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(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS.

This application is related to USSN 60/299,234, filed June 18, 2001; USSN 60/315,287, filed August 27, 2001; USSN 60/317,544, filed September 5, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002, each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

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The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in ovarian cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of ovarian cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit ovarian cancer.

BACKGROUND OF THE INVENTION

Ovarian cancer is the sixth most common cancer in women, accounting for 6% of all female cancers. It ranks fifth as the cause of cancer death in women. The American Cancer Society predicts that there will be about 23,100 new cases of ovarian cancer in this country in the year 2000 and about 14,000 women will die of the disease. Because many ovarian cancers cannot be detected early in their development, they account for a disproportionate number of fatal cancers, being responsible for almost half the deaths from cancer of the female genital tract; more deaths than any other reproductive organ cancer.

Most patients with epithelial ovarian cancer, the predominant form, are asymptomatic in early-stage disease and usually present with stage III or IV disease. Their five-year survival is less than 25%, with lower survival among African-American women. The minority of patients discovered with early-stage disease have a five-year survival rate of 80%-90%. See, Parker, et. al.. (1997) "Cancer Statistics, 1997" CA Cancer J. Clin. 47:5-27.

In the absence of a family history of ovarian cancer, lifetime risk of ovarian cancer is 1/70. Risk factors include familial cancer syndromes (risk of up to 82% by age 70 in women

with hereditary breast/ovarian syndrome); family history (1.4% lifetime risk with no affected relatives, 5% with one affected relative, 7% with two affected relatives; Kerlikowske, et.al. (1992) Obstet. Gynecol. 80:700-707); nulliparity; advancing age; obesity; personal history of breast, endometrial, or colorectal cancer; fewer pregnancies; or older age (>35 years) at first pregnancy. However, 95% of all ovarian cancers occur in women without risk factors. Use of hormonal contraceptives, oophorectomy, and tubal sterilization reduce risk of ovarian cancer (Kerlikowske, et. al. (1992) Obstet. Gynecol. 80:700-707; Grimes (1992) Am J. Obstet. Gynecol. 166:1950-1954; Hankinson, et. al. (1993) JAMA 270:2813-2818); however, even bilateral oophorectomy may not be completely effective in preventing ovarian cancer.

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Treatment of ovarian cancer consists largely of surgical oophorectomy, anti-hormone therapy, and/or chemotherapy. Although many ovarian cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons, et al. (2000) <u>Arch. Pathol. Lab. Med.</u> 124:966-978; Hamilton and Piccart (2000) <u>Ann. Oncol.</u> 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson (2000) <u>J. Clin. Oncol.</u> 18:113sup-118sup).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer.

Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma.

Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Potential immunotherapeutic targets have been identified for ovarian cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in ovarian cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically

distinct molecule, and is in early clinical trials as a vaccine target. Gilewski, et al. (2000) Clin. Cancer Res. 6:1693-1701; Scholl, et al. (2000) J. Immunother. 23:570-580. The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3. See, e.g., Bon, et al. (1997) Clin. Chem. 43:585-593. However, many patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease.

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Mutations in both BRCA1 and BRCA2 are associated with increased susceptibility to ovarian cancer. Mutations in BRCA1 occur in approximately 5 percent (95 percent confidence interval, 3 to 8 percent) of women in whom ovarian cancer is diagnosed before the age of 70 years. See Stratton, et al. (1997) N.E.J. Med. 336:1125-1130. And, in BRCA1 gene carriers, the risk for developing ovarian cancer is .63. See Easton (1995) Am. J. Hum. Genet. 56:267-xxx; and Elit (2001) Can. Fam. Physician 47:778-84.

Other biochemical markers such as CA125 have been reported to be associated with ovarian cancer, but they are not absolute indicators of disease. Although roughly 85% of women with clinically apparent ovarian cancer have increased levels of CA125, CA125 is also increased during the first trimester of pregnancy, during menstruation, in the presence of non-cancerous illnesses, and in cancers of other sites.

While industry and academia have identified novel gene sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in ovarian and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of ovarian cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate ovarian cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are upand down-regulated in ovarian cancer cells. Such genes are useful for diagnostic purposes,
and also as targets for screening for therapeutic compounds that modulate ovarian cancer,
such as hormones or antibodies. The methods of detecting nucleic acids of the invention or
their encoded proteins can be used for many purposes, e.g., early detection of ovarian
cancers, monitoring and early detection of relapse following treatment, monitoring response
to therapy, selecting patients for postoperative chemotherapy or radiation therapy, selecting
therapy, determining tumor prognosis, treatment, or response to treatment (of primary or
metastatic tumors), and early detection of pre-cancerous lesions. Other aspects of the
invention will become apparent to the skilled artisan by the following description of the
invention.

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In one aspect, the present invention provides a method of detecting an ovarian cancerassociated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the present invention provides a method of determining the level of an ovarian cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat ovarian cancer. In another embodiment, the patient is suspected of having metastatic ovarian cancer.

In one embodiment, the patient is a human.

In one embodiment, the ovarian cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids

before the step of contacting the biological sample with the polynucleotide.

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In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of an ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic ovarian cancer. In a further embodiment, the patient has a drug resistant form of ovarian cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-26.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological

sample with an antibody as described herein.

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In another aspect, the present invention provides a method of detecting antibodies specific to ovarian cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of:
(i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of an ovarian cancer-associated cell to treat ovarian cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having ovarian cancer or to a cell sample isolated from; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

In one embodiment, the control is a mammal with ovarian cancer or a cell sample that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or is non-malignant tissue.

In one embodiment, the test compound is administered in varying amounts or

concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-26 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

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In another aspect, the present invention provides a method for treating a mammal having ovarian cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having ovarian cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in an ovarian cancer. In one embodiment, a gene is selected from Tables 1-26. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the ovarian cancer modulatory protein, or an animal lacking the ovarian cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-26, wherein the biochip comprises fewer than 1000 nucleic acid probes.

Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with ovarian cancer is

provided. The method comprises determining the expression of a gene of Tables 1-26 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with ovarian cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in ovarian cancer.

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In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of an ovarian cancer modulating protein (ovarian cancer modulatory protein) or a fragment thereof and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining an ovarian cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. The method further includes determining the binding of said ovarian cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits ovarian cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an ovarian cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an ovarian cancer modulating protein, preferably encoded by a nucleic acid of Table 1-26 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an ovarian cancer modulating protein, preferably selected from the nucleic acids of Tables 1-26, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of an ovarian cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

In another aspect of the invention, a method of treating an individual for ovarian cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of an ovarian cancer modulating protein. In another embodiment, the method comprises administering to a patient having ovarian cancer an antibody to an ovarian cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for ovarian cancer (OC), including metastatic ovarian cancer, as well as methods for screening for compositions which modulate ovarian cancer. Also provided are methods for treating ovarian cancer and related conditions, e.g., ovarian carcinoma (e.g., epithelial (including malignant serous tumors, malignant mucinous tumors, and malignant endometrioid tumors), germ cell (including teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, and gonadoblastoma), and stromal carcinomas (e.g., granulosal stromal cell tumors)), fallopian tube carcinoma, and peritoneal carcinoma.

Tables 1-26 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in ovarian cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

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Definitions

The term "ovarian cancer protein" or "ovarian cancer polynucleotide" or "ovarian cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26. A polynucleotide or polypeptide

sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. An "ovarian cancer polypeptide" and an "ovarian cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" ovarian cancer protein or nucleic acid refers to an ovarian cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type ovarian cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

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"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an ovarian cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of particular interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default

parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

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For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) <u>Nuc. Acids Res.</u> 25:3389-3402 and Altschul, et al. (1990)

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J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5887). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

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The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

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Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (2001) Molecular Biology of the Cell (4th ed.) Garland Pub.; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the non-covalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds,

although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994)

Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., 15 phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986), Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucl. Acids Res. 20 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Angew. Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature, 25 365:566-568; Carlsson, et al. (1996) Nature 380:207, each of which is incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi, et al. (1991) Angew. 30 Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs,

et al. (1994) J. Biomolecular NMR 34:17-xx; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghvi and Cook (eds. 1994) Carbohydrate

Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (p. 35 June 2, 1997) C&E News. Each of these references is hereby expressly incorporated by reference.

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Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched base pairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic,

photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the ovarian cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945-xxx; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

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An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the

stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

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The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

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An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target

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sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the $\,$. probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are available, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, N.Y.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided, e.g., Ausubel, et al. (ed. 1991 and supplements) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that

modulate activity of an ovarian cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the ovarian cancer protein or nucleic acid, e.g., a functional, physical, physiological, or chemical effect, such as the ability to decrease ovarian cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

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By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an ovarian cancer protein sequence, e.g., functional, enzymatic, physical, physiological, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the ovarian cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on ovarian cancer can also be performed using ovarian cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. The functional effects can be evaluated by means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for ovarian cancer-associated sequences, measurement of RNA stability, or identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of ovarian cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of ovarian cancer polynucleotide and

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of ovarian cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate ovarian cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of ovarian cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Assays for inhibitors and activators include, e.g., expressing the ovarian cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of ovarian cancer can also be identified by incubating ovarian cancer cells with the test compound and determining increases or decreases in the expression of one or more ovarian cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more ovarian cancer proteins, such as ovarian cancer proteins encoded by the sequences set out in Tables 1-26.

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Samples or assays comprising ovarian cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25% or less. Activation of an ovarian cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., 2-5 fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, e.g., cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, change in contact inhibition or density limitation of growth, loss of growth factor or serum requirements, change in cell morphology, gain or loss of immortalization, gain or loss of tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss.

"Tumor cell" refers to pre-cancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is typically associated with phenotypic changes, such as immortalization of cells, aberrant growth control, non-morphological changes, and/or malignancy. See, Freshney (1994) Culture of Animal Cells.

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"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See, e.g., Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody,

one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

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For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al., pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, e.g., other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of ovarian cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is

characteristic of the state of the cell. That is, normal tissue (e.g., normal ovarian or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the ovarian, or ovarian cancer tissue or metastatic ovarian cancerous tissue can be compared with tissue samples of ovarian and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different ovarian cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

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The identification of sequences that are differentially expressed in ovarian cancer versus non-ovarian cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate ovarian cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, does existing treatment induce expression of a target. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of ovarian cancer in the tissue or origin of the primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the ovarian cancer expression profile. This may be done by making biochips comprising sets of the important ovarian cancer genes, which can then be used in these screens. These methods can also be based on evaluating protein expression; that is, protein expression levels of the ovarian cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the ovarian cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or RNAi nucleic acids, or the ovarian cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in ovarian cancer relative to normal tissues and/or non-malignant tissues, herein termed "ovarian cancer sequences." As outlined below, ovarian cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in ovarian cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the ovarian cancer sequences are from humans; however, as will be appreciated by those in the art, ovarian cancer sequences from other organisms may be useful

in animal models of disease and drug evaluation; thus, other ovarian cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Ovarian cancer sequences, e.g., counterpart genes, from other organisms may be obtained using the techniques outlined below.

Ovarian cancer sequences can include both nucleic acid and amino acid sequences. Ovarian cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids. Screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the ovarian cancer sequences, are also provided.

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An ovarian cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying ovarian cancer-associated sequences, the ovarian cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing ovarian cancer samples with metastatic cancer samples from other cancers, such as lung, ovarian, gastrointestinal cancers, etc. Samples of different stages of ovarian cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal ovarian, but also including, and not limited to, lung, heart, brain, liver, ovarian, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the ovarian cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, expression in non-essential tissues may be tolerated. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side

effects by interaction with target present in other organs.

In a preferred embodiment, ovarian cancer sequences are those that are up-regulated in ovarian cancer; that is, the expression of these genes is higher in the ovarian cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Other embodiments are directed to sequences up regulated in non-malignant conditions relative to normal.

Unigene cluster identification numbers and accession numbers herein refer to the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nucl. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, e.g., FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, ovarian cancer sequences are those that are down-regulated in ovarian cancer; that is, the expression of these genes is lower in ovarian cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three-fold change, with at least about five-fold or higher being preferred.

Informatics

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The ability to identify genes that are over or under expressed in ovarian cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. Expression profiles can be used in diagnostic or prognostic evaluation of patients with ovarian cancer. Subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA) or in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable

exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database, and can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

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The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing ovarian cancer, e.g., the identification of ovarian cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, and outcome data, among others. Although data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

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Fundamentals of bioinformatics are provided, e.g., in Mount, et al. (2001)

Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)

Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids

Cambridge Univ. Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical

Guide to the Analysis of Genes and Proteins (2d ed.) Wiley-Liss; Rashidi and Buehler (1999)

Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for ovarian cancer. In another variation, assay records cross-tabulate one or more of the following parameters for a target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or

characteristic separation coordinate (e.g., electrophoretic or genomic position coordinates); (2) sample source; and (3) absolute and/or relative quantity of target species present in the sample.

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The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells)

composing a bit pattern encoding data acquired from an assay of the invention.

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The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, e.g., which typically comprises one or more of: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by methods of the inventions, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of ovarian cancer-associated proteins

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Ovarian cancer proteins of the present invention may be categorized as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the ovarian cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins can also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are often involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in proteinprotein interaction. For example, Src-homology-2 (SH2) domains bind tyrosinephosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to prolinerich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

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In another preferred embodiment, the ovarian cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their

cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules, or may be processed or shed to the blood stream. In this respect, they can mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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Ovarian cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful ovarian markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the ovarian cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to an adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus, secreted molecules often find use in modulating or altering numerous aspects of physiology. Ovarian cancer proteins that are secreted proteins are particularly preferred as good diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be

antibody or small molecule therapeutic targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms, as protein or DNA vaccines.

Use of ovarian cancer nucleic acids

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As described above, ovarian cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The ovarian cancer nucleic acid sequences of the invention, e.g., in Table 1-26, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the ovarian cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once the ovarian cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ovarian cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised as a linear nucleic acid segment, the recombinant ovarian cancer nucleic acid can be further-used as a probe to identify and isolate other ovarian cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant ovarian cancer nucleic acids and proteins.

The ovarian cancer nucleic acids of the present invention are useful in several ways. In a first embodiment, nucleic acid probes to the ovarian cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, the ovarian cancer nucleic acids that include coding regions of ovarian cancer proteins can be put into expression vectors for the expression of ovarian cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to ovarian cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the ovarian cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

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A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent

attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of

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covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silicabased materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See, e.g., WO0055627 Reusable Low Fluorescent Plastic Biochip.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using

functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of ovarian cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an ovarian cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of ovarian cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are available. See, e.g., Innis, et al.(1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be

extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR; see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1980; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of ovarian cancer proteins from nucleic acids

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In a preferred embodiment, ovarian cancer nucleic acids, e.g., encoding ovarian cancer proteins are used to make a variety of expression vectors to express ovarian cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known and are used to express proteins. See, e.g., Ausubel, supra; and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the ovarian cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; and two sequences may be operably linked when they are physically part of the same polymer. Generally,

"operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the ovarian cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

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Promoter sequences typically encode constitutive or inducible promoters. The promoters may be naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The ovarian cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an ovarian cancer protein, under the appropriate conditions to induce or cause expression of the ovarian cancer protein. Conditions appropriate for ovarian cancer protein expression will vary with

the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculovirus systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

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In a preferred embodiment, the ovarian cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor 20 virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. See, e.g., Fernandez and Hoeffler, supra. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, ovarian cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters

are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the ovarian cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others. See Fernandez and Hoeffler, supra. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

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In one embodiment, ovarian cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, an ovarian cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The ovarian cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the ovarian cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the ovarian cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the ovarian cancer protein is an ovarian cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the ovarian cancer protein is purified or isolated after expression. Ovarian cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the ovarian cancer protein may be purified using a standard anti-ovarian cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the ovarian cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the ovarian cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

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Variants of ovarian cancer proteins

In one embodiment, the ovarian cancer proteins are derivative or variant ovarian cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative ovarian cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most any residue within the ovarian cancer peptide.

Also included within one embodiment of ovarian cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the ovarian cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant ovarian cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the ovarian cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed ovarian cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of ovarian cancer protein activities.

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Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the ovarian cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the ovarian cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the ovarian cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine,

valine, or alanine; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Covalent modifications of ovarian cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an ovarian cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an ovarian cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking ovarian cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-ovarian cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

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Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1983) <u>Proteins: Structure and Molecular Properties</u> Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the ovarian cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence ovarian cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence ovarian cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express ovarian cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to ovarian cancer polypeptides may also be

accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence ovarian cancer polypeptide (for O-linked glycosylation sites). The ovarian cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the ovarian cancer polypeptide at pre-selected bases such that codons are generated that will translate into the desired amino acids.

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Another means of increasing the number of carbohydrate moieties on the ovarian cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) <u>CRC Crit. Rev. Biochem.</u> CRC Press.

Removal of carbohydrate moieties present on the ovarian cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) <u>Arch. Biochem. Biophys.</u> 259:52-57; and Edge, et al. (1981) <u>Anal. Biochem.</u> 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) <u>Meth. Enzymol.</u>, 138:350-359.

Another type of covalent modification of ovarian cancer comprises linking the ovarian cancer polypeptide to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylene. See, e.g., U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Ovarian cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules, e.g., comprising an ovarian cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an ovarian cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the ovarian cancer polypeptide. The presence of such epitope-tagged forms of an ovarian cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the ovarian cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an ovarian cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of

the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; His6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include, e.g., the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other ovarian cancer proteins of the ovarian cancer family, and ovarian cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related ovarian cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the ovarian cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to ovarian cancer proteins

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In a preferred embodiment, when the ovarian cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the ovarian cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller ovarian cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a

mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at

least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Table 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

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In a preferred embodiment, the antibodies to ovarian cancer protein are capable of reducing or eliminating a biological function of an ovarian cancer protein, as is described below. That is, the addition of anti-ovarian cancer protein antibodies (either polyclonal or preferably monoclonal) to ovarian cancer tissue (or cells containing ovarian cancer) may reduce or eliminate the ovarian cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the ovarian cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a nonhuman species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanization can be essentially performed following the method of Winter and co-workers, e.g., by substituting rodent CDRs or CDR sequences for the

corresponding sequences of a human antibody. See, e.g., Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; Presta (1992) Curr. Op. Struct. Biol. 2:593-596; and Verhoeyen, et al. (1988) Science 239:1534-1536). Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

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Human antibodies can also be produced using various techniques known in the art, including phage display libraries (see, e.g., Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; and Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (see, e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. See, e.g., U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of ovarian cancer, e.g., with an antibody raised against ovarian cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the ovarian cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby

inactivating the secreted ovarian cancer protein.

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In another preferred embodiment, the ovarian cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the ovarian cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane ovarian cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, noncompetitive or uncompetitive inhibitor of protein binding to the extracellular domain of the ovarian cancer protein. The antibody is also an antagonist of the ovarian cancer protein. Further, the antibody prevents activation of the transmembrane ovarian cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the ovarian cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, ovarian cancer is treated by administering to a patient antibodies directed against the transmembrane ovarian cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the ovarian cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the ovarian cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with ovarian cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to ovarian cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with ovarian cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,

cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against ovarian cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane ovarian cancer proteins not only serves to increase the local concentration of therapeutic moiety in the ovarian cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

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In another preferred embodiment, the ovarian cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the ovarian cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The ovarian cancer antibodies of the invention specifically bind to ovarian cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of ovarian cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the ovarian cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing ovarian cancer) and in ovarian cancer tissue (and in some cases, for varying severities of ovarian cancer that relate to prognosis, as outlined below, or in non-malignant disease are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states,

information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

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"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus ovarian cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is modulated, either up-regulated, resulting in an increased amount of transcript, or down-regulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, e.g., Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., up-regulation or down-regulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the ovarian cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to ovarian cancer genes, e.g., those identified as being important in an ovarian cancer or disease phenotype, can be evaluated in an ovarian disease diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed, or on an individual basis.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular sample. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

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In a preferred embodiment nucleic acids encoding the ovarian cancer protein are detected. Although DNA or RNA encoding the ovarian cancer protein may be detected, of particular interest are methods wherein an mRNA encoding an ovarian cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an ovarian cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, ovarian cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as prognostic or diagnostic markers of ovarian disease. Detection of these proteins in putative ovarian cancer tissue allows for detection, diagnosis, or prognosis of ovarian disease, and for selection of therapeutic strategy. In one

embodiment, antibodies are used to detect ovarian cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the ovarian cancer protein is detected, e.g., by immunoblotting with antibodies raised against the ovarian cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

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In another preferred method, antibodies to the ovarian cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai (ed. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. Cells are contacted with from one to many antibodies to the ovarian cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the ovarian cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of ovarian cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing ovarian cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of ovarian cancer proteins. Antibodies can be used to detect an ovarian cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology, and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous ovarian cancer protein.

In a preferred embodiment, in situ hybridization of labeled ovarian cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including ovarian cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It

is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to ovarian cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of a plurality of genes being preferred. As above, ovarian cancer probes may be attached to biochips for the detection and quantification of ovarian cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

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In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified ovarian cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the ovarian cancer phenotype or an identified physiological function of an ovarian cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in ovarian cancer, test

compounds can be screened for the ability to modulate gene expression or for binding to the ovarian cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing ovarian cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in ovarian cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in ovarian cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

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The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the ovarian cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more ovarian cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-26. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate ovarian cancer, modulate ovarian cancer proteins, bind to an ovarian cancer protein, or interfere with the binding of an ovarian cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the ovarian cancer phenotype or the expression of an ovarian cancer sequence,

e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an ovarian cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced an ovarian cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

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Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of an ovarian cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an ovarian cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that

display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

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Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka (1991) Pept. Prot. Res. 37:487-493; and Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 15 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), non-peptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-218), analogous organic syntheses 20 of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-305), and/or peptidyl phosphonates (Campbell, et al.(1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic 25 acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al.(1996) Nature Biotechnology 14:309-314; and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522; and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33, Baum (Jan. 18, 1993) C&E News; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; 30 morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available.

See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J.; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The assays to identify modulators are amenable to high throughput screening.

Preferred assays thus detect enhancement or inhibition of ovarian cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

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In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of ovarian cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids.

For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

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After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with jabels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117; 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697, each of which is hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

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The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the ovarian cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an ovarian cancer expression pattern leading to a normal expression pattern, or to modulate a single ovarian cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated ovarian cancer tissue reveals genes that are not expressed in normal tissue

or ovarian cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for ovarian cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated ovarian cancer tissue sample.

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Thus, in one embodiment, a test compound is administered to a population of ovarian cancer cells, that have an associated ovarian cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., ovarian cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the ovarian cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on ovarian cancer activity. By defining such a signature for the ovarian cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins" or a "ovarian cancer modulatory protein". The ovarian cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the ovarian cancer modulatory protein is a fragment. In a preferred embodiment, the ovarian cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

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Preferably, the ovarian cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In another embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine. Or, the ovarian cancer proteins are conjugated to an immunogenic agent, e.g., to BSA.

Measurements of ovarian cancer polypeptide activity, or of ovarian cancer or the ovarian cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the ovarian cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of ovarian cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian ovarian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, an ovarian cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the ovarian cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the ovarian cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or

enzymatically labeled antibodies, and the like, as described herein.

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Alternatively, a reporter gene system can be devised using the ovarian cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins." The ovarian cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present.

Alternatively, cells comprising the ovarian cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an ovarian cancer protein and a candidate compound, and determining the binding of the compound to the ovarian cancer protein. Preferred embodiments utilize the human ovarian cancer protein, although other mammalian proteins, e.g., counterparts, may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative ovarian cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the ovarian cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is non-diffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the ovarian cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the ovarian cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the ovarian cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the ovarian cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one

component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

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In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., an ovarian cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically 4-40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hr will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the ovarian cancer protein and thus is capable of binding to, and potentially modulating, the activity of the ovarian cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the ovarian cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the ovarian cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the ovarian cancer proteins. In this embodiment, the methods comprise combining an ovarian cancer protein and a competitor in a first sample. A second sample comprises a test compound, an ovarian cancer protein, and a

competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the ovarian cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the ovarian cancer protein.

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Alternatively, differential screening is used to identify drug candidates that bind to the native ovarian cancer protein, but cannot bind to modified ovarian cancer proteins. The structure of the ovarian cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an ovarian cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an ovarian cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising ovarian cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an ovarian cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including

chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate ovarian cancer agents are identified.

Compounds with pharmacological activity are able to enhance or interfere with the activity of the ovarian cancer protein. Once identified, similar structures are evaluated to identify

In one embodiment, a method of inhibiting ovarian cancer cell division is provided. The method comprises administration of an ovarian cancer inhibitor. In another embodiment, a method of inhibiting ovarian cancer is provided. The method comprises administration of an ovarian cancer inhibitor. In a further embodiment, methods of treating cells or individuals with ovarian cancer are provided. The method comprises administration of an ovarian cancer inhibitor.

In one embodiment, an ovarian cancer inhibitor is an antibody as discussed above. In another embodiment, the ovarian cancer inhibitor is an antisense or RNAi molecule.

A variety of cell viability, growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

critical structural feature of the compound.

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of ovarian cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

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Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See, e.g., Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with an ovarian cancer-associated sequence and are grown for 24 hr at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, e.g., Freshney (1994), supra.

20 Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) <u>J. Nat'l Cancer Inst.</u> 37:167-175; Eagle, et al. (1970) <u>J. Exp. Med.</u> 131:836-879; and Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer Plenum</u>. Similarly,

tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u> Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

10 Invasiveness into Matrigel

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The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate ovarian cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Alternatively, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by pre-labeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of ovarian cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the ovarian cancer gene is disrupted or in which an ovarian cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous ovarian cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous ovarian cancer gene with a mutated version of the ovarian cancer gene, or by mutating the endogenous ovarian cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Nat'l Cancer Inst.</u> 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263-272; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing an ovarian cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of ovarian cancer

Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of an ovarian cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an ovarian cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturallyoccurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-

sugar linkages. Exemplary among these are the phosphorothicate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the ovarian cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for ovarian cancer molecules. A preferred antisense molecule is for an ovarian cancer sequences in Tables 1-26, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. An antisense or a sense oligonucleotide can be developed based upon a cDNA sequence encoding a given protein. See, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to down-regulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

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In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of ovarian cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. Pharmacol. 25: 289-

317 for a general review of the properties of different ribozymes).

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The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known to those of skill in the art. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Hum. Gene Ther. 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Hum. Gene Ther. 5:1151-120; and Yamada, et al. (1994) Virology 205:121-126.

Polynucleotide modulators of ovarian cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of ovarian cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating ovarian cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-ovarian cancer antibody that reduces or eliminates the biological activity of an endogenous ovarian cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding an ovarian cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the ovarian cancer sequence is down-regulated in ovarian cancer, such state may be reversed by increasing the amount of ovarian cancer gene product in the cell. This can be accomplished, e.g., by over-expressing the endogenous ovarian cancer gene or administering a gene encoding the ovarian cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when

the ovarian cancer sequence is up-regulated in ovarian cancer, the activity of the endogenous ovarian cancer gene is decreased, e.g., by the administration of an ovarian cancer antisense or RNAi nucleic acid.

In one embodiment, the ovarian cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to ovarian cancer proteins. Similarly, the ovarian cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify ovarian cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to an ovarian cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The ovarian cancer antibodies may be coupled to standard affinity chromatography columns and used to purify ovarian cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the ovarian cancer protein.

Methods of identifying variant ovarian cancer-associated sequences

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Without being bound by theory, expression of various ovarian cancer sequences is correlated with ovarian cancer. Accordingly, disorders based on mutant or variant ovarian cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant ovarian cancer genes, e.g., determining all or part of the sequence of at least one endogenous ovarian cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the ovarian cancer genotype of an individual, e.g., determining all or part of the sequence of at least one ovarian cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced ovarian cancer gene to a known ovarian cancer gene, e.g., a wild-type gene.

The sequence of all or part of the ovarian cancer gene can then be compared to the sequence of a known ovarian cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the ovarian cancer gene of the patient and the known ovarian cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the ovarian cancer genes are used as probes to determine the number of copies of the ovarian cancer gene in the genome.

In another preferred embodiment, the ovarian cancer genes are used as probes to determine the chromosomal localization of the ovarian cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the ovarian cancer gene locus.

Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of an ovarian cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Systems Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3)

Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceutical Assn.; and Pickar (1999) Dosage Calculations Thomson. Adjustments for ovarian cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in ovarian cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the ovarian cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-nasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the ovarian cancer

proteins and modulators may be directly applied as a solution or spray.

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The pharmaceutical compositions of the present invention comprise an ovarian cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that ovarian cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an ovarian cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gillman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill. Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions are readily available.

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The compositions containing modulators of ovarian cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and/or its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose."

The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, e.g., in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present ovarian cancer protein-modulating compounds can be administered alone or in combination with additional ovarian cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

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In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of ovarian cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, ovarian cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, ovarian cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the ovarian cancer coding regions) can be administered in a gene therapy application. These ovarian cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Ovarian cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) <u>J. Clin. Invest.</u> 95:341-

349), peptide compositions encapsulated in poly(D.L-lactide-co-glycolide, "PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS; see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243), multiple antigen . 5 peptide systems (MAPs; see, e.g., Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-10 540; Kieny, et al. (1986) AIDS Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Ann. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), 15 liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p. 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Ann. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted 20 delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be

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used as adjuvants.

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Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff et. al. (1990) Science 247:1465-1468; U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptidemediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode ovarian cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent. See, e.g., Shata, et al. (2000) Mol. Med. Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; and Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing an ovarian cancer gene or portion of an ovarian cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an ovarian cancer patient. The ovarian cancer gene used for DNA vaccines can encode full-length ovarian cancer proteins, but more preferably encodes portions of the ovarian cancer proteins including peptides derived from the ovarian cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an ovarian cancer gene. For example, ovarian cancer-associated genes or sequence encoding subfragments of an ovarian cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the ovarian cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment ovarian cancer genes find use in generating animal models of ovarian cancer. When the ovarian cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the ovarian cancer gene will also diminish or repress expression of the gene. Animal models of ovarian cancer find use in screening for modulators of an ovarian cancer-associated sequence or modulators of ovarian cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the ovarian cancer protein. When desired, tissue-specific expression or knockout of the ovarian cancer protein may be necessary.

It is also possible that the ovarian cancer protein is overexpressed in ovarian cancer. As such, transgenic animals can be generated that overexpress the ovarian cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of ovarian cancer and are additionally useful in screening for modulators to treat ovarian cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, ovarian cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, siRNA or antisense polynucleotides, ribozymes, dominant negative ovarian cancer polypeptides or polynucleotides, small molecules inhibitors of ovarian cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium

capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of ovarian cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an ovarian cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing ovarian cancer-associated activity. Optionally, the kit contains biologically active ovarian cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

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EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

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TABLE 1A lists about 1119 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59000 probasets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 80th percentile value amongst various ovarian cancers. The "average" normal adult tissue level was set to the 85th percentile amongst various non-matignant tissues.

30 TABLE 1A: ABOUT 1119 UP-REGULATED OVARIAN CANCER GENES Pkey: Primekey

Ex. Accn: Exemplar Accession UG ID: UniGene ID Title: UniGene title

35 ratio: ratio tumor vs normal tissues

	Pkey	Ex. Acon	UGID	Title	ratio
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
	423017	AW178761	Hs.227948	"serine (or cysteine) proleinase inhibitor, clade B(ovalbumi	63.6
40	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	58.3
	445810	AW265700	Hs.155660	ESTs	35.9
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
	407112	AA070801	Hs.51615	"ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAM	31.3
	425650	NM 001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0
45	402075			predicted exon	27.9
,,,	400301	X03635	Hs.1657	estrogen receptor 1	26.4

	402639 421948	L42583	Hs.111758	predicted exon kerstin 6A	25.3 24.7
	414540	BE379050		"gb:601236655F1 NIH_MGC_44 Homo sapiens cDNA clon	24.6
5	418994 401575	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1) predicted exon	24.5 23.6
,	457024	AA397546	Hs.119151	ESTs	23.2
	440684	Al253123	Hs.127356	"ESTs, Highly stmilar to NEST_HUMAN NESTI [H.saplen	23.1
	459008	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
10	400964 402421			predicted exon predicted exon	22.5 20.9
10	437329	AA811977	Hs.291761	ESTs	20.8
	414605	BE390440		*gb:601283601F1 NIH_MGC_44 Homo saplens cDNA clon	20.7
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapiens	20.4 20.3
15	401283 440633	AI140686	Hs.263320	predicted exon ESTs	19.9
13	445603	H08345	Hs.106234	ESTs	19.7
	403786			predicted exon	19.7
	436508	AW604381	Hs.121121	ESTS	19.6 19.2
20	459390 421823	BE385725 N40850	Hs.28625	"gb:601276347F1 NIH_MGC_20 Homo saptens cDNA clon ESTs	19.2
20	417366	BE185289	Hs.1076	small proline-rich protein 1B (comilin)	18.9
	422525	AA758797	Hs.192807	ESTs	18.5
	458121	S42416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from JM c	18.3
25	430520 450192	NM_016190 AA263143	Hs.242057 Hs.24596	chromosome 1 open reading frame 10 RAD51-interacting protein	18.1 18.0
23	416839	H94900	Hs.17882	ESTs	17.9
	440788	AI806594	Hs.128577	ESTs	17.9
	451072	AA013451	Hs.117929	ESTs	17.7 17.3
30	402203 417611	AW993983		predicted exon "gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapiens	17.3
50	438658	Al222068	Hs.123571	ESTs ·	17.3
	403747			predicted exon	17.2
	444958	AW292643	Hs.167047	ESTs .	17.2 17.1
35	404097 459375	BE251770		predicted exon *gb:601112470F1 NIH_MGC_16 Homo saptens cDNA clon	16.9
23	443198	Al039813		gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapl	16.9
	441557	AW452647	Hs.270482	ESTs	16.9
	433871	W02410	Hs.205555	ESTS	16.8 16.7
40	429163 443406	AA884766 Al056238	Hs.143316	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cD ESTs	16.7
	400613	74000200		predicted exon	16.6
	448372	AW445166	Hs.170802	ESTs	16.5
	410929 445887	H47233 Al263105	Hs.30643 Hs.145597	ESTs ·	16.5 18.1
45	422036	AA302647	Hs.271891	ESTs	16.0
	404767			predicted exon	15.9
	420831	AA280824	Hs.190035	ESTs and lated even	15.8 15.8
	405196 452947	AW130413		predicted exon "gb:xf50f04.x1 NCI_CGAP_Gas4 Homo saplens cDNA do	15.8
50	429538	BE182592	Hs.139322	small proline-rich protein 3	15.8
	435313	A1769400	Hs.189729	ESTs	15.7 15.6
	449635 424098	A1989942 AF077374	Hs.232150 Hs.139322	ESTs small proline-rich prolein 3	15.4
	411660	AW855718	110.1000	"gb:RC1-CT0279-070100-021-a06 CT0279 Homo saplens c	15.4
55	442653	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
	443534	Al076123	11- 400044	gb:oy92e04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	15.4 15.3
	458012 441018	AI424899 AI809587	Hs.188211 Hs.148782	ESTs .	15.1
	425972	BE391563	Hs.165433	*ESTs, Highly similar to T17342 hypothetical protein DKFZ	15.1
60	418092	R45154	Hs.106604	ESTs	15.1
	410909	AW898161	Hs.53112	*ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAM ESTs	15.1 15.0
	458234 434208	BE551408 T92641	Hs.127196 Hs.127648		15.0
	403177		************	predicted exon	15.0
65	423725	AJ403108	Hs.132127		14.9 14.7
	425090 409723	AA350552 AW885757	Hs.257862	"gb:EST57886 Infant brain Homo saplens cDNA 5' end, mR ESTs	14.6
	423735	AA330259	10.201002	"gb:EST33963 Embryo, 12 week II Homo saplens cDNA 5"	14.6
50	444266	AI424984	Hs.125465		14.5
70	443341	AW631480	Hs.8688	ESTs ·	14.4 14.4
	457336 440500	AW969657 AA972165	Hs.291029 Hs.150308		14.4
	446292	AF081497	Hs.279682	Rh type C glycoprotein	14.3
75	438086	AA336519	Hs.301167		14.3
75	434715 409387		Hs.116410 Hs.123526		14.2 14.2
	409272	AB014569	Hs.52526	KIAA0669 gene product	14.2
	454913	AW841462		gb:RC8-CN0014-080300-012-B09 CN0014 Homo saptens	14.0
80	439846		Hs.228320	"Homo saplens cDNA: FLJ23537 fis, clone LNG07690" "gb:EST112514 Adrenal gland tumor Homo saplens cDNA	14.0 13.9
οU	409695 422897		Hs.4290	ESTs	13.9
	404664			predicted exon	13.9
	458829		Un 200/44	*gb:PT2.1_6_G03.r turnor2 Homo seplens cDNA 3*, mRNA	13.8 13.8
	407327	AA487182	Hs.269414	ESTs	10.0

	455435	AW939445		*gb:QV1-DT0072-310100-056-b07 DT0072 Homo saplens	13.7
	449327	A1638743	Hs.224672	ESTs *gb:CM0-CT0307-210100-158-g09 CT0307 Homo saplens	13.7 13.7
	411693 407463	AW857271 AJ272034		gb:Homo saptens mRNA for putative capacitative calcium c	13.6
5	446767	AI380107	Hs.158954	EST8	13.6
•	433040	H70423	Hs.300511	ESTs .	13.5
	435209	AW027809	Hs.187698	*ESTs, Highly similar to cytomegalovirus partial fusion rece	13.5 13.5
	441459 401269	AI919142	Hs.214233	ESTs predicted exon	13.4
10	438663	Al199575	Hs.153070	ESTs	13.4
	426698	AA394104	Hs.97489	ESTs	13.4
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from clon	13.2
	448543	AW897741	Hs.21380	Homo saplens mRNA; cDNA DKFZp586P1124 (from clon	13.2 13.2
15	456714 458356	AW897265 AJ024855	Hs.131575 .	*gb:CMO-NN0057-150400-335-a04 NN0057 Homo saplens	13.2
13	431822	AA516049	113.131313 .	gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clo	13.1
	454822	AW833793		gb:QV4-TT0008-130100-080-a06 TT0008 Homo saplens c	13.1
	453358	A1990738	Hs.240066	ESTs	13.1
20	435542	AA687376	Hs.269533	ESTs	13.1 13.0
20	421286 452799	AA806584 Al948829	Hs.187895 Hs.213786	ESTs ESTs	13.0
	444355	BE383686	Hs.191621	ESTs .	13.0
	444271	AW452569	Hs.149804	ESTs	12.9
25	443860	AW866632		gb:QV4-SN0024-210400-181-g04 SN0024 Homo sapiens	12.9 12.9
25	428719	AA358193 AA215535	Hs.193128 Hs.98133	hypothetical projetin FLJ10805 ESTs	12.5
	418282 437308	AA749417	Hs.292353	ESTs	12.7
	400584			predicted exon	12.7
	426306	AA447310	Hs.164059	"Homo sapiens cDNA FLJ13338 fis, clone OVARC100188	12.7
30	448466	Al522109	Hs.171066	ESTs	12.7 12.7
	402738	A A D1 D214	Hs.114762	predicted exon ESTs	12.6
	451531 435243	AA018311 AW292886	Hs.261373	adenosine AZb receptor pseudogene	12.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	12.6
35	425108	AJ000489	Hs.96967	ESTs	12.5
	422330	D30783	Hs.115263	epiregulin	12.5 12.5
	432949	AA570749	Hs.298866 Hs.171872	ESTs DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA	12.4
	417009 456378	AA191719 AA843387	Hs.87279	ESTs	12.4
40	432966	AA650114		gb:ns92h09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clon	12.4
-	440571	AA904461	Hs.130798	ESTs	12.3
	411178	AW820852	11- 40475	*gb:RC2-ST0301-120200-011-f12 ST0301 Homo sapiens c	12.3 12.3
	445934 433917	AF131737 A1809325	Hs.13475 Hs.122814	hypothetical protein Human DNA sequence from done RP5-1028D15 on chrom	12.2
45	402018	MOUSOZO	110.122014	predicted exon	12.2
	424101	AA335394		gb:EST39787 Epididymus Homo saplens cDNA 5' end, mR	12.2
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	12.1
	458154	AW816379	11- 000000	*gb:QV4-ST0234-181199-035-g01 ST0234 Homo sapiens c	12.1 12.0
50	440919 415747	AW291274 AA381209	Hs.262826	ESTs - *gb:EST94257 Activated T-cells I Homo sapiens cDNA 5' e	12.0
50	411748	AW859920		gb:QV1-CT0364-260100-052-g05 CT0364 Homo sapiens	12.0
	452975	MB5521	Hs.69469	dendritic cell protein	12.0
	427276	AA400269	Hs.49598	ESTs	12.0 12.0
55	454315	AW373564	Hs.251928 Hs.33654	nuclear pore complex interacting protein ESTs	12.0
"	450786 402578	H86632	113.30004	predicted exon	11.9
	459591	AL037185		gb:DKFZp564A1169_r1 564 (synonym: hfbr2) Homo saple	11.9
	433449	AW772282		*gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA c	11.9
60	429108	AA890521	Hs.126035	ESTs *gb:MR4-ST0052-031199-018-d06 ST0062 Homo saplens	11:8 11.7
UU	454556 443513	AW807073		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo saplens cDNA c	11.7
	443613 400385	A1079356 NM_020389	Hs.283104	putative capacitative calcium channel	11.6
	411725	AW858396		gb:CM0-CT0341-181299-130-c06 CT0341 Homo sapiens	11.5
10	455174	A1694575	Hs.147801	ESTS	11.5 11.5
65	412402	AW984788	U= 202022	*gb:RC1-HN0015-120400-021-c07 HN0015 Homo saplens hypothetical protein PRO2015	11.5
	434205 450496	AF119861 AW449251	Hs.283032 Hs.257131		11.5
	411149	N68715	Hs.269128	I ESTA	11.5
	414210	BE383592		"gb:601297871F1 NIH_MGC_19 Homo sepiens cDNA clon	11.4
70	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	11.3 11.3
	453845	AL157568		gb:DKFZp761F0816_r1 761 (synonym: hamy2) Homo sapi predicted exon	11.3
	404849 442824	BE178065	Hs.14408		11.3
	428548	AA430058	Hs.98649	EST	11.3
75	434804	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cONA clo	11.3
	430486		Hs.24155		11.3 11.2
	400174 424324			predicted exon *gb:EST52440 Greater omantum tumor Homo saplens cDN	11.2
	424324 447724		Hs.24477		11.2
80	457028			ESTs	11.2
-	429900	AA460421	Hs.30875		11.2
	452240		Hs.61232		11,2 11,1
	458067 402222		Hs.35752	predicted exon	11.1
		•		00	

	446745	******	11- 450400	FOT-	44.4
	446745 453060	AW118189 AW294092	Hs.156400 Hs.21594	ESTs ESTs	11.1 11.1
	443482	AW188093	Hs.250385	ESTs	11.1
_	436843	AA824588		*gbroc83d02.s1 NCL_CGAP_GCB1 Homo saptens cDNA c	11.0
5	416320	H47867	Hs.34024	ESTs	11.0
	435772	AA700019	Hs.132992	*ATP-binding cassette, sub-family G (WHITE), member 5 (11.0
	451542 408522	AA018365 AI541214	Hs.32713 Hs.46320	ESTs "Small proline-rich protein SPRK [human, odontogenic kera	11.0 11.0
	414712	N88858.comp		ribosomal protein S3A	10.9
10	411940	AW876686		*gb:CM4-PT0031-180200-507-e05 PT0031 Homo sapiens c	10.9
	408733	AW264812	Hs.254290	ESTs	10.9
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	10.9 10.9
	458175 400612	AW296024	Hs.150434	ESTs . predicted exon	10.9
15	440159	AI637599	Hs.126127	ESTs	10.8
	429443	AB028967	Hs.202687	"potassium voltage-gated channel, Shal-related subfamily, m	10.8
	416319	AIB15601	Hs.79197	*CD83 antigen (activated B lymphocytes, immunoglobulin s	10.8
	405783			predicted exon predicted exon	10.7 10.7
20	405708 433266	A1863224	Hs.288677	"Homo saplens cDNA FLJ13872 fis, clone THYRO100132	10.6
20	456900	AA355442	Hs.169054	ESTs	10.6
	432408	N39127	Hs.76391	"myxovirus (influenza) resistance 1, homolog of murine (int	10.6
	451702	AW665452	Hs.246503	ESTs	10.6
25	418179	X51630	Hs.1145	Wilms turnor 1	10.6
25	408987	H85615		gb:yf03f11.r1 Soares retina N2b5HR Homo saplens cDNA predicted exon	10.6 10.5
	405285 419276	BE165909	Hs.134682	"Homo sapiens cDNA: FLJ23161 fis, clone LNG09730"	10.5
	407287	AI678812	Hs.201658	*ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	10.5
••	403065			predicted exon	10.5
30	414195	BE263293		gb:601144881F2 NIH_MGC_19 Homo saplens cDNA clon	10.4
	454258	A1457286	Hs.143979	"ESTs, Wealty simitar to KIAA1276 protein [H.saptens]" "Homo saptens cDNA: FLJ23107 ffs, clone LNG07738"	10.4 10.4
	412951 428888	BE018611 AA437010	Hs.251946 Hs.266584	ESTs	10.4
	440834	AA907027	Hs.128606	ESTs	10.4
35	437096	AA744406		gb:ny51h02.s1 NCI_CGAP_Pr18 Homo septens cDNA clo	10.4
	400135			predicted exon	10.4
	447849	Al538147	Hs.164277	ESTS	10.3 10.3
	400593 427469	AA403084	Hs.269347	predicted exon ESTs	10.3
40	402794	701103001	16.200017	predicted exon	10.2
. •	452743	AW965082	Hs.61455	ESTs	10.2
	448983	AI611654	Hs.224908	ESTs	10.2
	422696	AF242524	Hs.26323	hypothetical nuclear factor SBB122	10.2 10.2
45	428949 409191	AA442153 AW818390	Hs.104744	*ESTs, Weakly similar to AF208855 1 BM-013 [H.saplens] *gb:RC1-ST0278-160200-014-d10 ST0278 Homo saplens c	10.2
73	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	10.2
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	10.2
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA clon	10.1
50	445835	AW290999	Hs.145534	chromosome 21 open reading frame 23 *gb:QV-BT065-020399-103 BT065 Homo saplens cDNA, m	10.1 10.1
20	452507 433297	A1904646 AV658581	Hs.282633	EST8	10.1
	426724	AA383623	Hs.293616	ESTs	10.0
	436659	AI217900	Hs.144464	ESTs	10.0
	405675			predicted exon	10.0
55	413466	BE141737	Hs.254105	"enolase 1, (alpha)"	10.0 10.0
	447198 403306	D61523 NM_006825	Hs.283435 Hs.74368	ESTs "transmembrane protein (63kD), endoplasmic reticulum/Go	10.0
	413544	BE147225	113.17000	"gb:PM2-HT0225-031299-003-f11 HT0225 Homo saplens	9.9
	437094	AW103746	Hs.136907	ESTs	9.9
60	401497			predicted exon	9.9
	416203	H27794	Hs.269055	ESTs	9.9 9.9
	426882 454874	AA393108 AW836407	Hs.97365	ESTs *gb:PM3-LT0031-301299-002-b09 LT0031 Homo saplens	9.9
	406702	Z20658	Hs.278432		9.9
65	404952			predicted exon	9.9
	430691	C14187	Hs.103538		9.9
	444518	A1160278	Hs.146884	ESTs gb:yu28a10.s1 Soares fetal liver spleen 1NFLS Homo saple	9.8 9.8
	416665 438691	H72974 AA906288	Hs.212184		9.8
70	405636	77100000	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	predicted exon	9.8
	437242	AA747538	Hs.187942	ESTs	9.8
	425627	AF019612	Hs.297007		9.8
	452226	AA024898	Hs.296002		9.8 9.8
75	418986	Al123555 AW449009	Hs.81796 Hs.126647	ESTs ESTs	9.7
13	441139 427244	AA402400	Hs.178045		9.7
	423756	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clo	9.7
	457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDNA clone EURO	9.6
90	443526	AW792804	Hs.134002		9.6 9.6
80	440576	AW449775	Hs.126008 Hs.77496	ESTs small nuclear ribonucleoprotein polypeptide G	9.6 9.6
	419088 454707	AI538323 AW814989	110.11400	"gb:MR1-ST0206-170400-024-g05 ST0206 Homo saplans	9.6
	446252	Al283125	Hs.150009	EST8	9.6
	434374	AA631439		"gb:np85d02.s1 NCI_CGAP_Thy1 Homo septens cDNA cl	9.6

	100000			The state of the s	
	403093 454633	414M44200		predicted exon	9.6
		AW811380		"gb:IL3-ST0143-290999-019-005 ST0143 Homo saptens c	9.6
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo saplens cDNA	9.5
5	455203 403647	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapiens	9.5
5				predicted exon	9.5
	401530	00000764	U- 20000E	predicted exon	9.5
	414281	BE269751	Hs.288995	hypothetical protein FLJ20813	9.5
	411057 415953	AW815098 H14425	Un 27047	"gb:QV4-ST0212-091199-023-f10 ST0212 Homo sapiens c	9.5
10	450174	T82121	Hs.27947 Hs.177285	ESTs	9.5 9.5
10	422949	AA319435	ris.177203		
	402112	R58624	Hs.2186	"gb:EST21657 Adrenal gland tumor Homo saplens cDNA 5	9.5 9.5
	457886	AA742279	Hs.293346	eukaryotic translation elongation factor 1 gamma ESTs	9.4
	458145	AJ239457	Hs.130794	ESTS .	
15	452332	AW014859	Hs. 101657	ESTS	9.4 9.4
13	434950	AW974892	ns. 10 1037		
	409601	AF237621	Hs.80828	*gb:EST386997 MAGE resequences, MAGN Homo sapien keratin 1 (epidermolytic hyperkeratosis)	9.3 9.3
	419968	X04430	Hs.93913		
	436211	AK001581	Hs.80961	"Interleukin 6 (Interferon, beta 2)"	9.3 9.3
20	428412	AA428240	Hs.126083	"polymerase (DNA directed), gamma"	9.3
20	449441		Hs. 126063 Hs. 196532	ESTs ESTs	9.3
	458771	AI656040 AW295151	Hs.163612	ESTs	
	458543	ANZSS151 AA213403	Hs.257542		9.3 9.3
		AI828600	Hs.21124	ESTS	9.3
25	414257 442826	AI020000 AI018777	Hs.131241	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM ESTs	9.3 9.3
23	446740	Al611635	Hs.192605	ESTs ~	9.2
	408938	AA059013	Hs.22607	ESTs	9.2
	434157	AI538316	Hs.158451	ESTs	9.2
	408774	AW270899	Hs.254569	ESTS	9.2 9.2
30					9.2 9.2
50	424268	AA397653	Hs.144339	Human DNA sequence from clone 495010 on chromosome	
	415715	F30364		*gb:HSPD20786 HM3 Homo sapiens cDNA done s400009	9.1
	405277	414007020		predicted exon	9.1
	412167	AW897230	11- 404 550	"gb:CM0-NN0057-150400-335-a11 NN0057 Homo saplens	9.1
35	442771	AW409808	Hs.101550	ESTs	9.1
33	404898			predicted exon	9.1
	401230			predicted exon	9.1
	400623	41004020	11- 40000	predicted exon	9.1
	418808	AI821836	Hs.10359	ESTs	9.1
40	436396	A1683487	Hs.299112	*Homo sapiens cDNA FLJ11441 fis, clone HEMBA100132	9.1
40	440466	AA885871	Hs.135727	ESTS	9.0
	437568	A1954795	Hs.156135	ESTs	9.0 -
	405382	AF2020C4	11- 204200	predicted exon	9.0
	435673	AF202961	Hs.284200	"Homo saplens uncharacterized gastric protein ZG12P mRN	9.0
45	405848	*******		predicted exon	9.0
47	437229	AW976005	U- 24700	*gb:EST388114 MAGE resequences, MAGN Homo saplen	9.0
	417728	AW138437	Hs.24790	KIAA1573 protein	9.0
	454597	AW809648	LI- 07570	*gb:MR4-ST0124-261099-015-d01 ST0124 Homo sapiens	9.0
	427093	AA398118	Hs.97579	ESTS	9.0
50	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	9.0
30	440556	AW206958	Hs.125968	ESTs	9.0
	400163	41.040040	11-05040	predicted exon	8.9
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like 1	8.9
	417549	AA203651		gb:zx58f10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	8.9
55	406163	A1704 (4D	H- 404000	predicted exon	8.9
23	437918	A1761449	Hs.121629	ESTS	8.9
	449419	R34910	Hs.119172	ESTs	8.9
	434683	AW298724	Hs.202639	ESTS	8.9
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	8.9
60	454590	AW809762	Hs.222056	"Homo sapiens cDNA FLJ11572 fis, clone HEMBA100337	8.8 8.8
UU	454574	AW809109	11- 10710	*gb:MR4-ST0117-070100-027-a04 ST0117 Homo saplens c	
	441433	AA933809	Hs.42746	ESIS	8.8
	416858	AW979294	Hs.85634	ESTS	8.8
	421978	AJ243662	Hs.110196	NICE-1 protein	8.8
65	451528	AA018297	Hs.35493	ESTs	8.8
65	408751	N91553	Hs.258343	ESTs	8.7
	401862	*********		predicted exon	8.7
	417344	AW997313		"gb:RC2-BN0048-250400-018-112 BN0048 Homo saplens	8.7
	454455	AW752710		"gb:IL3-CT0219-281099-024-A03 CT0219 Homo sapiens c	8.7
70	455592	BE008002		"gb:QV0-BN0147-290400-214-h04 BN0147 Homo saplens	8.7
70	417650	T05870	Hs.100640	ESTS	8.7
	456309	AA225423	16. 440.00	"gb:nc24a12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clon	8.7
	432030	AI908400	Hs.143789	ESTs	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
75	402576			predicted exon	8.7
75	426874	N67325	Hs.247132	ESTs	8.7
	403334	****		predicted exon	8.7
	408562	AI438323	Hs.31141	"Homo sapiens mRNA for KIAA1568 protein, partial cds"	8.7
	439443	AF085261	Hs.127892	ESTS	8.7
00	428600	AW863261	Hs.15036	"ESTs, Highly similar to AF161358 1 HSPC095 [H.sapiens	8.7
80	414539	BE379046		"gb:601236646F1 NIH_MGC_44 Homo saplens cDNA clon	8.6
	432527	AW975028	Hs.102754	ESTs	8.6
	403273	004.4046		predicted exon	8.6
	452077	BE144949	11- 4 4000 4	gb:RC2-HT0187-041099-011-d12 HT0187 Homo sapiens	8.6
	444598	A1288830	Hs.149924	ESTs	8.6

	434066	AF116649	Hs.283944	"Homo sapiens PR00566 mRNA, complete cds"	8.6
	429643	AA455889	Hs.187548	ESTs	8.6
	432340	AA534222		gb:nj21d02.s1 NCL_CGAP_AA1 Homo saplens cDNA clon	8.6
	446142	AJ754693	Hs.145968	ESTs	8.6
5	417412				
,		X16898	Hs.82112	"Interleukin 1 receptor, type I"	8.6
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapiens	8.5
	451318	AA029888	Hs.95071	ESTs	8.5
	405547			predicted exon	8.5
	423843	AA332652		gb:EST36627 Embryo, 8 week I Homo sapiens cDNA 5' en	8.5
10	454145	AA045872	Hs.62798	ESTs	8.4
	401200	10010012	16.02700		
				predicted exon	8.4
	404166			predicted exon	8.4
	412761	AW995092		*gb:QV0-BN0041-030300-145-a10 BN0041 Homo saplens	8.4
	412333	AW937485		"gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapiens	8.4
15	455092	BE152428		*gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapiens	8.4
	419281	H96452	Hs.42189	ESTs	8.4
	446171	Al374927	110.72.100	gb:ta66c04.x1 Soares_total_fetus_Nb2HF8_9w Homo saple	8.3
			11-40/00		
	437362	AL359561	Hs.16493 ,	hypothetical protein DKFZp762N2316	8.3
20	402631			predicted exon	8.3
20	458573	AV653838	Hs.295131	ESTs	8.3
	439185	AF087976	Hs.233343	ESTs	8.3
	445881	A1263029	Hs.210689	EST ₈	8.3
	449737	AI668581	Hs.246316	ESTs	8.3
					8.3
25	401830	AJ004832	Hs.5038	neuropathy target esterase	
23	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
	416996	W91892	Hs.59609	ESTs	8.2
	443626	A1540644	Hs.138479	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	8.2
	407471	D55644		gb:Human spleen PABL (pseudoautosomal boundary-like se	8.2
	402664	555511		predicted exon	8.2
30		IAMOFG4			
20	417682	W69561		gb:zd47e08.r1 Soares_fetal_heart_NbHH19W Homo sapien	8.2
	424983	A1742434	Hs.169911	ESTs	8.2
	434353	AA630863	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	8.2
	453448	AL036710	Hs.209527	ESTs	8.2
	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo saplens	8.2
35	404270	ac 100 100		predicted exon	8.1
55		A14/E4/E400	11- 050000		
	438297	AW515196	Hs.258238	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	8.1
	418122	R42778	Hs.22217	ESTs	8.1
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.1
	400925			predicted exon	8.1
40	403350			predicted exon	8.1
-10		A A 000770	Un 444004	ESTs	
	426116	AA868729	Hs.144694		8.1
	441518	AW161697	Hs.294150	ESTs	8.1
	421888	AA299780	Hs.121036	ESTs	8.1
	402745			predicted exon	8.1
45	402071			predicted exon	8.1
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	8.0
	430372	A1206173	Hs.211375	ESTs	8.0
	449867	A1672379	Hs.73919	"clathrin, light polypeptide (Lcb)"	8.0
~~	422174	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (from clone	8.0
50	413382	BE090689		"gb:RC1-BT0720-280300-011-f08 BT0720 Homo sapiens c	8.0
	456502	A1798611	Hs.157277	ESTs	8.0
	405336			predicted exon	8.0
	405917			predicted exon	8.0
~ ~	436007	A1247716	Hs.232168	ESTs	8.0
55	439192	AW970536	Hs.105413	ESTs	8.0
	437724	AW444828	Hs.184323	ESTs	8.0
	452755	AW138937	Hs.213436	ESTs	8.0
	401781	7111100001	110.210100	predicted exon	7.9
60	406057			predicted exon	7.9
60	405289	AW068311	Hs.82582	"integrin, beta-like 1 (with EGF-like repeat domains)"	7.9
	421459	AI821539	Hs.97249	ESTs	7.9
	448251	BE280486	Hs.84045	"Homo sapiens cDNA FLJ11979 fis, clone HEMBB100128	7.9
•	429125	AA446854	Hs.271004	ESTs	7.9
	440154	8E077129	Hs.126119	"Homo septens cDNA FLJ13273 fis, clone OVARC100101	7.9
65					
UJ	413233	AW578713	Hs.47534	"ESTs, Weakly similar to ORF YKL201c [S.cerevisiae]"	7.9
	438268	AA782163	Hs.293502	ESTs	7.9
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on chromosome 6	7.9
	441194	BE274581		"gb:601120870F1 NIH_MGC_20 Homo sapiens cDNA cion	7.9
	425292	NM_005824	Hs.155545	37 kDa leudine-rich repeat (LRR) protein	7.9
70	445090	AW205208	Hs.147293	ESTs	7.9
. •	431292	AA370141		Human DNA sequence from clone 967N21 on chromosome	7.9
			Hs.251453		
	414266	BE267834		"gb:601124428F1 NIH_MGC_8 Homo sepiens cDNA clone	7.8
	407839	AA045144	Hs.161566	ESTs	7.8
	456101	AA159478		gb:zo74d06.s1 Stratagene pancreas (937208) Homo sapiens	7.8
75	455853	BE147225		gb:PM2-HT0225-031299-003-(11 HT0225 Homo sapiens	7.8
. •	414995	C18200		gb:C18200 Human placenta cDNA (TFullwara) Homo sapta	7.8
			11- 00-00-		
	447247	AW369351	Hs.287955	"Homo sepiens cDNA FLJ13090 fis, clone NT2RP3002142	7.8
	416151	T26661		"gb:AB65C7R Infant brein, LLNL erray of Dr. M. Soares 1	7.8
	446435	AW206737	Hs.253582	ESTs	7.8
80	403698			predicted exon	7.8
	424914	AA348410	Hs.119065	ESTs	7.8
				"thymosin, beta, identified in neuroblastoma cells"	7.8
	409731	AA125985	Hs.56145		
	401604			predicted exon	7.8
	413025	AA805265	Hs.291646	ESTs	7.8

	405898			predicted exon	7.8
	454505	AW801365		"gb:iL5-UM0067-240300-050-a01 UM0067 Homo sapiens	7.7
	448283	A1340462	Hs.182979	nbosomal protein L12	7.7
5	434098	AA625499	II- 000000	*gb:af69g08.r1 Soares_NhHMPu_S1 Homo saplens cDNA	7.7 7.7
,	431673 421029	AW971302 AW057782	Hs.293233 Hs.293053	ESTs ESTs	7.7
	408391	AW859276	1222000	*gb:MR1-CT0352-240200-105-d02 CT0352 Homo saplens	7.7
	422529	AW015128	Hs.256703	ESTs	7.7
10	454389	AW752571	N- 00000	*gb:IL3-CT0213-170100-055-F02 CT0213 Homo saplens c ESTs	7.7 7.7
10	427821 434657	AA470158 AA641876	Hs.98202 Hs.191840	ESTs .	7.7
	445628	AL344166	Hs.155743	ESTs	7.7
	424872	AA347923		"gb:EST54302 Fetal heart II Homo sapiens cONA 5' end, m	7.7
15	439232	N48590	Hs.46693	ESTs	7.7 7.7
15	441417 453596	AI733297 AA441838	Hs.144474 Hs.62905	ESTs ESTs	7.7 7.7
	430440	X52599	Hs.2561	"nerve growth factor, beta polypeptide"	7.7
	413306	AW303544	Hs.118654	ESTs	7.7
20	400968	4140000444	11- 200000	predicted exon	7.7 7.7
20	446726 427504	AW300144 AA776743	Hs.209209 Hs.191589	*Homo saplens cDNA FLJ11629 fis, clone HEMBA100424 ESTs	7.7
	405621	77110140	(13.101003	predicted exon	7.6
	414127	AI431863	Hs.135270	ESTs	7.6
25	409866	AW502152	11- 400047	gb:UI-HF-BR0p-alr-f-11-0-UI.r1 NIH_MGC_52 Homo sap	7.6 7.6
25	446232 403568	Al281848	Hs.165547	ESTs predicted exon	7.6 7.6
	451458	AI797558	Hs.270820	ESTs	7.6
	439157	AA912737	Hs.20160	ESTs	7.6
20	401793	******	11 440440	predicted exon	7.6
30	429839 445672	AJ190291 AJ907438	Hs.112143 Hs.282862	ESTs ESTs	7.6 7.6
	449444	AW818436	Hs.23590	"solute carrier family 16 (monocarboxyllc acid transporters)	7.6
	447499	AW262580	Hs.147674	KIAA1621 protein	7.6
25	.421773	W69233	Hs.112457	ESTs	7.6
35	439706 432189	AW872527 AA527941	Hs.59761	ESTs *gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens cDNA clon	7.5 7.5
	402050	704021341		predicted exon	7.5
	429687	A1675749	Hs.211608	nucleoparin 153kD	7.5
40	423193	R07299	Hs.254837	*Homo saplens cDNA FLJ13502 ffs, clone PLACE1004836	7.5
40	416548 443236	H62953 AI079496	Hs.134169	gb:yr47f06.r1 Soares fetal liver spleen 1NFLS Homo saplen ESTs	7.5 7.5
	435053	AI079496 AI057224	Hs.15443	ESTs	7.4
	437191	NM_006846	Hs.5476	*serine protease inhibitor, Kazal type, 5*	7.4
15	451829	AW964081	Hs.247377	ESTs	7.4
45	443151	AI827193	Hs.132714 Hs.293772	ESTs ESTs	7.4 7.4
	452055 445265	Al377431 Al218295	Hs.144942	ESTs	7.4
	401032			predicted exon	7.4
60	448184	BE541249	Hs.109697	ESTs	7.4
50	414808	T95945	Hs.90877	gb:ye42e02.r1 Soares fetal liver spleen 1NFLS Homo sapien "ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.4 7.4
	418540 410449	AJ821597 AW748954	Hs.18192	Ser/Arg-related nuclear matrix protein (plenty of prolines 1	7.4
	435568	AA688048	Hs.294080	ESTs	7.4
c	459160	AI904723		*gb:CM-BT066-120299-092 BT066 Homo sapiens cDNA,	7.4
55	419753 432383	N42531 AK000144	Hs.274449	gb:yy11c12.r1 Soares melanocyte 2NbHM Homo sapiens cD "Homo sapiens cDNA FLJ20137 fis, clone COL07137"	7.4 7.4
	404893	ANUUUIH	113.21 4443	predicted exon	7.4
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerese A (ribose 5-phosphate epimer	7.4
60	413864	BE175582		*gb:RC5-HT0580-100500-022-C01 HT0580 Homo saplens	7.3
60	426871	AA393041	Hs.216493	ESTs gb.yg18h11.r1 Soares Infant brain 1NIB Homo sapiens cDN	7.3 7.3
	415613 427025	R20233 AA397589	Hs.97523	ESTs	7.3
	444683	A1375101	Hs.158721	*ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
65.	447700	AJ420183	Hs.171077	"ESTs, Weakly similar to similar to serine/threonine kinase	7.3
65 ·		AW993984	Hs.226313	*gb:RC1-BN0035-130400-013-a05 BN0035 Homo saplens *ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3 7.3
	416642 416506	T96118 H59879	Hs.237306	ESTs	7.3
	426130	AA853282		gb:NHTBCee04f07r1 Normal Human Trabecular Bone Cell	7.3
70	407392	AB032369	11 07/1/0	gb:Homo sapiens MIST mRNA, partial cds.*	7.3 7.3
70	432365 451221	AK001106 'AI949701	Hs.274419 Hs.210589	hypothelical protein FLJ10244 ESTs	7.3
	443161	AI038316	166.21003	gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapi	7.3
	418186	BE541042	Hs.23240	"Homo sapiens cDNA FLJ13496 fis, clone PLACE1004471	7.3
75	439152	H65014	11- 4 4700-	gb:yu66f10.r1 Wetzmann Olfactory Epithelium Homo sapie	7.2 7.2
13	459534 443326	BE386808 BE156494	Hs.147905 Hs.188478	ESTs ESTs	7.2
	417351	T90278	Hs.15049	ESTs	7.2
	454182	AW177335		*gb:CM1-CT0129-180899-006-b08 CT0129 Homo sapians	7.2
٥٨	402298		11- 44800	predicted exon	7.2
80	458562	N34128	Hs.145268	ESTs *gb:Human mariner1 transposase gene, complete consensus	7.2 7.2
	407021 449276	U52077 AW241510	Hs.252713		7.2
	418251	AA832123	Hs.177723	ESTs	7.2
	420788	AA937957	Hs.193367	•	7.2
				02	

	401881			predicted exon	7.2
	456436 413425	AA251079	Hs.158386	ESTS	7.2
	448966	F20956 AW372914	Hs.287462	*gb:HSPD05390 HM3 Homo septens cDNA clone 032-X4- *Homo septens cDNA FLJ11875 fis, clone HEMBA100707	7.2 7.2
5	429340	N35938	Hs.199429	Homo saplens mRNA; cDNA DKFZp434M2216 (from clon	7.2
	406053			predicted exon	7.2
	405851 431009	BE149762	Hs.248213	predicted exon	7.2 7.2
	426662	AA879474	Hs.122710	"gap junction protein, beta 6 (connexin 30)" ESTs	7.2
10	408536	AW381532	Hs.135188	ESTs	7.1.
	455013	BE073250	11- 400700	"gb:MR0-BT0551-060300-102-e05 BT0551 Horno saplens	7,1
	428910 424634	W03667 NM_003613	Hs.193792 Hs.151407	ESTs *cartilage intermediate tayer protein, nucleotide pyrophosph	7.1 7.1
	449794	AW444502	Hs.256982	*ESTs, Highly similar to AF116865 1 hedgehog-interacting	7.1
15	423410	AF058989	Hs.128231	"G antigen, family B, 1 (prostate associated)"	7.1
	445460	AI797473	Hs.209468	ESTs ·	7.1
	447285 419750	Al371849 Al079741	Hs.200696 Hs.183114	"ATPase, Class VI, type 11C" "Home saplens cDNA FLJ14236 fts, clone NT2RP4000515	7.1 7.1
	438986	AF085888	Hs.269307	ESTs	7.1
20	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; testicular	7.1
	432479 449733	AL042844 R74546	Hs.275675 Hs.29438	katanin p80 (WD40-containing) subunit B 1 "Homo sapiens cDNA FLJ12094 fis, clone HEMBB100260	7.1 7.1
	437846	AA773866	Hs.244569	ESTs	7.1
25	454934	AW846080		gb:MR3-CT0176-081099-002-b09 CT0176 Homo saplens	7.1
25	421929	AA300543	Hs.247360	ESTs	7.1
	401780 448106	Al800470	Hs.171941	predicted exon	7.0 7.0
	448835	BE277929	Hs.11081	ESTs "ESTs, Weakly similar to S57447 HPBRII-7 protein [H.sap	7.0
••	400842	042.7025		predicted exon	7.0
30	429364	AA451797	Hs.201202	"ESTs, Moderately similar to Pro-Pol-dUTPase polyprotein	7.0
	454963 423891	AW847647 AK002042	Hs.134795	"gb:IL3-CT0213-280100-056-A06 CT0213 Homo saptens c "Homo saptens cDNA FLJ11180 fis, clone PLACE1007452	7.0 7.0
	423631	U71600	FIS. 134/ 50	gb:Human zinc finger protein zfp31 (zf31) mRNA, partial	7.0
	413802	AW964490	Hs.32241	ESTs	7.0
35	440051	BE559980		*gb:601345293F1 NIH_MGC_8 Homo saplens cDNA clone	7.0
	446283 419236	A1948801 AA330447	Hs.171073 Hs.135159	ESTS *Home contone cONA EL 111481 for clone UENDA100180	7.0 7.0
	405472	N-0000-11	na.133133	"Homo sapiens cDNA FLJ11481 fis, clone HEMBA100180 predicted exon	7.0
40	435024	AI863518	Hs.127743	*ESTs, Wealdy similar to V-ATPase G-subunit like protein	7.0
40	453969	AW090783	Hs.301731	*Homo saplens cDNA FLJ11738 fis, clone HEMBA100547	7.0
	404992 428129	AJ244311	Hs.26912	predicted exen ESTs	7.0 7.0
	414315	224878	113.20312	gb:HSB65D052 STRATAGENE Human skeletal muscle cD	7.0
	400491	H25530	Hs.50868	"solute carrier family 22 (organic cation transporter), memb	6.9
45	459275	AI808913	Hs.118321	ESTs	6.9
	450853 457460	AA479629 Al143312	Hs.44243 Hs.164004	ESTs ESTs	6.9 6.9
	434168	A1204525	Hs.116156	ESTs	6.9
	445153	Al214671		gb:qm32d02.x1 NCI_CGAP_Lu5 Homo saplens cDNA clo	6.9
50	450028	Al912012	Hs.200737	ESTs	6.9
	414954 459478	D81402 AW195566	Hs.253182	gb:HUM162A03B Human fetal brain (TFujiwara) Homo sa ESTs	6.9 6.9
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from clon	6.9
	401050			predicted exon	6.9
55	447588	AI394154	Hs.279659	"ESTs, Weakly similar to unknown protein [H.sapiens]"	6.9
	449002	AI620018 AW590773	Hs.117461 Hs.258996	ESTs ESTs	6.9 6.9
	452759 443220	R85304	Hs.132032	"Homo sapiens cDNA FLJ11683 fis, clone HEMBA100490	6.9
	400749			predicted exon	6.8
60	406277			predicted exon	6.8
	433785 434129	BE044593 AI807757	Hs.112704 Hs.221041	ESTs ESTs	6.8 6.8
	453369	BE551550	Hs.232630	EST8	6.8
	411722	AW875942	112120200	*gb:CM1-PT0013-131299-067-b10 PT0013 Homo saplens	6.8
65	455152	AW858621		*gb:CM0-CT0342-021299-115-f04 CT0342 Homo saplens	6.8
	412670	AA115456	U- 404540	gb:zk89b05.r1 Soares_pregnant_uterus_NbHPU Homo sapi "ESTs, Weakly similar to ORF2 [M.musculus]"	6.8 6.8
	419054 421316	N40340 AA287203	Hs.191510 Hs.251397	SMA5	6.8
	432363	AA534489	110.251001	gb:nf76g11.s1 NCI_CGAP_Co3 Homo saplens cDNA clone	6.8
70	458603	AW103046	Hs.6162	KIAA0771 protein	6.8
	439527	AW298119	Hs.202536	ESTs fibronectin leucine rich transmembrane protein 2	6.8 6.8
	408920 439127	AL120071 AW978465	Hs.48998 Hs.292368	ESTs	6.8
-	434890	AF161345	Hs.283930	"Homo saplens HSPC082 mRNA, partial cds"	6.8
75	429413	NM_014058	Hs.201877	DESC1 protein	6.7
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.7
	447252 455851	R90916 BE146879		gb:yn01e10.r1 Soares adult brain N2b4HB55Y Homo saplen "gb:QV4-HT0222-261099-014-c11 HT0222 Homo sapiens	6.7 6.7
	439509	AF086332	Hs.58314	EST8	6.7
80	418858	AW961605	Hs.21145	"Homo saplens cDNA: FLJ22489 fis, clone HRC10951"	6.7
	419323	AI092379	Hs.135275	ESTs	6.7
	415317 418654	Z43388 AA226334	Hs.5570 Hs.154291	hypothetical protein FLJ10006 ESTs	6.7 6.7
	407413	AF067801		"gb:Homo sapiens HDCGC21P mRNA, complete cds."	6.7

	400CD4	A A D 4304 C	11		
	439694	AA843915	Hs.54707	ESTs	6.7
	451191 454006	N67900 U12775	Hs.118446	ESTs	6.7
	443657	R14973	Hs.37006	agouti (mouse)-signaling protein	6.7 6.7
5	455879	BE153275		gb:yf42/10.s1 Soares fetal liver spieen 1NFLS Homo sapien "gb:PM0-HT0335-180400-008-e11 HT0335 Homo sapiens	6.7
9	451368	BE242152	Hs.288417	protein serine threonina kinasa CIK4	6.7
	453509	AL040021	1.002.00111	gb:DKFZp434N1812_r1 434 (synonym: htes3) Homo saple	6.7
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	6.7
	423372	A1246375	Hs.154458	ESTs	6.7
10	450316	W84448	Hs.17850	ESTs	6.7
	447795	AW295151	Hs.163612	ESTs	6.7
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo saplens	6.7
	405771			predicted exon	6.6
	411483	AW848115		gb:IL3-CT0214-301299-048-C09 CT0214 Homo sapiens c	6.6
15	420271	A1954365	Hs.42892	ESTs	6.6
	431948	AA917708	Hs.194616	ESTs	6.6
	409629	AW449589	Hs.279724	ESTs	6.6
	458841	W28965		gb:54d10 Human relina cDNA randomly primed sublibrary	6.6
20	416565	AW000960	Hs.44970	ESTs	6.6
20	409097	AA677927	Hs.144269	ESTs	6.6
	441832	AI018249	Hs.128082	ESTs	6.6
	457285	AI038858	Hs.228780	*ESTs, Highly similar to AF199597 1 A-type potassium cha	9.6
	406504	0033334		predicted exon	6.6
25	414606	BE387771	U- 121072	"gb:601283251F1 NIH_MGC_44 Homo sapiens cDNA clon	6.6 6.8
23	452956	AW003578 AA089474	Hs.231872 Hs.272153	ESTs ESTs	6.6
	410743 404599	AAA003414	NS.272133	predicted exon	6.6
	423575	C18863	Hs.163443	"Homo sapiens cDNA FLJ11576 fis, clone HEMBA100354	6.6
	443027	A1027847	Hs.253550	ESTs	6.6
30	458663	AV658444	Hs.280776	"Homo saplens cDNA FLJ13684 fis, clone PLACE2000021	6.6
50	431277	AA501806	Hs.249965	ESTs	6.6
	445232	BE294357	1 13.2 43300	*gb:601172878F1 NIH_MGC_17 Homo saplens cDNA don	6.6
	459170	AJ905518		gb:RC-BT091-210199-098 BT091 Homo saplens cDNA, m	6.6
	437876	AA770151	Hs.126424	ESTs	6.6
35	406752	AJ285598	Hs.217493	annexin A2	6.6
	401245			predicted exon .	6.6
	446102	AW168067	Hs.252956	ESTS	6.5
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.5
	421160	AL080215	Hs.102301	Homo saplens mRNA; cDNA DKFZp586J0323 (from clone	6.5
40	458831	. H71739	Hs.200227	ESTs	6.5
	408914	AW450309		gb:UI-H-BI3-akz-g-08-0-UI.s1 NCI_CGAP_Sub5 Homo sa	6.5
	411018	AW813428		*gb:MR3-ST0192-010200-210-c05 ST0192 Homo sapiens c	6.5
	436562	H71937	Hs.169756	"complement component 1, s subcomponent"	6.5
40	457620	AA602711		"gb:np03h06.s1 NCI_CGAP_Pr2 Homo saptens cDNA clon	6.5
45	438647	AA813118	Hs.163230	ESTs	6.5
	439570	T79925	Hs.269165	ESTs	6.5
	419273	BE271180	Hs.293490	EST ₈	6.5
	443745	AB039670	Hs.9728	ALEX1 protein	6.5
50	431029	BE392725	Hs.248571	Homo saplens PAC clone RP5-1163J12 from 7q21.2-q31.1	6.5
50	458695	AV660159	Hs.282284	ESTS	6.5
	410986	AW812088	11- 50547	"gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapiens c	6.4 6.4
	417135	AA422067	Hs.50547	ESTS Selventantesact MILL MCC 21 Name engines of NA class	6.4
	416441 413702	BE407197 BE170313		"gb:601301552F1 NIH_MGC_21 Homo saplens cDNA clon "gb:QV4-HT0536-040500-193-g02 HT0536 Homo saplens	6.4
55	452563	AI907552		"gb:RC-BT147-120499-044 BT147 Homo sapiens cDNA, m	6.4
55	408956	AK001868	Hs.295306	*ESTs, Highly similar to unnamed protein product (H.sapien	6.4
	406349	74.001000	110.20000	predicted exon	6.4
	425420	BE536911	Hs.234545	*ESTs, Weakly similar to AF155135 1 novel retinal pigmen	8.4
	459430	AW662886		gb:hi82h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
60	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	6.4
	458578	Al306162	Hs.170938	"ESTs, Wealdy similar to KIAA0705 protein [H.saplens]"	6.4
	429695	AAB35714	Hs.293556	ESTs	6.4
	426872	AA410446	Hs.112011	"ESTs, Wealty similar to unknown [H.sapiens]"	6.4
	437152	AL050027		gb:Homo saplens mRNA; cDNA DKFZp566C0324 (from c	6.4
65	440517	AW139632	Hs.132246	ESTs	6.4
	450877	AI799608 i	Hs.29178	ESTs ·	6.4
	410564	NM_006033	Hs.65370	"Ilpase, endothelial"	8.4
	405793			predicted exan	6.4
70	418709	AA227394		gb:zr17c10.r1 Stratagene NT2 neuronal precursor 937230 H	6.4
70	428584	AAA31792	Hs.44784	ESTs *ab:RC1-NN0073-260400-011-009 NN0073 Homo septens	6.4
	448516	AW898595			6.4 6.3
	400983 422365	AF035537	Hs.115521	predicted exon "REV3 (yeast homolog)-like, catalytic subunit of DNA poly	6.3
	425612	BE004257	113.113321	"gb:CM0-BN0103-180300-296-c04 BN0103 Homo saplens	6.3
75	401521	DEVOTEST		gradicted exon	6.3
	430290	AI734110	Hs.136355	ESTs	6.3
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (from clon	6.3
	437939	AW298600	Hs.141840	*ESTs, Weakly similar to S59501 interferon receptor JFNA	6.3
	451842	AI820539	Hs.267087	"ESTs, Moderately similar to ALU4_HUMAN ALU SUBF	6.3
80	405810			predicted exon	6.3
50	443747	AV646352		gb:AV646352 GLC Homo saplens cDNA clone GLCAME	· 6.3
	427287	NM_014903	Hs.174188		6.3
	413521	BE145814		ab:MR0-HT0208-101299-202-a04 HT0208 Homo sapiens	6.3
	429090	AW820278	Hs.99066	ESTs .	6.3
				•	

		1100000			
	451488 455713	H22999 BE069891	Hs.208846	ESTS	6.3 6.3
	452161	R43077	Hs.221747	*gb:QV4-BT0401-201299-064-b01 BT0401 Homo saptens ESTs	6.3
	428647	AA830050	Hs.124344	ESTs	6.3
5	445083	Al246275	Hs.149198	ESTs	6.3
	456671	AB011142	Hs.114293	KIAA0570 gene product	6.3
	401508			predicted exon .	6.3
	412677	AW029608	Hs.17384	ESTs	6.3
10	441720	AJ346487	Hs.28739	ESTs	6.3
10	418051	AW192535	Hs.19479	ESTS	6.3 6.3
	438014 432101	N71183 AI918950	Hs.121806 Hs.11092	"Homo sapiens cDNA FLJ11971 fis, clone HEMBB100120 "Homo sapiens cDNA FLJ14290 fis, clone PLACE1006795	6.3
	421032	AW293133	Hs.101340	ESTs	6.3
	436532	AA721522	(10.101010	"gb:nv54h12_r1 NCt_CGAP_Ew1 Homo sepiens cDNA clo	6.3
15	431318	AA502700	Hs.293147	ESTs	6.3
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Homo saplens c	6.3
	402425			predicted exon	6.3
	455993	BE179085		gb:RCO-HT0613-140300-021-d06 HT0613 Homo saplens	6.3
20	400160	41040470	U- 440000	predicted exon	6.3 6.2
20	413795	AL040178	Hs.142003	ESTs predicted exon	6.2
	405071 403741			predicted exon	6.2
	432489	AI804855	Hs.207530	EST8	6.2
	402296	. 400 .000		predicted exon	6.2
25	446091	AW022192	Hs.200197	ESTs	6.2
	444788	AI871122	Hs.202821	ESTs	6.2
	404972			predicted exon	6.2
	400227			predicted exon	6.2
20	433804	A1936561	Hs.112740	ESTs	6.2
30	448807	Al571940	Hs.7549	ESTs	6.2 6.2
	404340 424632	AB014523	Hs.151406	predicted exon KIAA0623 gene product	6.2
	449547	H93543	Hs.117963	ESTs	6.2
	406945	K01383	Hs.203967	metallothionein 1A (functional)	6.2
35	433663	AF083131	Hs.229535	CATX-15 protein	6.2
	407809	AW082279	Hs.244106	ESTs	6.2
	418342	BE002723	Hs.293504	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.2
	438007	AA133008	Hs.158675	ribosomal protein L14	6.2
40	410536	N39533	11. 470070	gb:yv27d04.s1 Soares fetal liver spleen 1NFLS Homo saple	6.2
40	448005	AW207437	Hs.170378	ESTs	. 6.2 6.2
	414083 405362	AL121282	Hs.257786	ESTs predicted exon	6.2
	410102	AW248508	Hs.279727	*Homo sapiens cDNA FLJ14035 fis, clone HEMBA100463	6.2
	457868	AW975133	I IGLET OF ET	"gb:EST387239 MAGE resequences, MAGN Homo sepien	6.2
45	407395	AF005082	•	gb:Homo sapiens skin-specific protein (xp33) mRNA, part	6.2
	443603	BE502601	Hs.134289	"ESTs, Weakly similar to KIAA1063 protein [H.saplens]"	6.2
	430051	AA464611	Hs.52515	transducin (bela)-like 2	6.1
	434569	Al311295	Hs.58609	ESTs	6.1
50	430481	AA479678	Hs.203269	*ESTs, Moderately similar to ALU8_HUMAN ALU SUBF	6.1
50	402859			predicted exon	6.1 · 6.1
	401260 406544			predicted exon predicted exon	6.1
	428446	AJ024600 .	Hs.98612	ESTs	6.1
	412246	A1160873	Hs.69233	"ESTs, Weakly similar to KIAA1064 protein [H.sapiens]"	6.1
55	400420	AJ277247	Hs.287369	interleukin 22	6.1
	455662	BE065387		"gb:RC1-BT0314-030500-016-d03 BT0314 Homo saplens	6.1
	428613	AB037749	Hs.186928	KIAA1328 protein	6.1
	443267	AW450630	Hs.133851	ESTs	6.1
60	433405	AW157568	Hs.156892	ESTS	6.1
60	416795	A1497778	Hs.168053	"ESTs, Highly similar to AF227948 1 HBV pX associated p	6.1 6.1
	435706	W31254 AA057418	Hs.7045 Hs.33654	GL004 protein ESTs	6.1
	450769 427174	AA398848	Hs.97541	ESTs	6.1
	425389	AW974499	Hs.192183	ESTs	6.1
65	416675	H73802	Hs.35381	ESTs	6.1
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	8.1
	401809			predicted exon	6.1
	403041			predicted exon	6.0
70	408523	AW833259		"gb:RC2-TT0007-131099-011-c01 TT0007 Homo sapiens c	6.0
70	416515	N91716	Hs.194140	ESTS	6.0 6.0
	452591 437146	BE173164 AA730977	Hs.1516	Insulin-like growth factor-binding protein 4 "gb:nw55f05.s1 NCL_CGAP_Ew1 Homo saplens cDNA clo	6.0
	450094	Al174947	Hs.295789	Homo saplens mRNA; cDNA DKFZp564D1164 (from clon	6.0
	402529			predicted exon	6.0
75	430706	NM_003540	Hs.247818	"H4 histone family, member C"	6.0
	459186	AI908287		gb:RC-BT168-020499-035 BT168 Homo sapiens cDNA, m	6.0
	452158	Al699120	Hs.61198	ESTS	6.0
	411237	AW833676		*gb:QV4-TT0008-181199-038-h04 TT0008 Homo saplans	6.0
٥٨	400441	M15530	Hs.99879	8-cell growth factor 1 (12kD)	6.0
80	439398	AA284267	Hs.221504		- 6.0 6.0
	440862	H39048	Hs.127432 Hs.268720		6.0
	415451 459587	H19415 AA031958	110.200120	cb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Homo sapi	6.0
	456072	H54381		gb:yq89a03.s1 Soares fetal liver spleen 1NFLS Homo saple	6.0

	100054	414740000		FOT	
	409954 443488	AW512770	Hs.266457	ESTs	6.0
	430825	A1073495 A1734186	Hs.133912 Hs.185105	"ESTs, Weakly similar to methyl-CpG blnding domain-cont ESTs	6.0 6.0
	454466	AA984138	Hs.279895	"Homo saplens mRNA for KIAA1578 protein, partial cds"	6.0
5	456506	AA278277	Hs.194212	ESTs	6.0
•	449228	AJ403107	Hs.148590	"ESTs, Wealty similar to AF208846 1 BM-004 [Haapiens]	6.0
	457727	AW974687		"gb:EST386776 MAGE resequences, MAGM Homo saplen	6.0
	442440	BE464435	Hs.146180	"ESTs, Wealty similar to non-receptor protein tyrosine kina	5.9
10	455110	BE154505		*gb:PM0-HT0343-281299-003-e06 HT0343 Homo saptens	5.9
10	402790	DECOURSO.		predicted exon	5.8
	409982	BE005839	Un 170000	*gb:RC2-BN0120-250400-012-f03 BN0120 Homo sapiens	5.9
	427635 408948	BE397988 AW298713	Hs.179982 Hs.221441	tumor protein p53-binding protein ESTs	5.9 5.9
	402046	AIIZUIIS	113-221441	predicted exon	5.9
15	416438	R89238	Hs.34262	ESTs	5.9
	403083			predicted exon	5.9
	402481			predicted exon	5.9
	409867	AW502161		gb:Ui-HF-BR0p-air-g-12-0-Ul.r1 NIH_MGC_52 Homo sap	5.9
20	420362	U79734	Hs.97206	huntingtin Interacting protein 1	5.9
20	421375	AA489200	Hs.100595	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.9
	437630	AI252782	Hs.153029	ESTs	5.9
	443500	AV646388	Hs.137071	ESTs	5.9
	448995 438214	A1613276 H06076	Hs.5662 Hs.26320	"guanine nucleotide binding protein (G protein), beta polyp TRABID protein	5.9 5.9
25	428046	AW812795	Hs.155381	"ESTs, Moderately similar to I38022 hypothetical protein (H	5.9
LJ	431941	AK000106	Hs.272227	"Homo sapiens cDNA FLJ20099 fis, clone COL04544"	5.9
	403356	, , , , , , , , , , , , , , , , , , , ,	110127 2221	predicted exon	5.9
	439031	AF075079		gb:Homo saplens full length insert cDNA YQ80A08	5.9
	430032	AW936136	Hs.99610	ESTs	5.9
30	423457	F08208	Hs.155606	paired mesoderm homeo box 1	5.9
	422158	L10343	Hs.112341	"prolease inhibitor 3, skin-derived (SKALP)"	5.9
	406592			predicted exon	5.9
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo saplens	5.8
25	429399	AA452244	Hs.16727	ESTs	5.8
35	408590	AW238162	Hs.253873	ESTs	5.8
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	5.8
	417421	AL138201	Hs.82120	"nuclear receptor subfamily 4, group A, member 2"	5.8
	401129	4144074445	15 100100	predicted exon	5.8
40	434745	AW974445	Hs.185155	"ESTs, Weakly similar to HuEMAP [H.sapiens]"	5.8
40	402800 436185	AW753380	Hs.49753	predicted exon "Homo saplens mRNA for KIAA1561 protein, partial cds"	5.8 5.8
	419519	A1198719	Hs.176376	ESTs	5.8
	452542	AW812256	10.170010	*gb:RC0-ST0174-191099-031-a07 ST0174 Homo saplens c	5.8
	427166	AA431576	Hs.155658	ESTs	5.8
45	416168	H23687		gb:yn72d12.r1 Soares adult brain N2b5HB55Y Homo sapie	5.8
	431467	N71831	Hs.256398	Homo saplens mRNA; cDNA DKFZp434E0528 (from clon	5.8
	421558	AB011125	Hs.105749	KIAA0553 protein	5.8
	458055	AW979121	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN III! ALU CLAS	5.8
~ ^	418345	AJ001696	Hs.241407	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.8
50	426544	AA492325		gb:ng81b11.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone	5.8
	433544	Al793211	Hs.165372	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.8
	442007	AA301116	Hs.142838	"Homo saplens cDNA: FLJ23444 fis, clone HSI01343"	5.8
	443422	R10288	Hs.301529	ESTs "Homo septens cDNA FLJ14115 fis, clone MAMMA10017	5.8 5.8
55	434311 424966	BE543469 AU077312	Hs.266263 Hs.153985	"solute carrier family 7 (cationic amino acid transporter, y+	5.8
55	441744	AA960922	Hs.200938	ESTs	5.8
	413101	BE065215	110.20000	*gb:RC1-BT0314-310300-015-f01 BT0314 Homo saplens c	5.7
	445687	W80382	Hs.149297	ESTs	5.7
	441369	AA931535		gb:oo56a04.s1 NCL_CGAP_Lu5 Homo sapiens cDNA don	5.7
60	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associated pr	5.7
	431211	M86849	Hs.5566	"gap junction protein, beta 2, 26kD (connexin 26)"	5.7
	411541	W03940		gb:za62b02.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.7
	448612	A1696363	Hs.171285	ESTs	5.7
65	419118	AA234223	Hs.139204	ESTs	5.7
65	406322	A14MP 4000		predicted exon	5.7
	454690	AW854639	Un 24000	*gb:MR1-CT0258-140100-203-d10 CT0258 Homo saplens	5.7 5.7
	450313 416292	AI038989 AA179233	Hs.24809 Hs.42390	hypothetical protein FLJ 10826 nasopharyngeal carcinoma susceptibility protein	5.7 5.7
	449309	AW589823	Hs.224189	ESTs	5.7 5.7
70	408418	AW963897	Hs.44743	KIAA1435 protein	5.7
	416100	H18700	Hs.268799	ESTs	5.7
	437845	AA769578	Hs.90488	ESTs	5.7
	443345	AI052508	Hs.164482	"ESTs, Weakly similar to contains similarity to TPR domain	5.7
	418407	AL044818	Hs.84928	"nuclear transcription factor Y, beta"	5.7
75	434557	AW855466	Hs.271866	*ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.7
	431688	AA513906		gb:ng67c08.s1 NCt_CGAP_Lip2 Homo saplens cDNA do	5.7
	437641	AA811452	Hs.291911	ESTs	5.7
	409319	AW752736	Hs.33565	ESTs	5.7
90	403967	AF030107	Hs.17165	regulator of G-protein signalling 13	5.7
80	445189	A1936450	Hs.147482	ESTs	5.7
	414418	H62943	Hs.154188		5.7 5.7
	446563	BE326588	Hs.141454	ESTs ESTs	5.7 5.7
	446075 428068	AW451457 AW016437	Hs.279179 Hs.233462	ESTS ESTS	5.7
	720000	VIIIIIII	1 10.200102		U. 1

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	438425 415532	AW292922 R14780	Hs.293170 Hs.12826	ESTs ESTs
	441442	AL043282	Hs.131824	ESTs
5	443380 445527	AJ792478 W39694	Hs.135377 Hs.83286	ESTs
,	414378	BE393856	Hs.66915	"ESTs, Weakly similar to 16.7Kd protein [H.saplens]"
	457960	AA771881	Hs.298149	ESTs
	453293	AA382267	Hs.10653	ESTs
^	452503	AB000509	Hs.29736	TNF receptor-associated factor 5
)	405227 442257	AW503831		predicted exon gb:Ui-HF-BNO-sib-b-05-0-Ui.r1 NIH_MGC_50 Homo sep
	403403	711303031		predicted exon
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library Hom
_	438656	H85310	Hs.209456	"ESTs, Wealdy similar to NG22 [H.sapiens]"
5	419936 437267	AI792788 AW511443	Hs.258110	*gb:ol91d05.y5 NCI_CGAP_Kid5 Homo saplens cDNA clo ESTs
	437267	AA481269	Hs.178381	ESTs
	444835	Al198994	Hs.158479	ESTs
^	444902	AJ132099	Hs.12114	vanin 1
0	451800	AW977435	Hs.31890	ESTs
	405465 403891			predicted exon predicted exon
	425557	Al694300	Hs.46730	ESTs
_	432162	AA584062	Hs.272798	hypothetical protein FLJ20413
5	450152	AI138635	Hs.22968	ESTS
	410053 421285	AW579707 NM_000102	Hs.59332 Hs.1363	ESTs "cytochrome P450, subfamily XVII (steroid 17-alpha-hydro
	421265	AA353953	Hs.20369	"ESTs, Wealthy similar to gonadotropin inducible transcript
	418844	M62982	Hs.1200	arachidonale 12-lipoxygenase
)	429616	Al982722	Hs.120845	ESTs
	423528	AB011137	Hs.129740	KIAA0565 gene product predicted exon
	403089 414373	AW162907	Hs.75969	proline-rich protein with nuclear targeting signal
_	403687			predicted exon
5	417079	U65590	Hs.81134	interleukin 1 receptor antagonist
	432501	BE546532	Hs.287329	Fas binding protein 1
	403691 409545	BE296182		predicted exon *gb:601177324F1 NIH_MGC_17 Homo saptens cDNA clon
	435990	AI015862	Hs.131793	EST8
0	444409	Al792140	Hs.49265	ESTs
	435478	AA682622	11- 404075	gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo
	439981 433644	A1348408 AW342028	Hs.124675 Hs.256112	"ESTs, Weakly similar to unnamed protein product (H.sapie ESTs
	441541	AA938663	Hs.199828	ESTs
5	400709	74.00000	1.0	predicted exon
	407615	AW753085		gb:PM1-CT0247-151299-005-a03 CT0247 Homo saplens
	424153	AA451737	Hs.141496 Hs.34244	MAGE-like 2 ESTs
	452465 406030	AA610211	F13.34244	predicted exon
0	431071	AA491379		gb:aa65f05_r1 NCI_CGAP_GC81 Homo saplens cDNA cl
	418086	AA211791	Hs.269666	*Homo sapiens cDNA FLJ13415 fis, clone PLACE1001799
	453034	BE246010	Hs.184109 Hs.238809	ribosomal protein L37a
	412953 425351	Z45794 Al206234	Hs.155924	ESTs cAMP responsive element modulator
55	406149	AZUZU	113,13324	predicted exon
-	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)
	458378	A1040535	Hs.150524	ESTs
	401213			predicted exon
50	405904 445132	Z44811		predicted exon gb:HSC29G031 normalized Infant brain cDNA Homo saple
,,,	405138	LTTOIL		predicted exon .
	442238	AW135374	Hs.270949	ESTs
	416852	AF283776	Hs.80285	Homo saplens mRNA; cDNA DKFZp586C1723 (from clon
5	448691 452242	AA481119 R50956	Hs.283558 Hs.59503	hypothetical protein PRO1855 "ESTs, Weakly similar to AF157318 1 AD-017 protein [H.s.
,,,	456994	AA383623	Hs.293616	ESTs
	440913	Al267491	Hs.160593	ESTs
	435380	AA679001	Hs.192221	ESTs
10	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (metrin alph
70	414035 459084	Y00630 H01699	Hs.75716 Hs.27289	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi CGI-125 protein
	405867	1101033	110.21203	predicted expn
	414093	BE544867		"gb:601078872F1 NIH_MGC_12 Homo saplens cDNA clon
15	447306	Al373163	Hs.170333	ESTs
75	413083	BE064528		*gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapiens
	404828 402543			predicted exon predicted exon
	421988	AW450481	Hs.161333	ESTs
	413404	BE503463	Hs.297431	ESTs
80	459043	AI808444	Hs.208113	
	404410	A A 470540		predicted exon "gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clon
	430264 431499	AA470519 NM_001514	Hs.258561	
	412566	AW962574	113.240001	"gb:EST374647 MAGE resequences, MAGG Homo saplen

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5 0 5 5 60 35 40 45 55 60	458163 446205 415578 415578 425275 415578 425275 415578 42052 424717 420111 432140 409479 404727 420111 456083 424834 425071 426065 415602 432839 455088 423715 424834 425071 426065 415679 45688 423716 424834 425071 436873 405454 436873 405454 431887 442783	AA884304 AA884304 AW172662 AW977808 AA165232 AA323073 AI653774 H03754 AA255652 AA5000404 AA157881 BE163800 AI623778 U46922 AK001432 NKL_013989 N32049 F12920 AA573945 H98899 BE177320 WZ7595 AA464840 T93500 AA38791 AI966103 AW897321 AW661783 AJ701609 AA523660 AL048534 NM_002914 AF174394 U82435 AF226667 T16981 T89473 N56820 H50167	Hs.131163 Hs.149479 Hs.222069 Hs.289083 Hs.195648 Hs.152213 Hs.272688 Hs.143056 Hs.136912 Hs.145809 Hs.77252 Hs.153408 Hs.153408 Hs.154424 Hs.165575 Hs.287332 Hs.165575 Hs.287332 Hs.165575 Hs.28699 Hs.11061 Hs.18653 Hs.26999 Hs.11061 Hs.189908 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.21963 Hs.21963 Hs.21963 Hs.225133 Hs.225133	ESTs "gb:EST389810 MAGE resequences, MAGO Homo saplen ESTs ESTs ESTs ESTs ESTs ESTs "wingless-type MMTV integration site family, member 5A" gb:zs2!ht1.rl NCL CGAP_GCB1 Homo saplens cDNA clo hypothetical protein FLJ20397 ESTs ESTs ESTs predicted exon ESTs fragile histidine triad gene "Homo saplens cDNA FLJ10570 fis, clone NT2RP2003117 "delodinase, iodothyronine, type il" gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to9W ESTs ESTs ESTs "Homo saplens cDNA: FLJ23082 fis, clone LNG06451" ESTs ESTs eSTs "Homo saplens cDNA: FLJ23082 fis, clone LNG06451" ESTs gb:zx43h11.rl Soares_lotal_fetus_Nb2HF8_9w Homo saple "Homo saplens cDNA FLJ11041 fis, clone PLACE1004405 nascant-potypeptide-associated complex alpha potypeptide "Homo saplens cDNA FLJ12836 fis, clone NT2RP2003206 ESTs ESTs predicted exon ESTs ESTs PESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo saplens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicotinic, alpha potypeptide 6" CTP synthase il predicted exon ESTs ESTs
0 5 60 35 40 45 55	415579 423200 424717 420111 432140 409479 446011 456083 424834 425071 426065 415602 432839 416879 424823 42423 425701 447645 402974 438607 428873 405454 42768 424323 425701 447645 402974 436607 428873 405454 435711 405292 435433 4410123 435435 4410123 435435 4410123 435435	AA165232 AA323073 AI633774 H03754 AA255652 AA6000404 AA157881 BE163800 AI623778 U46922 AK001432 NKL_013989 N32049 F12920 AA573945 H98899 BE177320 WZ7595 AA464840 T93500 AA338791 AI966103 AW897321 AW661783 AJ701609 AA523660 AL046534 NKL_002914 AF174394 U82435 AF226667 T16981 T89473 N56820 H50167	Hs.222069 Hs.289083 Hs.195648 Hs.195648 Hs.152213 Hs.272688 Hs.143056 Hs.136912 Hs.145809 Hs.77252 Hs.153408 Hs.153408 Hs.15424 Hs.165575 Hs.287332 Hs.42599 Hs.156148 Hs.18653 Hs.28792 Hs.46763 Hs.28799 Hs.156169 Hs.191727 Hs.48458 Hs.19226 Hs.177461 Hs.98908 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.585553 Hs.21963 Hs.21963 Hs.21963 Hs.21963 Hs.275133	ESTs ESTs "wingless-type MMTV integration site family, member 5A" gbzs2/th11.rl NCL_CGAP_GCB1 Homo sapiens cDNA clo hypothetical protein FLJ20397 ESTs ESTs predicted exon ESTs fragile histidine triad gene "Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117 "delodinase, iodothyronine, type if" gbzyw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to9W ESTs ESTs "Homo sapiens cDNA: FLJ23082 fis, clone LNG06451" ESTs ESTs eSTs "Homo sapiens cDNA: FLJ23082 fis, clone LNG06451" ESTs gbzx43h11.rl Soares_total_fetus_Nb2HF8_9w Homo sapie "Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405 nascent-potypeptide-associated complex alpha potypeptide "Homo sapiens cDNA FLJ12836 fis, clone NT2RP2003206 ESTs predicted exon ESTs ESTs predicted exon ESTs ESTs Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo sapiens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicotinic, alpha potypeptide 6" CTP synthase il predicted exon ESTs ESTs
0 5 60 35 40 45 55	423200 440052 420111 422140 414904 409479 404727 446011 426065 432839 416672 432839 416672 432839 416672 424524 425055 42281 425011 447645 42423 426701 447645 42423 426701 447648 42423 426701 44768 42423 42571 42571 42581	AA323073 AIS33774 H03754 AA255652 AK000404 AA157881 BE163800 AIS23778 U46922 AK001432 NL_013989 N32049 F12920 AA579465 H98899 F12920 AA579465 H98899 F12920 WZ7595 AA464840 T93500 AA338791 AIS68103 AW897321 AW661783 AI701609 AA523660 AL048534 NL_002914 AF174394 U62435 AF226667 T16981 T16981 T16981 T16981 N56820 H50167	Hs.289083 Hs.195648 Hs.195648 Hs.152213	ESTs ESTs ### ESTs #### ESTs ##### ESTs ##### ESTs ##### ESTs ##### ###### ######### ##########
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0 0 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	452281 424223 425701 447645 402974 435607 428873 405454 431887 442768 424085 424085 425098 421284 435711 405292 410123 435435 417071 438958 457405	T93500 AA338791 AI968103 AW897321 AW661783 AI701609 AA523660 AL048534 NM_002914 AF174394 U82435 AF226667 T16981 T89473 N55820 H50167	Hs.146763 Hs.209461 Hs.159699 Hs.211061 Hs.98908 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	"Homo septens cDNA FLJ11041 fis, clone PLACE1004405 nascent-polypeptide-essociated complex atpha polypeptide "Homo septens cDNA FLJ12836 fis, clone NT2RP2003206 ESTs predicted exon ESTs ESTs predicted exon ESTs "ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo septens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicotinic, alpha polypeptide 6" CTP synthase il predicted exon ESTs ESTs ESTs
0 0 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	426701 447645 402974 436607 428873 405458 431887 442768 424085 435098 435098 435711 405292 410723 435435 417071 438958 457405	AI968103 AW897321 AW661783 AI701609 AA523660 AL048534 NM_002914 AF174394 U62435 AF226667 T16981 T89473 N56820 H50167	Hs.209481 Hs.159699 Hs.211061 Hs.98908 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	"Homo sapians cDNA FLJ12836 fis, clone NT2RP2003206 ESTs predicted exon ESTs ESTs predicted exon ESTs "ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo sapians apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicolinic, alpha polypeptide 6" CTP synthase II predicted exon ESTs ESTs
35 30 35 50	447645 402974 4366073 405454 431867 442768 424085 424085 424085 425098 421284 435719 405292 410123 435435 417071 438958 457405	AW897321 AW661783 AI701609 AA523660 AL048534 NM_002914 AF174394 U82435 AF226667 T16981 T89473 N56820 H50167	Hs.159699 Hs.211061 Hs.98908 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	ESTs predicted exon ESTs ESTs predicted exon ESTs ESTs Predicted exon ESTs "ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo sepiens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicolinic, alpha polypeptide 6" CTP synthase II predicted exon ESTs ESTs
35 360 355	402974 436607 428873 405454 431887 442768 424085 435098 421284 435711 405292 410123 435435 417071 438958 457405	AW661783 AJ701609 AA523660 AL048534 NM_002914 AF174394 U82435 AF226667 T16981 T89473 N56820 H50167	Hs.211061 Hs.98908 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.58553 Hs.21963 Hs.192328 Hs.21963 Hs.275133	predicted exon ESTs ESTs predicted exon ESTs "ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo septens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicolinic, alpha polypeptide 6" CTP synthase il predicted exon ESTs ESTs
5 60 65 55	436607 428873 405454 431867 442768 424085 435098 421284 435711 405292 410123 435435 417071 438958 457405	A7701609 AA523660 AL048534 NM_002914 AF174394 U62435 AF226667 T16981 T89473 N56820 H50167	Hs.98908 Hs.191727 Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	ESTs ESTs ESTs Predicted exon ESTs "ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo seplens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicotinic, alpha polypeptide 6" CTP synthase II predicted exon ESTs ESTs
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35 50	431867 442768 424085 435098 421284 435711 405292 410123 435435 417071 438958 457405	AL048534 NM_002914 AF174394 U62435 AF226667 T16981 T89473 N58820 H50167	Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	ESTs "ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo septens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicotinic, alpha polypeptide 6" CTP synthase il predicted exon ESTs ESTs
0 55 60	442768 424085 435098 421284 435711 405292 410123 435435 417071 438958 457405	AL048534 NM_002914 AF174394 U62435 AF226667 T16981 T89473 N58820 H50167	Hs.48458 Hs.139226 Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	"ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAM replication factor C (activator 1) 2 (40kD) "Homo sapiens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicolinic, alpha polypeptide 6" CTP synthase II predicted exon ESTs ESTs
0 55 60	424085 435098 421284 435711 405292 410123 435435 417071 438958 457405	NM_002914 AF174394 U62435 AF226667 T16981 T89473 N58820 H50167	Hs.139226 Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	replication factor C (activator 1) 2 (40kD) "Homo septens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicotinic, alpha polypeptide 6" CTP synthase II predicted exon ESTs ESTs
0 55 60	435098 421284 435711 405292 410123 435435 417071 438958 457405	AF174394 U62435 AF226667 T16981 T89473 N58820 H50167	Hs.177461 Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	"Homo sapiens apoptotic-related protein PCAR mRNA, par "cholinergic receptor, nicotinic, alpha polypeptide 6" CTP synthase II predicted exon ESTs ESTs
55 50	421284 435711 405292 410123 435435 417071 438958 457405	U62435 AF226667 T16981 T89473 N58820 H50167	Hs.103128 Hs.58553 Hs.21963 Hs.192328 Hs.275133	"cholinergic receptor, nicolinic, alpha polypeptide 6" CTP synthase il predicted exon ESTs ESTs
55 50	405292 410123 435435 417071 438958 457405	T16981 T89473 N58820 H50167	Hs.21963 Hs.192328 Hs.275133	predicted exon ESTs ESTs
55 50	410123 435435 417071 438958 457405	T89473 N58820 H50167	Hs.192328 Hs.275133	ESTs ESTs
5	435435 417071 438958 457405	T89473 N58820 H50167	Hs.192328 Hs.275133	ESTs
0 5	417071 438958 457405	N58820 H50167	Hs.275133	
0	457405		L1- 00440	ESTs
0 5			Hs.33113	ESTs
0 5	413047	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202 Homo sapiens
5	433868	BE154837 AA612960		*gb:PM1-HT0345-121199-001-c08 HT0345 Homo saplens gb:nq38g06.s1 NCI_CGAP_Co10 Homo saplens cDNA clo
5	444461	R53734	Hs.25978	ESTs
55	427088	AA398085	Hs.142390	ESTs
55	451307	AW293207	Hs.211516	ESTs
	403831			predicted exon
	402892 433420	Al674093	Hs.293961	predicted exon ESTs
	455759	BE080469	115.250501	"gb:QV1-BT0630-280200-086-d06 BT0630 Homo saplens
	411379	AI816344	Hs.12554	"ESTs, Weakly similar to Nucleosome Assembly Protein 1-
50	428483	AI908539	Hs.184592	KIAA0344 gene product
50	429208	AA447990	Hs.190478	ESTS
50	447572 434896	AJ631546 AW022054	Hs.159732 Hs.136591	ESTS ESTs
50	417616	R07728	Hs.268668	ESTs
	411805	AW884183		*gb:PM0-SN0014-260400-002-d02 SN0014 Homo saplens
	419000	T79855	Hs.268592	ESTs
	413488	BE144017	Hs.184693	"transcription elongation factor B (SIII), polypeptide 1 (15k
	400975 407453	AJ132087		predicted exon gb:Homo saplens mRNA for exonemal dynein heavy chain (
55	430757	AJ458623		"gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clo
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B"
	401877	AB011094	Hs.129892	KIAA0522 protein
	457122	AI026157	Hs.33728	*ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM
70	410708 435807	A1732404 A1033299	Hs.68846 Hs.113614	ESTs ESTs
	42839B	A1249368	Hs.98558	EST ₈
	401088			predicted exon
	414501	N43991	Hs.171984	ESTS
75	419083	A1479560	Hs.98613	"Homo septens cDNA FLJ12292 fis, clone MAMMA10018 "ESTs, Weakly similar to ZN91_HUMAN ZINC FINGER P
, ,	421107 411489	AA283822 AW848346	Hs.55606	"qb:IL3-CT0214-150200-076-F03 CT0214 Homo saplens c
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A receptor, beta 1°
	430082	AW514083	Hs.190135	ESTs
00	425698	NM_016112		
80	451686	AA059246	Hs.110293	
	NF 400-4	A1929383 H66373	Hs.108196 Hs.15973	HSPC037 protein "ESTs, Highly similar to bA393J16.3 [H.sapiens]"
	453867	AA382814	119.10313	"gbtEST96097 Testis I Homo saplens cDNA 5' end, mRNA
	419985 426650	AA335497	Hs.293965	

	405576			predicted exon	5.2
	409584	AA076010		gb:zm89f12.s1 Stratagene ovarian cancer (937219) Homo sa	5.2
	454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	5.2
5	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.2
,	439155 432267	H81076 AK000872	Hs.269001 Hs.274227	ESTs "Homo septens cDNA FLJ10010 fis, clone HEMBA100030	5.2 5.2
	459024	AA020799	Hs.179825	RAN binding protein 2-like 1	5.2
	404088	70020133	113.113023	predicted exon	5.2
	403525			predicted exon	5.2
10	445882	AI948717	Hs.225155	ESTs, Wealty similar to PSF_HUMAN PTB-ASSOCIATE	5.2
	448257	AW772070	Hs.253146	ESTs	5.2
	410500	R09442		gb:yf26c09.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.2
	456084	AA155859	Hs.79708	ESTS	5.2
15	410523 434623	BE143839 AB023163	Hs.4014	"gb:MR0-HT0164-151299-012-d03 HT0164 Homo saplens KIAA0946 protein; Huntinglin interacting protein H	5.2 5.2
13	454484	AW795196	Hs.215857	ring finger protein 14	5.2
	402131			predicted exon	5.2
	438913	AJ380429	Hs.172445	ESTs	5.2
•	402628			predicted exon	5.1
20	415973	R24707	Hs.260201	ESTs	5.1
	455640	BE064059		*gb:QV3-BT0296-010300-111-e04 BT0296 Homo sapiens	5.1
	442750	AI016803	Hs.131096	ESTs	5.1 5.1
	404638 431117	AF003522	Hs.250500	predicted exon delta (Drosophila)-like 1	5.1
25	428819	AL135623	Hs.193914	KIAA0575 gene product	5.1
	439519	AA837118	Hs.118366	ESTs	5.1
	427335	AA448542	Hs.251677	Gantigen 78	5.1
	416450	AA180467	Hs.142556	ESTs	5.1
20	440876	AW613524	Hs.279570	ESTs	5.1
30	414584	BE409585		"gb:601301836F1 NIH_MGC_21 Homo sapiens cDNA don	5.1
	443175	N57863	Un 40276	gb:yv60c02.s1 Soares fetal liver spleen 1NFLS Homo saple	5.1 5.1
	408968 415654	A1652236 AW968363	Hs.49376	hypothetical protein FLJ20644 "gb:EST380439 MAGE resequences, MAGJ Homo saptens	5.1
	440559	AW629054	Hs.125976	*ESTs, Weakly similar to metalloprotease/disintegrin/cystel	5.1
35	421236	Al287622	Hs.151956	ESTs	5.1
••	416258	N45661	Hs.275131	ESTs	5.1
	405982			predicted exon .	5.1
	406589			predicted exon	5.1
40	412458	AW953229	Hs.169142	ESTs	5.1
40	435693	Al033134	Hs.119887	ESTs .	5.1
	449182	AW292381	Hs.224150	ESTs	5.1 5.1
	403963 440830	AI733112	Hs.176101	predicted exon ESTs	5.1
	415412	F08049	Hs.52132	EST8	5.1
45	442832	AW206560	Hs.253569	ESTs	5.1
	445359	Al808725	Hs.147783	EST8	5.1
	412088	AI689496	Hs.108932	ESTa	5.1
	428785	AI015953	Hs.125265	ESTs	5.1
50	430163	X66610	Hs.234748	"enolase alpha, tung-specific"	5.1
50	455441	AW945964	Hs.113261	*gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapiens c "Homo sapiens skin-specific protein (xp33) mRNA, partial	5.1 5.1
	400304 403944	AF005082	NS.113201	predicted exon	5.1
	457069	BE159191	Hs.114318	"ESTs, Weakly similar to ORF1 [H.saplens]"	5.1
	414125	BE253197		"gb:601116804F1 NIH_MGC_16 Homo sapiens cDNA clon	5.1
55	448566	AW291319	Hs.194574	EST8	5.1
	457948	A1498640	Hs.159354	ESTs	5.1
	438240	N92638	Hs.124004	ESTs	5.1
	404070			predicted exon	5.1
60	402709 416425	BE077308		predicted exon "gb:RC1-BT0606-060200-012-h12 BT0606 Homo saplens	5.1 5.0
OO	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) Homo sapiens cDN	5.0
	452502	AI904296		gb:PM-BT048-220199-286_1 BT046 Homo sepiens cDNA	5.0
	446657	Al335191	Hs.260702	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	5.0
	459124	AW301478	Hs.299178	ESTs	5.0
65	409940	BE548143		gb:601073109F1 NIH_MGC_12 Homo saplens cDNA clon	5.0
	443547	AW271273	Hs.23767	"Homo saplens cDNA FLJ12666 fis, clone NT2RM400225	5.0
	447452	BE618258	Hs.102480	ESTS Madagatah similar ta NAC 4 aratain ID naggalasis	5.0 5.0
	414327	BE408145 AI807264	Hs.185254 Hs.205442	"ESTs, Moderately similar to NAC-1 protein [R.norvegicus] "ESTs, Weakly similar to AF117610 1 inner centromere pro	5.0
70	416155 408081	AW451597	Hs.167409	ESTs	5.0
	426834	AI091533	Hs.135167	ESTs	5.0
	433368	AW877277		*gb:MR4-PT0051-150200-001-d03 PT0051 Homo saptens	5.0
	433098	AW190593	Hs.151143	ESTs	5.0
75	439721	W92142	Hs.271963	*ESTs, Wealty similar to ALU5_HUMAN ALU SUBFAM	5.0
75	441818	AI630451	Hs.7976	KIAA0332 protein	5.0
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2) Homo sapi	5.0
	411905	BE265067	Ue 107702	"gb:601193893F1 NIH_MGC_7 Homo sapiens cDNA clone ESTs	5.0 5.0
	434248 423967	AA628151 AW296758	Hs.187783 Hs.11641	"Homo sapiens cDNA: FLJ21432 fis, clone COL04219"	5.0
80	456212	N51636		gb:yy87b01.s1 Soares_multiple_sclerosis_2NbHMSP Homo	5.0
- •	442914	AW188551	Hs.99519	"Homo sapiens cDNA FLI14007 fis, clone Y79AA1002407	5.0
	436084	AK000185		"gtxHomo sapiens cDNA FLJ20178 fis, clone COL09990"	5.0
	449252	AW594482	Hs.253315		5.0
	454653	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo saplens c	5.0

	414699	Al815523	Hs.76930	"synuclain, alpha (non A4 component of amyloid precursor) 5.0					
	443335	T89697	Hs.16645	ESTs 5.0					
	448419 425574	AL080072	Hs.21195	Homo saplens mRNA; cDNA DKFZp584M0616 (from clon 5.0					
5	435174	AA359663 AA687378	Hs.194624	*gb:EST68717 Fetal tung II Homo seplens cDNA 5' end, mR 5.0 ESTs 5.0					
•	429548	AW138872	Hs.135288	ESTs 5.0					
	450613	A1702055	Hs.287767	*gb:tq20g10.x1 NCL_CGAP_Ut1 Homo septens cDNA clon 5.0					
	400432 421751	AX015809 AW813731	Hs.159153						
10	405800			predicted exon 5.0					
	429430	Al381837	Hs.155335	ESTs 5.0					
	439518 430884	W76326 AF053748	Hs.248114	gbzd60d04.r1 Soares_fetal_heart_NbHH19W Homo septen 5.0 glial cell derived neurotrophic factor 5.0					
	452741	BE392914	Hs.30503	"Homo seplens cDNA FLI11344 fis, clone PLACE1010870 5.0					
15	441001	AW137017	Hs.126373	Human DNA sequence from clone RP5-1184F4 on chromos 5.0 ESTs 5.0					
	438490 408170	AW593272 AW204516	Hs.26261 Hs.31835	ESTS 5.0 ESTS 5.0					
	449104	R08702 .		gb:yf24c06.r1 Soares fetal liver spleen 1NFLS Homo sapien 5.0					
20	TABLE 18								
20		que Eos probese	t identifier nur	nber					
	CAT numb	er. Gene duster	number						
	Accession	: Genbank acces	ssion numbers	,					
25	Pkey	CAT Number	Accessio						
	407615	1005404_1		35 AW753082 AW054744 AW753107 AW753087					
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	409191 409545	1107176_1 1138823_1		30 AW818237 AW858911 AW858977 BE072544 W26498 12 AW629821					
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25	409695	114878_1		1 AA296889 AA076945 AA077528 AA077497					
35	409866 409867	1156522_1 1156530_1		52 H41202 H29772 51 AW502587 AW502345					
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	410626	12126211	BE40772						
	410966 411004	1228071_1 1228975_1		88 AW812105 AW812082 42 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582					
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	411057	1230493_1		98 BE154843 BE154831					
	411178 411237	1234752_1 1236377_1		52 AW820773 AW821088 76 AW833814 AW833798 AW833677 AW833449 AW833630 AW833626 AW833444 AW833366 AW833791 AW833659 AW833432					
	4,120	1200017_1		34 AW833556 AW833553					
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	411489 411541	1247360_1 1249044_1		46 AW848760 AW848340 AW848818 AW849043 AW849061 T98335 AW850705					
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55	411693	1254206_1		71 AW857308 AW857296 AW857258 42 AW858234 AW875938 AW875941 AW858235 AW875958					
))	411722 411725	1254914_1 1255047_1		96 AW858505 AW858476 AW861971 AW858556 AW861908 AW858514 AW858601 AW861909 AW858434 AW858400 AW858405					
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Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
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Strend: Indicates DNA strend from which exons were predicted NL position: Indicates nucleofide positions of predicted exons

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                                      Plus
                                                   21240-21399
             403403
                         9438460
                                      Plus
                        7960440
                                                   152431-153243
                                      Plus
             403525
  80
                         8101145
                                      Minus
                                                   85509-85658
             403568
                         8699843
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                                                   35849-36204
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                                      Plus
                                                   9009-9534
             403687
                                                   88280-88463
             403691
                         7387384
                                      Minus
                                                   10464-10907
                                      Plus
             403698
                         4263532
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2833-3468
          403741
                       7630932
7658395
                                    Minus
                                                  20493-20621
          403747
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                                                  73028-73217
61468-61575
          403786
                       8083636
                                     Minus
           403831
                       7249249
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                                                   191508-193220
                       7331467
7711864
           403891
                                     Minus
                                                   129213-129415
                                     Minus
           403944
                                                  149466-149665
7210-7414,10043-10195
184131-184295
           403963
                       8568150
                                     Plus
           404070
                       2996642
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                       9958257
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                       7770701
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                                                   86147-86509
3649-3750,4161-4306,5962-6049,6849-6965
                       7596822
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           404166
           404270
                       9828129
                                     Minus
                                                   10898-11506
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                       7630856
                                     Plus
                                                   49052-49176,56177-56273,59384-59488
                       7342122
           404410
                                     Phis
                                                   110443-110733
99433-99528,100035-100161
104257-105215
15
                        8705107
                                     Plus
           404599
           404638
                        9796751
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                        9797142
                                     Minus
                                                   115534-115747
           404727
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                                     Plus
                        7882827
                                                   23244-23759
                                     Minus
           404767
                                                   26291-27253
144843-144964,149846-150121
65083-65223
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           404828
                        6580415
                                      Minus
           404849
                        7706886
                                     Plus
           404893
                        6850447
                                     Plus
                                                    177015-177328
                                      Minus
           404898
                        7331420
                                                    136326-136618
           404952
                        7382669
                                      Minus
                                                    48711-49524
106104-106199,111659-111781
11115-11552
25
                        3213020
           404972
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           404992
                         4662677
                                      Minus
           405071
                        7708797
                                      Minus
                                                    90303-90516
                        8576241
7230083
            405138
                                      Plus
                                                    135716-135851
                                      Minus
            405198
 30
                         6731245
                                      Minus
                                                    22550-22802
            405227
                                      Plus
                                                    23471-23572
55744-55903,57080-57170,61478-61560
                         3980473
            405277
            405285
                         6139075
                                      Minus
                                                    33227-33442
            405292
                         3845420
                                      Plus
                         6094635
                                                    33267-33563
            405336
405362
                                      Pius
                                                     105008-105142,105980-106091,140445-140556,142519-142641
 35
                         2337862
                                      Minus
                                                    31923-32311
133807-134053
            405382
                         6552767
                                      Plus
            405454
                         7656675
                                      Plus
                                                    8935-9073,12242-12367,13364-13506,14965-15493
            405465
                         7767904
                                      Plus
                                                    106297-106447,108462-108596
124361-124520,124914-125050
84000-85009
                         8439781
                                      Plus
            405472
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            405547
                                      Ptus
                          1054740
                          4003382
                                      Plus
            405576
                                                     59362-59607
             405621
                          5523811
                                      Plus
                                                     56384-56587
            405636
                         5123990
                                      Phis
                                      Plus
                                                     70304-70630
                          4557087
            405675
 45
                          4156182
                                       Plus
                                                     55030-55604
            40570B
                                                    91191-91254,91510-91589
27238-27885
                          7018349
                                       Plus
            405771
             405783
                          5738434
                                       Minus
                                                     89197-89453
                          1405887
2791346
             405793
                                       Minus
                                                     19271-19813
                                       Plus
             405800
  50
                          4938307
                                       Minus
                                                     64543-64966
             405810
                                                     28135-28244
26407-27151
             405848
                          7651809
                                       Minus
             405851
                          6164995
                                       Minus
                                       Minus
                                                     74553-75173
             405867
                          6758731
                          6758795
                                                     57311-57874
                                       Plus
             405896
405904
  .55
                          7705118
                                        Minus
                                                     16375-16584
                                                     106829-107213
             405917
                          7712162
                                       Minus
                                                     36028-36408
             405982
                          8247790
                                       Minus
                                                     96123-96547
             406030
                          8312328
                                       Minus
                                                     30921-31532
                                       Plus
             406053
                          6758997
  60
                                                     20830-21222
                          6691254
                                        Minus
             406057
                                        Minus
                                                     44464-45164
66690-66835
                          7144791
              406149
                           7158901
                                        Plus
              406163
                                                     4759-5490
              406277
                           5686030
                                        Minus
                                                      130230-130418
              406322
                          9212102
                                        Minus
                                                      21251-21526
   65
                                        Minus
              406349
                           9256007
                           7711360
                                                      107068-107277
                                        Minus
              406504
                                                      46576-46757
              406544
                           7711508
                                        Plus
                                                      38806-38989
              406589
                           8224211
                                        Plus
                                                      352560-352963
                                        Plus
              406592
                           4567182
   70
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TABLE 2A lists about 167 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 1A, except that the ratio was greater than or equal to 2.5, and the predicted protein contained a PFAM domain that is indicative of extracellular localization (e.g., ig, fig., egf, 7m domains).

TABLE 2A: ABOUT 187 UP-REGULATED OVARIAN CANCER GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS Pkey: Primekey

Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title

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Title: Unigena Title PFAM domains ratio: tumor vs. normal tissues

				Tid.	PFAM domain	ratio
	Pkey 423017			Title serine (or cystelne) proteinase inhibito	serpin	63.6
	431938		Hs.115242	developmentally regulated GTP-bindi	SCP	32.0
	425650		Hs. 1925	desmodein 3 (pemphigus vulgaris ant	cadherin	30.0 24.5
5	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molec	EGF;tectin_c;sushi alpha-emytase	15.B
	452947	AW130413	Hs.106604	gbod50f04.x1 NCI_CGAP_Gas4 Hom ESTs	pkinase;Activin_recp	15.1
	418092 431725	R45154 X65724	Hs. 2839	Norrie disease (pseudoglioma)	Cys_knot	12.6
	422330	D30783	Hs.115263	epiregulin	EGF	12.5
10	446745	AW118189	Hs.156400	ESTS	AMS	11.1 10.8
	416319	AI815601	Hs.79197	COB3 antigen (activated 8 lymphocyt	tg ion_trans;K_tetra	10.6
	432408 405285	N39127	Hs.76391	myxovirus (influenza) resistance 1, ho predicted exon	A2NtA2M_N	10.5
	405265 405636			predicted exon	EGF;ldl_recept_a;ldl_recept_b	9.8
15	403093			predicted exon	fn3	9.6 9.2
	446740	AI611635	Hs.192605	ESTs	RYDR_TPR ABC_tran;ABC_membrane	8.5
	405547	AW937485		predicted exon gb:QV3-DT0044-221299-045-b09 DT	7tm_1	8.4
	412333 404270	AVV93/403		predicted exon	SCP	8.1
20	402745			predicted exon	EGF;tdl_recept_b;thyroglobulin_1	8.1
	452755	AW138937	Hs.213436	ESTs	cystalin .	8.0 7.9
	421459	AI821539	Hs.97249	ESTS	disintegrin;ReprolysIn taminin_G;EGF	7.8
	416151	T26661	Hs.165547	gb:AB65C7R Infant brain, LLNL arra ESTs	7tm_3	7.6
25	446232 431009	Al281848 BE149762	Hs.248213	gap junction protein, beta 6 (connextn	connexin	7.2
20	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, n	ig;tsp_1	7.1
	400749	_		predicted exon	fn3;kil_recept_a;tdl_recept_b	6.8 6.8
	419054	N40340	Hs.191510	ESTs, Wealdy similar to ORF2 [M.m	ig;SPRY ABC_tran;ABC_membrane	6.6
30	459170	A1905518		gb:RC-BT091-210199-098 BT091 Ho gb:601301552F1 NIH_MGC_21 Hom	SDF	6.4
30	416441 410664	BE407197 NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22	6.4
	402425	1111/200000		predicted exon	ion_trans	6.3
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_H	Ephrin	6.0 5.9
25	403083			predicted exon	fn3 SDF	5.9 5.9
35	448995	AI613276	Hs.5662 Hs.241407	guanine nucleotide binding protein (G serine (or cysteine) proteinase inhibito	serpin	5.8
	418345 424966	AJ001696 AU077312	Hs.153985	solute carrier family 7 (cationic amino	aa_permeases	5.8
	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (co	connexin	5.7
	430563	AA481269	Hs.178381	ESTs	ABC_tran;ABC_membrane	5.6 5.6
40	450152	Al138635	Hs.22968	ESTs	ig;pkinase lipoxygenase;PLAT	5.6
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase predicted exon	fn3	5.6
	403089 403687			predicted exon	tsp_1;Reprolysin	5.6
	403891			predicted exon	tsp_1;Reprolysin	5.5
45	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	semin	5.4 5.3
	421284	U62435	Hs.103128	cholinergic receptor, nicolinic, alpha p	neur_chan lipase;PLAT	5.3
	435435	T89473 Al026157	Hs.192328 Hs.33728	ESTs ESTs, Weakly similar to ALU1_HUM	lipoxygenase;PLAT	5.2
	457122 419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A	neur_chan	5.2
50	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	ion_trans	5.2
• •	431117	AF003522	Hs.250500		EGF;DSL	5.1 5.1
	457948	A1498640	Hs.159354		G-alpha;arf SPRY	5.0
	435174	AA687378 AW204516	Hs.194624 Hs.31835	ESTs ESTs	art;ras	5.0
55	408170 434351	AW974991	Hs.191852		artras	4.9
55	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	7tm_1	4.8 4.8
	422597	BE245909	Hs.118634		ABC_tran;ABC_membrane ABC_tran;ABC_membrane	4.8
	405545		Hs.170009	predicted exon transforming growth factor, alpha	EGF	4.7
60	426471 409632	M22440 W74001	Hs.55279	serine (or cysteine) proteinase inhibito	serpin	4.7
00	420206	M91463	Hs.95958	solute carrier family 2 (facilitated gluc	sugar_tr	4.6
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	Kunitz_BPTI;G-gamma	4.6 4.5
	424402	M63108	Hs.1769	tuteinizing harmone/chartogonadotrop	7tm_1 ASC	4.5
65	436480	AJ271643	Hs.87469	putative acid-sensing ion channel adrenergic, beta-2-, receptor, surface	7tm_1	4.4
65	430226 436126	BE245562 AW449757	Hs.2551 Hs.163036		SNF	4.4
	406812	AF000575	Hs.67846	teukocyte immunogłobulin-like recep	ig	4.4
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (TIMP	4.3 4.3
~ ^	449184	AW296295	Hs.19649	I ESTS	TNFR_c6 disintegrin;Reprotysin	4.3
70	410555	U92649	Hs.64311		cadhedn	4.3
	422389 405281	AF240635	Hs.11589	protocedness 12	A2M;A2M_N	4.3
	413548	BE147555	Hs.28854	1 Homo sagiens mRNA for KIAA1558	EGF;tdi_recept_a;tdl_recept_b	4.3
	449535	W15267	Hs.23672	low density lipoprotein receptor-relate	kdi_recept_a;EGF;kdi_recept_b	4.3 4.3
75	425864	U56420	Hs.15990	3 olfactory receptor, family 5, subfamily	7tm_1 Peplidase_S9	4.3 4.2
	410611	AW954134		KIAA1628 protein desmoglein 1	cadherin;Cadherin_C_term	4.1
	430686 418693	NM_00194 AI750878	2 Hs.2000 Hs.87409		vwc,TSPN	4.0
	445924	A1264671	Hs.16416	6 ESTs	sugar_tr	3.9
80	457148	AF091035	Hs.18462	7 KIAA0118 protein	arfras	3.9 3.9
	428568	AC004755			E1-E2_ATPase EGF;kd]_recept_a;kdl_recept_b	3.8
	412170		Hs.73729 Hs.12111		enk;death;RHD;TIG	3.8
	442566 403763		1 13.12.11	predicted exan	7tm_1	3.8
	100.00				105	

				. Hatad area	fn3	3.8
	403074 413605	BE152644		predicted exon ab:CM1-HT0329-250200-128-109 HT	apha-amytase	3.8
	442295			Homo sapiens cDNA FLJ11469 fis, c	Collagen;COLFI	3.7
	403681	70001210		predicted exon	7tm_3;ANF_receptor	3.7
5	407305 AA715284			gbanv35f03.r1 NCL_CGAP_Br5 Horn	pkinase;Sema;Plexin_repeat;TIG	3.7 3.7
	457353			melanocortin 2 receptor (adrenocortic	7tm_1 laminin_EGF;taminin_B	3.6
	431176			ESTs ESTs	pa parameter bearing	3.6
	436233 431808			amphiregulin (schwannoma-derived g	ĔGF	3.6
10	445798	NM_012421		rearranged L-myc fusion sequence	zf-C2H2	3.6
	400380	NM_018485		G protein-coupled receptor C5L2	7tm_1	3.6 3.5
	453893	NM_000835		glutamate receptor, lonotropic, N-met	lig_chan	3.5 3.5
	409402	AF208234	Hs.695	cystatin 8 (stefin 8)	cystatin IRK	3.5
15	421166	AA305407	Hs.102308 Hs.172004	potassium inwardly-rectifying channe titin	tn3	3.5
13	445575 428957	Z25368 NM_003881	Hs.194679	WNT1 inducible signaling pathway p	tsp_1;vwc;tGFBP	3.5
	403909	NM_016255	Hs.95260	Homo sapiens mRNA; cDNA DKFZp	Na_H_Exchanger	3.5
	403077	11112010200		predicted exon	fn3	3.5
	455612	BE042896	Hs.274848	ESTs	ABC_tran;ABC_membrane	3.5 3.5
20	424091	AF235097	Hs.139263	calcium channel, voltage-dependent, a	ion_trans	3.4
	403955	75m (cadherin;Cadherin_C_term 7tm_1	3.4	
	457470	AB040973	Hs.272385 Hs.81360	G protein-coupled receptor 72 CGI-35 protein	disintegrin; Reprolysin	3.4
	401522 404886	N47812	NS.01300	predicted exon	lon_trans	3.4
25	437692	AA176959	Hs.172004	fiffn	fn3	3.4
	407944	R34008	Hs.239727	desmocollin 2	cadherin	3.4
	407393	AB038237		gb:Homo sapiens mRNA for G protei	7tm_1	3.3
	436936	AL134451	Hs.197478	ESTs	EGF;laminin_G	3.3 3.3
20	423309	BE006775	Hs.126782	sushi-repeat protein	sushi;HYR	3.3
30	402172	41070000		predicted exon gb:tc72g07.x1 Soares_NhHMPu_S1 H	ig ank;pkinase;death	3.3
	447420 438901	AI378628 AF085834	Hs.29036	ESTs	sushi	3.3
	424362	AL137646	Hs.146001	Homo sepiens mRNA; cDNA DKFZp	trypsin;sushi;CUB	3.3
	430453	8E387060	Hs.3903	Cdc42 effector protein 4; binder of Rh	fn3	3.3
35	416631	H69466		gb:yr88f07.r1 Soares felal liver spleen	idl_recept_a;MACPF	3.3
•	453174	A1633529	Hs.135238	ESTs	7tm_1	3.3 3.2
	433848	AF095719	Hs.93764	carboxypeptidase A3	Zn_carbOpeptPropep_M14	3.2
	408546	W49512	Hs.46348	bredykinin receptor B1	7tm_1 7tm_1 '	3.2
40	423573	AA328504	Hs.169149	gb:EST31993 Embryo, 12 week I Hom karyopherin alpha 1 (importin alpha 5	7tm_3;ANF_receptor	3.2
40	458662 433430	AI823410 AI863735	Hs.186755	ESTs	thyroglobulin_1;1GFBP	3.2
	438850	R33727	Hs.24688	EST	ank;pkinase;death	3.2
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	Gal-bind_lectin	3.2
	409968	U56102	Hs.57699	adhesion glycoprotein	ig .	3.1 3.1
45.	430630	AW269920	Hs.2621	cystalin A (stefin A)	7tm_3;ANF_receptor	3.1
	420737	L08096	Hs.99899	tumor necrosis factor (tigand) superfa	TNF tectin_c	3.1
	422279	H69644	Hs.114231 Hs.2258	C-type tectin-like receptor-2 matrix metalloproteinase 10 (stromely	hemopexin;Peptidase_M10	3.1
	400289 412597	X07820 AU077051	Hs.74561	alpha-2-macroglobulin	A2M;A2M_N	3.1
50	453420	AJ003459	110.14001	gb:AJ003459 Selected chromosome 2	IRK	3.1
50	404243 predicted exon zf-C3HC4;SPRY;zf-B		zi-C3HC4;SPRY;zi-B_box	3.1		
	449987	AW079749	Hs.184719	ESTs, Wealdy similar to AF116721 1	ABC_tran;ABC_membrane	3.1 3.0
	422471	AA311027	Hs.271894	ESTs	ig Peptidase_S9	3.0
<i>5</i>	400464	05044400	II- obazoz	predicted exon ESTs	EGF	3.0
55	458713	BE044496 F07783	Hs.282707 Hs.1369	decay accelerating factor for complem	sushi	3.0
	421340 449523	NM_000579		chemokine (C-C motif) receptor 5	7tm_1	3.0
	400704			predicted exon	lig_chan;ANF_receptor	3.0
	416239	AL038450	Hs.48948	ESTs	E1-E2_ATPase;Hydrolase	3.0
60	433664	AW292176	Hs.245834	ESTs	Ricin_B_lectin	3.0 2.9
	423994	X01057	Hs.1724	interleukin 2 receptor, sipha	AMS	2.9
	447726	AL137638	Hs.19368	Homo saplens mRNA; cDNA DKFZp Homo saplens protocadherin Fat 2 (FA	EGF:cadherin:laminin_G	2.9
	425483 423513	AF231022 AF035960	Hs.301273 Hs.129719		Transglut_core;TransglutamIn_N	2.9
65	423513	M-033300	113.125710	predicted exon	lg;pklnase;LRRNT;LRRCT	2.9
05	405790			predicted exon	Sema; Plexin_repeat; TIG	2.9
	422669	H12402	Hs.119122	ribosomal protein L13a	arf;ras;Ribosomal_\$17	2.9 2.9
	430793	MB3181	Hs.247940		7tm_1	2.8
70	403411			predicted exon	ABC_tran;ABC_membrane Transglutamin_N;Transglut_core	2.8
70	428188	M98447	Hs.22 Hs.76252	transglutaminase 1 (K polypeptide ep endothelin receptor type A	7tm_1	2.8
	414482	S57498	Hs.174031		COX68	2.8
	427223 404187	BE208189	115,174001	predicted exon	ig	2.8
	443537	D13305	Hs.203	cholecystakinin B receptor	7tm_1	2.8
75	428701	NM_013276	5 Hs.190207		vwa;Integrin_A;P2X_receptor	2.7 2.7
, -	411213	AA676939	Hs.69285	neuropilin 1	CUB;MAM;F5_F8_type_C	2.7
	453999	BE328153	Hs.24008		kazal vwa;vwd;TIL	2.7
	401244	1114 00004	0 Nº 01610	predicted exon sema domain, immunoglobulin domai	Sema	2.7
80	458930 434411	NM_00361 AA632649	2 Hs.24640 Hs.20137		sushi	27
OV	434411	AF263537	Hs.28737		FGF ·	2.7
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like	kazal	2.7
	417350		Hs.82001	polycystic kidney disease 2 (autosoma	ion_trans	2.6 2.6
	419452		Hs.90572	PTK7 protein tyrosine kinase 7	pkinase;ig	20

	401657			predicted exon	7tm_1	2.6				
	456711	AA033699	Hs.83938	ESTs, Moderately similar to MASP-2	sushi;trypsin;CUB	2.6				
	432042	AW971345	Hs.292715	ESTs	sugar_tr	2.6 ·				
5	433138 452530	AB029496 Al905518	Hs.59729	semaphorin sem2 gb:RC-8T091-210199-098 BT091 Ho	ig;Sema ABC_tran;ABC_membrane	2.6 2.6				
3	426418	M90464	Hs.169825	collagen, type IV, atpha 5 (Alport syn	Collagen; C4	2.6				
	403796			predicted exon	cadherin	2.6				
	431728	NM_007351	Hs.268107	multimerin	EGF;C1q	2.6				
10	441595	AW206035	Hs.192123	ESTs	sugar_t	2.6				
10	445537 447197	AJ245671 R36075	Hs.12844	EGF-like-domain, multiple 6 gb:yh88b01.s1 Soares placenta Nb2H	EGF;MAM SDF	2.6 2.5				
	428765	X54150	Hs.193122	Fc fragment of IgA, receptor for	b	2.5				
	450245	AA007536	Hs.271767	ESTs, Moderately similar to ALU1_H	tg	2.5				
1.5	416429	H54658	Hs.268942		E1-E2_ATPase;Hydrolase	2.5				
15	417067 433182	AJ001417 AB039920	Hs.81086 Hs.127821	solute carrier family 22 (extraneurona BWRT protein	sugar_tr lon_trans	2.5 2.5				
	403092	ADWJJZU	113.121021	predicted exon	m3	2.5				
	406850	Al624300	Hs.172928	collagen, type I, alpha 1	vwc;Collagen;COLFI	2.5				
20	438698	AW297855	Hs.125815	ESTS	lipoxygenase;PLAT	2.5				
20	456815	NM_013348	Hs.144011	potassium inwardly-rectifying channe	IRK .	2.5				
	TABLE 2B:									
	Pkey: Unic	que Eos probesei		nber						
25		er: Gene cluster		·						
23	Accession:	Genbank acces	ision numbers	¥						
	Pkey	CAT Number	Accession							
	409385	112523_1		T65940 T64515 AA071334						
30	412333	1289037_1		AW937589 AW937658 AW937654 AW937492		75450555 DE469550 DE469745 DE469560				
30	413605	1379792_1		8E152712 BE152668 BE152659 BE152810 BE1 BE152661 BE152672 BE152653 BE152716 BE1						
				BE152775 BE152666 BE152768 BE152813 BE1						
				BE152815 BE152678 BE152673 BE152782 BE1						
0.5				BE152774 BE152763 BE152769						
35	416151	1573926_1		4135 H23016						
	416441 416631	159480_1 1605019_1		AA182474 AA180369 BE275628 BE276131 3884 N59684						
	423573	229714_1		AA327783 AW962370						
	447197	711623_1		366546 R36167						
40	447420	721207_1	A1378628 N32350 H85772							
	452530	920646_1		N905516 Al905457 Al905515 AW176013 AW176	5037					
	452947 453420	939810_1 966433_1	AW130413 AJ003459							
	459170	920646_1		AI905516 AI905457 AI905515 AW176013 AW176	5037	•				
45										
	TABLE 20			-						
				an Eos probeset bers in this column are Genbank klentifier (GI) nu	mhere "Dimham I at al "refers to the ou	Nicetion entitled "The DNA sequence of				
				, et al. (1999) <u>Nature</u> 402:489-495	mbers. Dumbarra et al. reiers ware pu	STATE OF THE STATE				
50	Strand: Indicates DNA strand from which exons were predicted									
	Nt_positio	n: Indicates nucl	ectide position	ns of predicted exons						
	Clanu	Dof	Strand	All aggiffen						
	Pkey 400454	Ref 9929670		Nt_position 22074-22214						
55	400704	8118864		63110-63241						
	400749	7331445		9162-9293						
	401244	4827300		55359-56376 186786-187029,190607-190779,198218-198348						
	401537 401657	7960358 9100664		7312-8163						
60	402172	8575911		143378-143671						
	402425	9796347	Minus	50224-50395						
	402745	9212200		76516-76690						
	403074	8954241		143375-143561 146023-147222-147326-147628						
65	403077 403083	8954241 8954241	Plus Plus	146923-147222,147326-147628 163070-163351						
00	403089	8954241	Plus	171964-172239						
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813	l e					
	403093	8954241		177083-177373,177464-177751						
70	403411 403661	9438635 8705027	Minus Minus	104247-104420 30268-30482						
70	403687	7387384	Plus	9009-9534						
	403691	7387384	Minus	88280-88463						
	403763	7229888	Minus	43575-43887						
75	403796	8099896	Minus	75073-77664 7544-7001						
13	404187 404243	4481839 5672609	Plus Plus	7644-7991 74695-75123						
	404243	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965		•				
	404886	4884062	Plus	30058-30596						
oΛ	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731	45958,47296-47457,49549-49658,49790	-49904,50231-50342,53583-53667,54111-				
80	105005	£42057E	More	54279 55744,55003 57080,57170 61478,61560						
	405285 405545	6139075 1054740	Minus Plus	55744-55903,57080-57170,61478-61560 118677-118807,119091-119296,121626-12182	3					
	405547	1054740	Plus	124361-124520,124914-125050	-					
	405636	5123990	Plus	56384-56587						
				10	77					

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136364-136509,136579-136699,136805-136941 405790 1203968 Plus

TABLE 3A lists about 1643 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 1A, except that the ratio was greater than or equal to 15, and the denominator was the arithmetic mean value for various non-malignant ovary specimens obtained. 5

TABLE 3A: ABOUT 1643 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY Pkey: Primekey
Ex. Acon: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title
PFAM domains
ratio: tumor vs. normal tissues

10

	1800. 1011	01 13. 10111101 000			
15	Pkey	Ex. Acon No.	UGID	Title	ratio
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	219.9
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)	180.2 165.0
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP) fatty acid binding protein 5 (psoriasis-associated)	161.5
20	424799 442402	8E550723 NM_000954	Hs.153179 Hs.8272	prostaglandin D2 synthase (21kD, brain)	150.2
20	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human, odontogenic k	149.5
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (antileukoprotein	144.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	. 136.6
~ ~	428471	X57348	Hs.184510	stratifin	129.5
25	421978	AJ243662	Hs.110196	NICE-1 protein	108.7
	437191	NM_006846	Hs.5476	serine protease inhibitor, Kazal type, 5	106.2 105.5
	407788	BE514982	Hs.38991	S100 catclum-binding protein A2 solute carrier family 2 (facilitated glucose transporter),	103.6
	441565 431211	AW953575 M86849	Hs.169902 Hs.5566	gap junction protein, beta 2, 26kD (connexin 26)	102.1
30	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	95.3
30	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fundus d	87.0
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	86.1
	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	85.0
0.5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated protein	84.8
35	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	84.5 84.4
	452669	AA216363	Hs.262958	ESTs, Wealdy similar to alternatively spliced product u	83.8
	406711	N25514 M31212	Hs.77385 Hs.77385	myosin, light polypeptide 6, alkeli, smooth muscle and n myosin, light polypeptide 6, alkeli, smooth muscle and n	81.0
	406712 432680	T47364	Hs.278613	Interferon, alpha-inducible protein 27	81.0
40	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	77.8
10	409453	AJ885516	Hs.95612	ESTs	75.3
	424670	W61215	Hs.116651	epithelial V-like antigen 1	67.5
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium protein, calv	67.0
4.5	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	65.7
45	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, protein-glutamine-g	64.7 64.6
	456898	NM_001928	Hs.155597	D component of complement (adipsin) serine (or cysteine) proteinsse inhibitor, clade B (ovalbu	63.6
	423017 447990	AW178761 BE048821	Hs.227948 Hs.20144	small inducible cytokine subfamily A (Cys-Cys), memb	60.7
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from	60.3
50	414438	Al879277	Hs.76136	thioredoxin	59.9
•	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, sorta	58.9
	433336	AF017986	Hs.31386	ESTs, Highly similar to JE0174 frizzled protein-2 (H.sa	58.8
	403741			predicted exon	57.0 56.1
55	430637	BE160081	Hs.256290	S100 catclum-binding protein A11 (catgizzartn)	55.8
55	424098	AF077374	Hs.139322 Hs.183	small proline-rich prolein 3 Duffy blood group	55.6
	441591 426521	AF055992 AF161445	Hs.170219	hypothetical protein	55.5
	406713		Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	55.3
	406725		Hs.288061	actin, beta	54.1
60	422168		Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	54.1
• •	406755		Hs.94360	metallothionein 1L	54.0
	425593		Hs.1908	proteoglycan 1, secretory granute	53.3
	442257			gb:UI-HF-BNO-alb-b-05-0-UI.1 NIH_MGC_50 Homo	53.1 52.3
65	421957		Hs.109857	hypothetical protein DKFZp434H0820 small inducible cytokine A2 (monocyte chemotactic pro	51.2
65	447526		Hs.340 Hs.283305	Homo sapiens SNC73 protein (SNC73) mRNA, comple	51.0
	406722 427223		Hs.174031	cytochrome c oxidase subunit VIb	51.0
	414420		Hs.76095	Immediale early response 3	50.9
	417259		Hs.81800	chondroifin sulfate proteoglycan 2 (versican)	50.3
70	414191		Hs.75807	PDZ and LIM domain 1 (elfin)	49.5
	436906		Hs.181244	major histocompatibility complex, class I, A	49.0
	408000		Hs.620	bullous pemphigoid antigen 1 (230/240kD)	49.0 48.8
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	48.8
75	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma cluster 4 antig	48.7
13	421948 414662		Hs.111758 Hs.76807	keratin 6A major histocompatibility complex, class II, DR alpha	48.5
	414002		Hs.154424		48.5
	404767		110.101161	predicted exon	48.4
	418327		Hs.84136	paired-like homeodomain transcription factor 1	48.2
80	43672		Hs.3337	transmembrane 4 superfamily member 1	47.7
	41418	3 AW957446	Hs.301711		47.2
	40016			predicted exon	47.0 46.9
	43342		Hs.8997	heat shock 70kD protein 1A paired masodern homeo box 1	46.9 46.6
	42345	7 F08208	Hs.155606	hance these requirement with a	*****

	414085	AA114018		eldehyde dehydrogenase 6	46.0 45.6
	423189 438240	M59371 N92638		EphA2 ESTs	45.5
	430240	BE185289		small proline-rich protein 1B (comilin)	45.3
5	412774	AA120865	Hs.23136	ESTs	45.1
	407242	M18728		gb:Human nonspecific crossreacting entigen mRNA, co Human DNA sequence from clone 957N21 on chromos	44.8 44.8
	431292 403695	AA370141		predicted exon	43.5
	417365	D50683	Hs.82028	transforming growth factor, beta receptor II (70-80kD)	43.4
10	432331	W37862		Homo saplens mRNA; cDNA DKFZp586i1524 (from c	43.4 43.3
	424479	AF064238		smoothefin Interferon regulatory factor 6	43.2
	444726 432314	NM_006147 AA533447		ESTS	43.2
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	43.1
15	441406	Z45957		Homo sapiens cDNA FLJ10457 fis, clone NT2RP1001	42.7 42.6
	412969	A1373162	Hs.75103 Hs.23388	tyrosine 3-monoxygenase/typtophan 5-monoxygenas Homo sapiens cDNA: FLJ21310 fis, clone COL02160	42.5
	423720 400111	AL044191	NS.23300	predicted exon	42.4
	407207	T03651	Hs.179661	tubulin, beta polypeptide	42.4
20	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein A/B	42.2 41.9
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3 ESTs, Wealdy similar to WDNM RAT WDNM1 PROT	41.9
	439394 406657	AA149250 A1678644	Hs.56105 Hs.277477	major histocompatibility complex, class I, C	41.8
	451092	Al207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein, partial ods	41.6
25	412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-binding epidermal gro	41.6
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein-like protein HS	41.5 41.3
	428785 450988	Al015953 BE618571	Hs.125265 Hs.429	ESTs ATP synthase, H+ transporting, mitochondrial F0 comp	41.0
	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	40.8
30	405022			predicted exon	40.8
	408221	AA912183	Hs.47447	ESTs	40.8 40.7
	446500 421416	U78093 BE302950	Hs.15154 Hs.104125	sushi-repeat-containing protein, X chromosome adenytyl cyclase-essociated protein	40.6
	412247	AF022375	Hs.73793	vascular endothelial growth factor	40.5
35	410541	AA065003	Hs.64179	hypothetical protein ,	40.5
	406658	Al920965	Hs.77961	major histocompatibility complex, class I, B	40.0 40.0
	420225	AW243046	Hs.94789 Hs.84298	ESTs CD74 antigen (Invariant polypeptide of major histocom	39.4
	406825 443623	Al982529 AA345519	Hs.9641	complement component 1, q subcomponent, alpha poly	39.4
40	404201		Hs.103983	solute carrier family 5 (sodium lodide symporter), mem	39.3
	405138			predicted exon	39.1 39.0
	408733		Hs.254290 Hs.75721	ESTs profilin 1	38.9
	414044 430152		Hs.234642	equaporin 3	38.8
45	428121		Hs.182536	Homo saplens cDNA: FLJ21370 fis, clone COL03092	38.8
	434311		Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MAMMA10	38.7 38.5
	406140		Hs.279813	predicted exon hypothetical protein	38.4
	432918 420107		Hs.7886	pellino (Drosophila) homolog 1	38.4
50	427693		Hs.180370	cofilin 1 (non-muscle)	38.1
	448835		Hs.11081	ESTs, Wealdy similar to S57447 HPBRII-7 protein [H.	38.1 37.9
	432374		Hs.301885 Hs.184029	Homo sapiens cDNA FLJ11346 fis, clone PLACE1010 hypothetical protein DKFZp761A052	37.7
	428383 43625		Hs.107125	ESTs, Weakly similar to S57447 HPBRIL-7 protein [H.	37.7
55	42079		Hs,99936	keratin 10 (epidermolytic hyperkeratosis; keratosis paim	37.7
-	40032	7 M18679	Hs.247942	Human variant 5S rRNA-like gene and ORF, complete	37.6 37.6
	40178		Hs.253146	predicted exon ESTs	37.3
	44825 42841		Hs.184222	Down syndrome critical region gane 1	37.2
60	42420		. Hs.198241	amine oxidase, copper containing 3 (vascular adhesion p	37.2
	40681		Hs.67846	leukocyte immunogłobulin-like receptor, subfamily B (37.2 37.2
	42588		Hs.161002 Hs.287329		37.1
	43250 42178		Hs.21351	EST8	37.1
65	42798		Hs.181311	asparaginyl-tRNA synthetase	37.0
	41014		Hs.288819		36.8 36.7
	45132		Hs.109012 Hs.2128	ESTs dual specificity phosphatase 5	36.7
	41413 41460		Hs.76550	Homo saplens mRNA; cDNA DKFZp564B1264 (from	36.7
70	40178			predicted exon	36.5
	41146		Hs.70327	cysleine-rich protein 2	36.2 36.1
	41969		Hs.92323 Hs.80986	FXYD domain-containing ion transport regulator 3 ATP synthase, H+ transporting, milochondrial F0 comp	36.1
	41703 40671		Hs.169476		36.0
75	40254			predicted exon	36.0
	40860	9 Al493591	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	35.9 35.9
	4149		Hs.165544 Hs.155660		35.9
	4458 4066		Hs.77961	mator histocompatibility complex, class I, B	35.7
80	4074			gb:Human HMGI-C chimeric transcript mRNA, partial	35.6
	4125	24 AA417813	Hs.11177	ESTs	35.5 35.4
	4015		Hs.22144	predicted exon 1 ESTs	35.1
	4089 4067		Hs.18370		34.9
	-1007			100	

	440669 422658	Al206964 AF231981	Hs.250175	gbxqr30g06.x1 NCL_CGAP_GC6 Homo sapiens cDNA homolog of yeast long chain polyunsaturated fatty acid	34.8 34.8
		AW580939	Hs.97139	complement component C1g receptor	34.7
_	428600	AW883261	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC095 (H.sapi	34.7 34.5
5	409828	AW501137		gb:UI-HF-BP0p-zii-e-12-0-Ul.r1 NIH_MGC_51 Homo gb:601276347F1 NIH_MGC_20 Homo saplens cDNA	34.5
	459390 445055	BE385725 BE512856		glycoprotein, synaptic 2	34.3
	411789	AF245505	Hs.72157	Homo sapiens adlican mRNA, complete cds	34.3
10	410626	BE407727	Un C0046	gb:601299771F1 NIH_MGC_21 Homo saptens cDNA	34.2 34.2
10	410705 419273	AJ732404 BE271180	Hs.68846 Hs.293490	ESTs ESTs	34.2
	407839	AA045144	Hs.161566	ESTs	34.0
	444286	A1625304	Hs.190312	ESTs	34.0 34.0
15	449226	AB002365	Hs.23311 Hs.71721	KIAA0367 protein ESTs	33.9
15	414290 401245	Al568801	FIS. / 1 / 2 1	predicted exon	33.9
	425222	M85430	Hs.155191	villn 2 (ezrin)	33.8
	409950	R42678	Hs.301669	KIAA0564 protein amyloid beta (A4) precursor protein (protease nexin-ti,	33.8 33.7
20	437201 406566	F29279 AF088886	Hs.177486 Hs.11590	cathepsin F	33.7
20	405071	A 000000	113,11000	predicted expn	33.7
	455426	AW937792		gb:QV3-DT0045-140200-082-b07 DT0045 Homo sapl	33.6 33.5 ·
	415160	T82802		gb:yd38a04.r1 Soares felal liver spleen 1NFLS Homo s gb:HSC2FA041 normalized infant brain cDNA Homo s	33.5
25	424995 453870	Z45023 AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone LNG10019	33.5
23	433470	AW960564	Hs.3337	transmembrane 4 superfamily member 1	33.4
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermai type I, pro	33.3 33.3
	417409	BE272506	Hs.82109	syndecan 1 ESTs	33.3
30	425389 434658	AW974499 A1624436	Hs.192183 Hs.194488	ESTS	33.2
50	456562	AA306049	Hs.102669	DKFZP434O125 protein	33.1
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	33.0 32.9
	432360	BE045243	Hs.274416 Hs.1735	NADH dehydrogenase (ubiquinone) 1 alpha subcomple inhibin, beta B (activin AB beta polypeptide)	32.7
35	424125 419968	M31669 X04430	Hs.93913	Interleukin 6 (Interferon, beta 2)	32.7
55	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	32.6
	451541	BE279383	Hs.26557	plakophilin 3	32.6 32.4
	424499	N90344	Hs.149436	kinasin family mamber 58 predicted exon	32.4
40	402144 422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	32.4
-10	400231	7.00.07.12		predicted exon	32.3
	437712		Hs.85844	neurotrophic tyrosine kinase, receptor, type 1	32.3 32.2
	417433		Hs.82128 Hs.92186	5T4 oncofetal trophoblast glycoprotein Leman coiled-coil protein	32.0
45	419659 428582		Hs,185055	BENE protein	32.0
7.5	421401		Hs.104019	transforming, acidic colled-coll containing protein 3	32.0
	414064		Hs.16165	expressed in activated T/LAK lymphocytes	32.0 32.0
	431938		Hs.115242	developmentally regulated GTP-binding protein 1 gb:HSC19G051 normalized infant brain cDNA Homo s	31.9
50	411930 428150		Hs.182684	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	31.8
-	401887			predicted exon	31.8 31.7
	412570		Hs.74047	electron-transfer-flavoprotein, beta polypeptide growth differentiation factor 5 (cartilage-derived morph	31.6
	422738 453092		Hs.1573 Hs.31638	restin (Reed-Steinberg cell-expressed intermediate filam	31.5
55	413924		Hs.75616	KIAA0018 gens product	31.4
-	420231	R06866	Hs.19813	ESTs .	31.3 31.3
	434715		Hs.116410	ESTs gb:ye86f06.r1 Soares fetal liver spleen 1NFLS Homo sa	31.2
	422831 416854		Hs.80296	Purkinje celi protein 4	31.2
60	42297		Hs.1600	sec61 homolog	31.1
	42635			gb:601064837F1 NIH_MGC_10 Homo sapiens cDNA	31.0 30.8
	43393		Hs.44163 Hs.227823	13kDa differentiation-associated protein pM5 protein	30.8
	43004 40634		Hs.180370	contin 1 (non-muscle)	30.8
65	42605		Hs.166096	E74-like factor 3 (ets domain transcription factor, epith	30.7
	42510	5 BE280066	Hs.24956	hypothetical protein FLJ22056	30.7 30.7
	40206		Hs.13932	predicted exon 2 small proline-rich protein 3	30.6
	42953 41837		Hs.84298	CO74 antigen (invariant polypeptide of major histocom	30.4
70	42125		Hs.10294	3 enigma (LIM domain protein)	30.3 30.3
	45608		Hs.79708		30.3
	40202			predicted exon predicted exon	30.2
	40435 41597		Hs.26020		30.2
75	44598		Hs.13221	9 ESTs	30.1
. •	4504	40 AB024334	Hs.25001		30.1 30.1
	45878		Hs.20157	Homo saptens cDNA FLJ20848 fis, clone ADKA01732 predicted exon	30.1
	4008- 4068:		Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.0
80	4232		Hs.12617	7 Homo saplens mRNA; cDNA DKFZp4340192 (from c	30.0
	4513	83 AW239364		hypothetical protein FLJ12788	30.0 30.0
	4370		Hs.5420	hypothetical protein FLJ20695 gb:601299745F1 NIH_MGC_21 Homo septens cDNA	30.0
	4593 4256		4 Hs.1925	dasmoglein 3 (pemphigus vulgaris anligen)	30.0
	-200				

	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membrane protein	29.9
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 30)	29.7
	436651	BE045962	Hs.275998	ESTs	29.6
5	419766	BE243101	Hs.22391	chromosome 20open reading frame 3	29.5
5	420747	BE294407	Hs.99910	phosphofructoldnase, ptatelet	29.5 29.5
	436895 412765	AF037335 AK000620	Hs.5338 Hs.74571	carbonic anhydrase XII ADP-ribosylation factor 1	29.4
	419223	X60111	Hs.1244	CD9 antigen (p24)	29.4
••	413798	AW408094	Hs.75545	Interlaukin 4 receptor	29.4
10	447795	AW295151	Hs.163612	ESTs	29.4
	431103	M57399	Hs.44	plelotrophin (heparin binding growth factor 8, neurite g	29.4 29.3
	415314 428411	N88802 AW291464	Hs.5422 Hs.10338	glycoprotein M6B ESTs	29.3
	430580	AA806105	Hs.140	immunoglobulin heavy constant gamma 3 (Gm marker)	29.3
15	430451	AA836472	Hs.249982	cathepsin B	29.2
	453949	AU077146	Hs.36927	heat shock 105kD	29.2
	413859	AW992356	Hs.8364	pyruvale dehydrogenase kinase, Isoenzyme 4	29.2 29.1
	407845 453500	AL036518 Al478427	Hs.118598 Hs.43125	ESTs ESTs	29.1
20	456054	BE313241	110.40120	gb:601151545F1 NIH_MGC_19 Homo saplens cDNA	29.0
	453467	Al535997	Hs.30089	ESTs	29.0
	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	28.9
	421773	W69233	Hs.112457	ESTS	28.9 28.8
25	423621 408935	BE002904 BE539706	Hs.285363	gb:QV4-8N0090-070400-163-c07 BN0090 Homo sapi ESTs	28.8
23	450847	NM_003155	Hs.25590	stanniocalcin 1	28.8
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	28.7
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	28.7
20	433469	F12741		gb:HSC3DG061 normalized infant brain cDNA Homo	28.7
30	405783	UCO720	Hs.81892	predicted exon	28.7 28.7
	417308 400749	H60720	ns.0 (032	KIAA0101 gene product predicted exon	28.7
	413442	BE140643		gb:RCO-HT0015-310599-016 HT0015 Homo sapiens c	28.6
	404828			predicted exon	28.6
35	407453	AJ132087	•	gb:Homo saplens mRNA for exonemal dynein heavy ch	28.6
	418529	AW005695	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and nam	28.6 28.5
	413787 450690	Al352558 AA296696	Hs.75544 Hs.25334	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas FXYD domain-containing ion transport regulator 5	28.5
	402430	AAZ30030	FIS.23334	predicted exon	28.4
40	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	28.2
	423803	NM_005709	Hs.132945	POZ-73 protein	28.2
	406086			predicted exon	28.2
	416585	X54162	Hs.79386	telomodin 1 (smooth muscle)	28.2 28.1
45	417055 449184	N39489 AW296295	Hs.7258 Hs.196491	Homo saplens cDNA: FLJ22021 fis, clone HEP08253 ESTs	28.1
70	446542	NM_004281	Hs.15259	BCL2-associated athanogene 3	28.1
	412793	AW997986		gb:RC1-BN0056-230200-021-e11 BN0056 Homo sapie	28.0
	452818	W21909	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subunit	28.0
50	402869	44050044	U- 5204	predicted exon	27.9 27.9
30	436810 402075	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog predicted exon	27.9
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	27.8
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell adhesion molecul	27.8
~ ~	439766	AB033492	Hs.301241	Homo sapiens mRNA; cDNA DKFZp586A0424 (from	27.7
55	424482	BE268621	Hs.149155	voltage-dependent anion channel 1	27.6
	420737 414663	L08096	Hs.99899	tumor necrosis factor (ligand) superfamily, member 7 gb:601289258F1 NIH_MGC_8 Homo sapiens cDNA c	27.6 27.6
	409703		Hs.56009	2-5 olipoadenylate synthetase 3	27.6
1 -	445108		Hs.102773	ESTs	27.5
60	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	27.5
	445688	A1248205	Hs.153244	ESTs	27.5
	405411	Horceo	Hs.61796	predicted exon transcription factor AP-2 gamma (activating enhancer-b	27.5 27.5
	410275 424675		Hs.151641	glycoprolein A repetitions predominant	27.3
65	450455		Hs.25035	chloride intraceilular channel 4	27.3
	414855		Hs.104640	HIV-1 Inducer of short transcripts binding protein	27.2
	433578		Hs.3416	adipose differentiation-related protein	27.2
	401994		11- 455445	predicted exon ESTs	27.2 27.2
70	445033 402277		Hs.155145	predicted exon	27.1
, 0	428106		Hs.182470	PTD010 protein	27.1
	448625		Hs.178470	Homo septens cDNA: FLJ22662 fis, clone HSI08080	27.1
	422587	AI879352	Hs.118625	hexokinase 1	27.0
75	457204		Hs.221994	ESTs	27.0
75	444094		Hs.202394 Hs.75725	ESTs transgelin 2	27.0 26.9
	414053 430511		Hs.2575	calpain 1, (mu/l) large subunit	26.9
	434039		Hs.3712	ubiquinol-cytochrome c reductase, Rieske iron-sulfur po	26.9
00	424939		Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, partial cds	26.9
80	414539			gb:601236646F1 NIH_MGC_44 Homo sapiens cDNA	26.9
	404675		Hs.110950	predicted exon	26.8 26.8
	401597 401405		113.110330	Rag C protein predicted exon	26.8
	411541			gb:za62b02_r1 Soares (eta) liver spleen 1NFLS Homo sa	26.8

	412025	AI827451	Hs.24143	ESTs	26.7
	414276	BE297862		gb:601174780F1 NIH_MGC_17 Homo sapiens cDNA	26.7
	444065	AW449415	Hs.10260	Homo saplens cDNA FLJ11341 fis, clone PLACE1010	26.7
	447981		Hs.8929		
5		R53772		hypothetical protein FLJ11382	26.7
5	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	26.5
	400982			predicted exon	26.5
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone HRC08686	26.5
	407233	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecul	26.4
	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit, alpha type, 7	26.3
10	448218	Al188489		gb:qd09b12.x1 Soares_placenta_8to9weeks_2NbHP8to	26.3
•			th 75449		26.2
	413511	AI627178	Hs.75412	Arginina-rich protein	
	459511	Al142379		gb:qg64c01.r1 Soares_testis_NHT Homo sepiens cONA	26.2
	410668	BE379794	Hs.65403	hypothetical protein	26.2
	458662	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	26.2
15					
15	451219	AA054209	Hs.167904	ESTs	26.2
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	26.2
	400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	26.2
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from c	26.2
00	421177	AW070211	Hs.102415	Homo saplens mRNA; cDNA DKFZp586N0121 (from	26.1
20	433848	AF095719	Hs.93764	carboxypeptidase A3	26.1
	448497	BE613269	Hs.21893	ESTs, Wealty similar to glycerol 3-phosphate permease	26.1
	415279	F04237	Hs.1447	glial fibrillary acidic protein	26.0
•	419323	A1092379	Hs.135275	ESTs	26.0
	430265	L36033	Hs.237356	stromal cell-derived factor 1	25.9
25	437679	NM_014214	Hs.5753	Inositol(myo)=1(or 4)-monophosphatase 2	25.9
23					
	425535	AB007937	Hs.158287	KIAA0468 gene product	25.8
	412923	AA179922	Hs.75056	adapter-related protein complex 3, delta 1 subunit	25.8
	447980	Al703397	Hs.202355	ESTs	25.8
	419118	AA234223	Hs.139204	ESTs	25.8
30	421224	AW402154	Hs.125812	ESTs	25.8
	414890	BE281095	Hs.77573	uridine phosphorylase	25.8
	447330	BE279949	Hs.18141	ladinin 1	25.7
	405610			predicted exon	25.7
	447604	AW089933	Hs.293674	ESTs	25.7
35					25.7
22	445677	H96577	Hs.6838	ras homolog gene family, member E	
	456088	BE177320	Hs.156148	Homo sapiens cDNA: FLJ23082 fis, clone LNG06451	25.7
	417120	N79687	Hs.46616	ESTs	25.6
	405194			predicted exon	25.6
		110 1000	11-05400		
40	410687	U24389	Hs.65436	lysyl oxidase-like 1	25.6
40	421888	AA299780	Hs.121036	ESTs	25.6
	420459	AF016045	Hs.97905	ovo (Drosophila) homolog-like 1	25.5
	416323	N72630	Hs.33981	Homo sapiens genomic DNA, chromosome 21q, section	25.5
	446292	AF081497	Hs.279682	Rh type C glycoprotein	25.5
	416274	AW160404	Hs.79126	guanine nucleotide binding protein 10	25.5
45					25.5
43	430028	BE564110	Hs.227750	NADH dehydrogenase (ublquinone) 1 beta subcomplex	
	438450	A1050866	Hs.65853	nodal, mouse, homolog	25.5
	400215			predicted exon	25.4
		H59354	Hs.182485		25.4
	430014			actinin, alpha 4	
	453582	AW854339	Hs.33476	hypothetical protein FLI11937	25.4
50	405867			predicted exon	25,4
	459170	AI905518		gb:RC-BT091-210199-098 BT091 Homo saplens cDNA	25.4
			11- 000707		25.4
	407944	R34008	Hs.239727	desmocollin 2	
	415748	D90086	Hs.979	pyruvate dehydrogenase (lipoamide) beta	25.3
	423287	H38340		gb:yp70h07.r1 Soares adult brain N2b4HB55Y Homo s	25.3
55	450944	AA554989	Hs.209061	sudD (suppressor of blmD6, Aspergillus nidulans) homo	25.3
55					
	432906	8E265489	Hs.3123	lethal glant larvae (Drosophila) homolog 2	25.3
	400104			predicted exon	25.3
	449019	AI949095	Hs.67776	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	25.3
			113.07770		
C O	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, partial cds.	25.3
60	402639			predicted exon	25.3
-	447147	AA910353	Hs.292815	ESTs	25.3
					25.3
	453379	AA035261	Hs.61753	ESTs	
	414217	A1309298	Hs.279898	Homo saplens cDNA: FLJ23165 fis, clone LNG09846	25.3
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	25.3
65	406685	M18728		gb:Human nonspecific crossreacting antigen mRNA, co	25.3
UJ			11- 007004		
	444747		Hs.257291	ESTs, Weakly similar to PSS8_HUMAN PROSTASIN	25.2
	417883	R22519	Hs.23398	ESTs	25.2
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	25.2
70	459001	Al761313	Hs.204605	ESTs	25.2
70	434368	AW519020	Hs.212640	Homo sapiens cDNA FLJ13265 fis, clone OVARC1000	25.2
	415917	Z43912		gb:HSC1OA111 normalized infant brain cDNA Homo	25.2
	444409		Hs.49265	ESTs	25.2
	428578		Hs.82148	hypothetical protein	25.1
_	433417	AA587773	Hs.136494	ESTs	25.1
75	426372		Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeplide 21	25.1
, 5		GC304000	1 10 10 200 1		
	402131			predicted exon	25.1
	450545	AW135582	Hs.201767	ESTs	25.0
	434162		Hs.116136	ESTs	25.0
			110.110130		
00	406571			predicted exon	24.9
80	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (P	24.9
-	409402		Hs.695	cystalin B (stefin B)	24.9
					24.9
	400135			predicted exon	
	428403	AJ393048	Hs.239894	leucine rich repeat (in FLII) interacting protein 1	24.9
	403223			predicted exon	24.8
	100000				

	435236	T03890	Hs.157208	ESTs, Highly similar to Arx homeoprotein (M.musculu	24.8
	457439	AW410408	Hs.271167	L-olpecolic acid oxidase	24.8
	448667	Z78394			
			Hs.4896	Homo saplens cDNA: FLJ22046 fis, clone HEP09276	24.8
•	440605	Z40094	Hs.185698	ESTs	24.8
5	426724	AA383623	Hs.293616	ESTs	24.8
	403359			predicted exon	24.7
	442826	AI018777	Hs.131241	ESTs	24.7
	411503	AW190338	Hs.28029		
			115.20029	purinergic receptor P2X, ligand-gated ion channel, 4	24.6
10	414540	8E379050		gb:601236655F1 NIH_MGC_44 Homo sapiens cDNA	24.6
10	421595	AB014520	Hs. 105958	Homo saplens cDNA: FLJ22735 fis, clone HUV00180	24.5
	438802	AA825976	Hs.136954	ESTs	24.5
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation transporter), me	24.5
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
	426383		15.05540		
15		BE537380		gb:601064570F1 NIH_MGC_10 Homo saplens cDNA	24.4
15	418408	AA219321	Hs.173294	ESTs	24.4
	416186	W87575	Hs.269177	ESTs	24.4
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	24.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	24.4
	439706			ESTs	24.4
20		AW872527	Hs.59761		
20	441619	NM_014056	Hs.7917	DKFZP564K247 protein	24.4
	417198	F11533	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 comp	24.3
	433662	W07162	Hs.150826	CATX-8 protein	24.3
	453986	M13232	Hs.36989	coagulation factor VII (serum prothrombin conversion a	24.3
	457123	AA770021	Hs.16332	ESTs	24.3
25	433864	AA931550	Hs.192785	ESTs	24.3
	409865	AW502208	15.152700		24.3
			U- 005400	gb:UI-HF-BR0p-sju-e-09-0-UI.r1 NIH_MGC_52 Hom	
	448175	BE296174	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	24.3
•	406277			predicted exon	24.3
22	451957	Al796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PLACE1006	24.3
30	408802	AL048269	Hs.288544	Homo sapiens cDNA: FLJ20882 fis, clone ADKA0320	24.2
	401757			predicted exon	24.2
	444751	AI207406	Hs.11866	hypothetical protein PRO1197	24,2
			115.11000		
	408647	AW245831		gb:2822937.5prime NIH_MGC_7 Homo saplens cDNA	24.2
25	418870	AF147204	Hs.89414	chemokine (C-X-C molif), receptor 4 (fusin)	24.2
35	436913	AA789074	Hs.187478	ESTs	24.2
	434745	AW974445	Hs.185155	ESTs, Weakly similar to HuEMAP [H.saplens]	24.2
	451743	AW074266	Hs.23071	ESTs	24.2
	421853	AL117472	Hs.108924	DKFZP586P1422 protein	24.2
	407926	AW956382	Hs.59771	ESTs	24.1
40					
40	413973	BE279858	Hs.128417	Homo saplens cDNA FLJ14009 fis, clone Y79AA1002	24.1
	439078	AF085936		gb:Homo sapiens full length insert cDNA clone YR58F	24.1
	401913			predicted exon	24.1
	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo saplens cDNA	24.1
	405311			predicted exon	24.0
45	413127	BE066529	Hs.83484	SRY (sex determining region Y)-box 4	24.0
	430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) receptor 1A	24.0
	434445	Al349306	Hs.11782	ESTS	24.0
	418166	Al754416	Hs.260024	Cdc42 effector protein 3	24.0
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	23.9
50	401167			predicted exon	23.9
	454163	AW175997		gb:QV0-8T0078-190899-005-E02 BT0078 Homo sapl	23.9
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic reticulum/	23.9
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	23.9
<i>E E</i>	450796	NM_001988	Hs.25482	envoplakin	23.8
55	442199	BE277633	Hs.286027	eloposide-induced mRNA	23.8
	402699			predicted exon	23.8
	426143	BE379838	Hs.167106	proteasome (prosome, macropain) subunit, alpha type, 3	23.8
	437592	NM_003851	Hs.5710 ·	cellular repressor of E1A-stimulated genes	23.8
	433598	AI762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN ALU SU	23.8
60		- WI 02000	113.41 1400		23.8
UU	401088	11001074	11- 404400	predicted exon	
	445924	AI264571	Rs.164166	ESTS	23.8
	420902	AA742277		gb:ny28e09.s1 NCI_CGAP_GC81 Homo saplens cDN	23.8
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog	23.8
	458698	AW452189	Hs.257528	ESTs	23.7
65	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	23.7
	413460	R61610	Hs.21527	ESTs, Weakly similar to KIAA0918 protein (H.sapiens	23.6
	401575				23.6
		AAE46040		predicted exon	23.6
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	
70	427276	AA400269	Hs.49598	ESTs	23.6
70	417069	AA442192	Hs.81097	cytochrome c oxidase subunit VIII	23.5
	400161			predicted exon	23.5
	417190	NM_001359	Hs.81548	2,4-dianoyi CoA reductase 1, mitochondrial	23.5
	443667	Al129066	Hs.135457	ESTs	23.5
	413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo saple	23.5
75		5017120			23.5
, 5	400685	MMC045	11. 00000	predicted exon	
	422090	W05345	Hs.293884	ESTs	23.4
	432517	AF275816	Hs.283096	PR domain containing 9	23.4
	405307			predicted exon	23.4
	416328	H48389	Hs.268886	ESTs	23.4
80	427174	AA398848	Hs.97541	ESTs	23.4
	426148	AI751071	Hs.167135	Homo saplens cDNA FLJ10728 fis, clone NT2RP3001	23.3
	452544	AW851888		gb:QV0-CT0225-131099-034-d05 CT0225 Homo saple	23.3
		ATTO-1000			23.3
	404890	*****	11-4-6	predicted exon	
	408725	AA131539	Hs.15669	ESTs	23.3

	400000				
	428362	AA426555	Hs.169333	ESTs	23.3
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5-phosphate ep	23.3
	422440	NM_004812	Hs.116724	aldo-kelo reductase family 1, member 811 (aldose redu	23.3
_	410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	23.2
5	411796	AA807197	Hs.6918	ESTs	23.2
	458954	AW379075	Hs.141742	Homo saplens cDNA FLJ12211 fis, clone MAMMA10	23.2
	408896	AI610447	Hs.48778	niban protein	23.2
	457024	AA397546	Hs.119151	ESTs	23.2
10	414591	AI888490	Hs.55902	ESTs	23.2
10	437846	AA773866	Hs.244569	ESTs .	23.2
	401220			predicted exon	23.1
	421747	AI816224	Hs.107747	DKFZP566C243 protein	23.1
	452950	AA428123	Hs.7745	17kD fetal brain protein	23.1
16	414327	BE408145	Hs.185254	ESTs, Moderately similar to NAC-1 protein [R.norvegic	23.1
15	405256			predicted exon	23.1
	452416	AA026115	Hs.114777	ESTs	23.1
	440684	Al253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NESTI (H.sap	23.1
	445603	H08345	Hs.106234	ESTs	23.1
20	436306	AA805939	Hs.117927	ESTs	23.1
20	434867	AF159442	Hs.103382	phospholipid scramblase 3	23.0
	404727	A120.4022	U- 974464	predicted exon	23.0 23.0
	407317 405580	Al204033	Hs.271461	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA predicted exon	23.0
	437898	W81260	Hs.43410	ESTs .	22.9
25	448781	AW243419	Hs.254048	ESTs .	22.9
23	457297	AW968188	Hs.290999	ESTs S	22.9
	405545	A11300100	1 15.230333	predicted exon	22.9
	431562	AI884334	Hs.11637	ESTs	22.9
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from c	22.9
30	439848	AW979249	113.1310	gb:EST391359 MAGE resequences, MAGP Homo sap	22.9
50	418149	AA811473	Hs.291877	ESTS	22.9
	439332	AW842747	Hs.293314	ESTs, Highly similar to unnamed protein product [H.sa	22.8
	401566	MIGHE	18.20014	predicted exon	22.8
	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	22.8
35	406684	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecul	22.8
-	421651	AW860612	Hs.283586	ESTs	22.8
	421064	Al245432	Hs.101382	tumor necrosis factor, alpha-induced protein 2	22.8
	441249	AA971585	Hs.166250	ESTs	22.8
	457624	AA809159	Hs.287581	Homo seplens cDNA FLJ13544 fis, clone PLACE1006	22.8
40	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33) mRNA, p	22.8
	459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
	436827	H72187	Hs.5322	guantne nucleotide binding protein (G protein), gamma	22.7
	418174	1.20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	22.7
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin transporter), mem	22.7
45	456035	N54956	Hs.271726	ESTs	22.7
	457867	AA045767	Hs.5300	bladder cancer associated protein	22.7
	440401	Al126341	Hs.143887	ESTs	22.7
	400126			predicted exon	22.7
	414931	AK000342	Hs.77646	Homo saplens mRNA; cDNA DKFZp761M0223 (from	22.7
50	406719	A1832962	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	22.6
	439675	W95357	Hs.138860	Rho GTPase activating protein 1	22.6
	456058	N94587	Hs.55063	ESTs	22.6
	441926	Al015051	Hs.130953	ESTs	22.6
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exchanger), is	22,6
55	438518	BE561958	Hs.285823	immunoglobulin heavy constant mu	22.6
	420674	NM_000055	Hs.1327	butyrylcholinesterase	22.6
	422160	AW582898		gb:ta07e04.y1 Human Pancreatic Islets Homo saplens c	22.5
	412408	D51103	Hs.73851	ATP synthase, H+ transporting, mitochondrial F0 comp	22.5
60	400964	41104545	11. 40	predicted exon	22.5
OU	434360	AW015415	Hs.127780	ESTs	22.5
	427977	AW630727	Hs.181307	H3 histone, family 3A	22.4 22.4
	450339	AI693281	Hs.54547	EST8	
	424059	AW451266	Hs.107418	ests gb:601303308F1 NIH_MGC_21 Homo sapiens cDNA	22.4 22.4
65	414626	BE410589			
UJ	401991 419741	NM_007019	Hs.93002	predicted exon ublquitin carrier protein E2-C	22.4 22.3
		U25750	Hs.210783	Human chromosome 17g21 mRNA clone 1046:1-1	22.3
	457952 422597	8E245909	Hs.118634	ATP-binding cassette, sub-family B (MDR/TAP), mem	22.3
	429504		Hs.204238	lipocalin 2 (oncogene 24p3)	22.3
70	447306	AJ373163	Hs.170333	ESTs	22.3
, ,	424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino acid transporter,	22.3
	422739		Hs.119591	edaptor-related protein complex 2, sigma 1 subunit	22.2
	432504		Hs.277704	oxygen regulated protein (150kD)	22.2
_	423804		Hs.1706	interferon-stimulated transcription factor 3, gamma (48k	22.2
75	404683	A1924294	Hs.173259	uncharacterized bons marrow protein BM033	22.2
. •	441624		Hs.179666	uncharacterized hypothalamus protein HSMNP1	22.2
	425751	T19239	Hs.1940	crystallin, alpha B	22.2
	452976		Hs.101189	ESTs	22.2
	414642			gb:zi03h01.r1 Soares_pregnant_uterus_NbHPU Homo	22.2
80	437452		Hs.7104	Homo septens mRNA; cDNA DKFZp761P06121 (from	22.2
	417426		Hs.82124	laminin, beta 1	22.2
	414774		Hs.77274	plasminogen activator, urokinase	22.1
	424631	AA688021	Hs.179808	ESTs	22.1
	413967	AW204431	Hs.117853	ESTs	22.1

	400174			and the state of t	
				predicted exon	22.1
	431837	T79326	Hs.298262	ESTs, Wealthy similar to dJ88J8.1 [H.saplens]	22.1
	401628			predicted exon	22.1
_	418374	AJ011916	Hs.84359	hypothetical protein	22.0
5	429297	X82494	Hs.198862	fibulin 2	22.0
-	403508	TOLIOT	113.130002		
		41047747		predicted exon	22.0
	432638	AI017717	Hs.126525	chromosome 21 open reading frame 15	22.0
	407382	AA503620		gb:ne49b08.s1 NCI_CGAP_Co3 Homo saplans cDNA	22.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	22.0
10	420185	AL044056	Hs.158047	ESTs	22.0
	409545	BE296182		gb:601177324F1 NIH_MGC_17 Homo saptens cDNA	22.0
	426662		U- 400740		
		AA879474	Hs.122710	ESTs	22.0
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	22.0
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDNA clone EU	21.9
15	422447	AA310711	Hs.124340	ESTs	21.9
	421574	AJ000152	Hs.105924	defensin, beta 2	21.9
	435302	Al076259	Hs.190337	ESTs	21.9
	414527	BE241739	Hs.76359	catalase	21.9
~~	441436	AW137772	Hs.185980	ESTs	21.9
20	454178	AW177274		gb:CM2-CT0128-230899-005-a02 CT0128 Homo saple	21.8
	448838	BE614761		gb:601281335F1 NIH_MGC_39 Homo saplens cDNA	21.8
			11- 404040		
	427889	Al400968	Hs.181046	dual specificity phosphatase 3 (vaccinia virus phosphat	21.8
	441114	AA917466	Hs.126600	ESTs	21.8
~ -	451831	NM_001674	Hs.460	activating transcription factor 3	21.8
25	405600	_		predicted exon	21.8
	446981	AI652743	Hs.197497	ESTs	21.8
	432839	AA579465		ESTs	
		AA3/9403	Hs.287332		21.8
	405208			predicted exon	21.8
• •	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeast) homolog	21.7
30	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	21.7
	423515	AA327017	Hs.162204	ESTs	21.7
	452329	N36626	Hs.29106	mitogen-activated protein kinase phosphatase x	21.7
	423050	AA320946		gb:EST23529 Adipose tissue, brown Homo saplens cD	21.7
	413679	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo saple	21.7
35	442166	AW845280	Hs.204723	ESTs	21.6
• •	4455B5	Al243836	Hs.147066	ESTs	21.6
		AIZ-10000	113.141000		
	406160			predicted exon	21.6
	433025	AA374743	Hs.279920	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	21.6
	446598	AW250546		gb:2821774.5prime NIH_MGC_7 Homo sapiens cDNA	21.6
40	434493	AA635305	Hs.121574	ESTs	21.6
	429582	AI569068	Hs.22247	ESTs	21.6
		M303000	113.22.21		
	403796			predicted exon	21.6
	405028			predicted exon	21 <i>.</i> 6
	426597	AA382250	Hs.145601	ESTs	21,6
45	437308	AA749417	Hs.292353	ESTs	21.6
	447384	Al377221	Hs.4052B	ESTs	21.6
	429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	21.6
	437068	AA743643	Hs.291427	ESTs	21.6
	418509	AB028624	Hs.85539	ATP synthase, H+ transporting, mitochondrial F0 comp	21.5
50	432999	BE294029	Hs.279903	Ras homolog enriched in brain 2	21.5
	407663	NM_016429	Hs.37482		
				COPZ2 for nonclathrin coat protein zeta-COP	21.5
	446627	AI973016	Hs.15725	hypothetical protein SB8I48	21.5
	413605	BE152644		gb:CM1-HT0329-250200-128-f09 HT0329 Homo sapie	21.5
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway substrate 8	21.5
55	405226			predicted exon	21.4
	402570				
			11. 000440	predicted exon	21.4
	457960	AA771881	Hs.298149	ESTS	21.4
	400684			predicted exon	21.4
	425943	H46986	Hs.31861	ESTs	21.4
60	434240	AF119912	Hs.258119	hypothetical protein PRO3073	21.4
	448376		Hs.196963		
		AI494332		ESTs	21.4
	408089	H59799	Hs.42644	thioredoxin-like	21.4
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33) mRNA, part	21.4
	412652	AI801777	Hs.6774	ESTs	21.4
65	428373	Al751656	Hs.183986	poliovirus receptor-related 2 (herpesvirus entry mediato	21.3
	416138	C18946	Hs.79026	myeloid leukernia factor 2	21.3
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen included)	21.3
	411028	AW813703		gb:RC3-ST0197-130100-014-h09 ST0197 Homo sapien	21.3
	417438	Z43989	Hs.82141	Human clone 23612 mRNA sequence	21.3
70	417534	NM_004998	Hs.82251	myosin IC	21.3
. •					
	427767	AI8792B3	Hs.180714	cytochrome c oxidase subunit Via polypeptide 1	21,2
	433300	AA582307		gb:nn49d09.s1 NCI_CGAP_Kd6 Horno sapiens cDNA	21.2
	452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	21.2
	411939	Al365585	Hs.146246	ESTs .	21.2
75	435060	Al422719	Hs.233349	ESTs, Weakly similar to fork head like protein [H.saple	21.2
	432412	A1470549	Hs.162201	ESTs	21.2
	407491	S82769		gb:GABAA receptor gamma 3 subunit [human, fetal bra	21.2
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mobility group p	21.1
	426254	BE018103	Hs.168541	Homo saplens mRNA full length insert cDNA clone EU	21.1
80	458188				
55		AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	21.1
	406215			predicted exon	21.1
	425461	AK000602	Hs.157938	hypothetical protein FLJ20595	21.1
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fls, clone NT2RM4002	21.1
	409415	AA579258	Hs.6083	Homo saplens cDNA: FLJ21028 fis, clone CAE07155	21.1
				,	~***

	408546	W49512	11- 40240	h-444-1 1-04	
	450008	H52970	Hs.46348 Hs.36688	bradykinin receptor B1 WAP four-disutifide core domain 1	21.1 21.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	21.1
_	438901	AF085834	Hs.29038	ESTs	21.1
5	440500	AA972165	Hs.150308	ESTs .	21.1
	413101 447452	8E065215 8E618258	Hs.102480	gb:RC1-BT0314-310300-015-f01 BT0314 Horno saple ESTs	21.1
	412446	AI768015	Hs.92127	ESTs .	21.1 21.1
10	418975	T75496	Hs.296980	ESTs	21.0
10	454961	AW847807		gb:lL3-CT0213-190200-040-E12 CT0213 Homo saplen	21.0
	401072			predicted exon	21.0
	401204 433526	AF078859	Hs.86347	predicted exon hypothetical protein	21.0 21.0
	418047	R37633	Hs.4847	ESTs	21.0
15	443380	Al792478	Hs.135377	ESTs	21.0
	427424	AA402453	Rs.113011	ESTs	21.0
	433412 422599	AV653729 BE387202	Hs.8185 Hs.118638	CGI-44 protein; sulfide dehydrogenase like (yeast)	21.0 20.9
	435656	R93409	Hs.120759	non-metastatic cells 1, protein (NM23A) expressed in ESTs	20.9
20	413745	AW247252	Hs.75514	nucleoside phosphorylase	20.9
	418874	T60872		gb:yb72h11.s1 Stratagene ovary (937217) Homo sapten	20.9
	452574 400332	AF127481 S66407	Hs.35093	lymphoid blast crisis oncogene	20.9
	400332	300407	Hs.248032	FLT4 predicted exon	20.9 20.9
25	427138	N77624	Hs.173717	phosphatidic acid phosphalase type 28	20.9
	432038	AA524746	Hs.162110	EST8	20.8
	423711	AF059194	Hs.131953	v-mai musculoaponeurolic fibrosarcoma (avlan) oncoge	20.8
	402297 405133			predicted exon	20.8
30	436661	Al125270	Hs.128069	predicted exon ESTs, Weakly similar to similar to collagen [C.elegans]	20.8 20.8
•	437836	BE269291	Hs.292458	ESTs	20.8
	437329	AA811977	Hs.291761	ESTs .	20.8
	445830	H10451	Hs.42656	Horno saplens cDNA FLJ12667 fis, clone NT2RM4002	20.8
35	406824 421271	AW515961 AW170057	Hs.84298 Hs.133179	CD74 antigen (Invariant polypeptide of major histocom ESTs	20.7 20.7
55	400256	ATTIOON	16.100173	predicted exon	20.7
	41402B	AA782576	Hs.4944	Homo saptens cDNA FLJ12783 fts, clone NT2RP2001	20.7
	456728	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	20.7
40	417707 438713	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	20.7
+0	450306	H16902 AL080080	Hs.6749 Hs.24766	ESTs DKFZP564E1962 protein	20.7 20.7
	438898	Al819863	Hs.106243	ESTs	20.7
	403273			predicted exon	20.7
45	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens cDNA	20.7
43	401283 403703			predicted exon	20.7
	416969	AI815443	Hs.283404	predicted exon organic cation transporter	20.6 20.6
	442400	AW381148	Hs.3593	ESTs	20.6
50	447563	BE536115	Hs.160983	ESTs	20.5
50	419754	H52299	Hs.75243	bromodomain-containing 2	20.5
	408204 450507	AA454501 AW295603	Hs.43666 Hs.250891	protein tyrosine phosphatase type IVA, member 3 ESTs	20.5 20.5
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	20.5
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo saple	20.5
55	432140	AK000404	Hs.27268B	hypothetical protein FLJ20397	20.5
	400642 431582	E07420	U- 004000	predicted exon	20.4
	442724	F07136 AA355525	Hs.261828 Hs.159604	G protein-coupled receptor kinase 7 cysteinyl-IRNA synthetase	20.4 20.4
	417861	AA334551	Hs.82767	sperm specific anligen 2	20.4
60	402948			predicted exon	20.4
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo saple	20.4
	435478 447955	AA682622 BE544271	Hs.288390	gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Ho Homo sapiens cDNA: FLJ22795 fis, clone KAIA2543	20.4
	433592	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog) 1	20.3 20.3
65	420865	N73241	Hs.100001	solute carrier family 17 (sodium phosphate), member 1	20.3
	449482	Al784266	Hs.28774	ESTs	20.3
	400807	1105490	11- 02044	predicted exon	20.3
	419942 420783	U25138 Al659838	Hs.93841 Hs.99923	potassium large conductance calcium-ectivated channel lectin, galactoside-binding, soluble, 7 (galectin 7)	20.3 20.3
70	402986	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)	20.3
	451375	. AI792066	Hs.283902	Homo saplens BAC done RP11-481J13 from 2	20.3
	453586	AA248089	Hs.50841	ESTs, Weakly similar to tuftelin [M.muscutus]	20.3
	433090 425053	Al720050 AF046024	Hs.145362 Hs.154320	Immortalization-upregulated protein	20.3 20.3
75	425053	U41518	Hs.74602	ubiquitin-activating enzyme E1C (homologous to yeast aquaporin 1 (channel-forming integral protein, 28kD)	20.3
•	409738	BE222975	Hs.56205	insulin induced gane 1	20.3
	428245	AF151048	Hs.183180	hypothelical protein	20.2
	412582	BE270631	Hs.74077	proteasome (prosome, macropain) subunit, alpha type, 6	20.2
80	406207 400931			predicted exon predicted exon	20.2 20.2
-	410709	AL122109	Hs.65735	Homo sapiens mRNA; cDNA DKFZp434M1827 (from	20.2
	428438	NM_001955	Hs.2271	endothelin 1	20.2
	446918	AL135125	Hs.13913	KIAA1577 protein	20.2
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.2

	420112	Danae	Un 40000/		20.2
	429113 414511	D28235 AA148725	Hs.196384 Hs.12969	prostaglandin-endoperoxide synthase 2 (prostaglandin G hypothetical protein	20.2 20.2
	451548	AF051782	Hs.26584	Homo sapiens clone CDABP0038 mRNA sequence	20.1
_	441899	Al372588	Hs.8022	TU3A protein	20.1
5	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	20.1
	411014	AW816072		gb:MR3-ST0220-070100-021-h07 ST0220 Homo saple	20.1
	451400 459247	BE160479 N46243	Hs.110373	gb:QV1-HT0413-210200-081-g05 HT0413 Homo sapi ESTs	20.1 20.1
	441633	AW958544	Hs.112242	ESTS	20.1
10	427466	AA523543	Hs.7678	cellular retinoic acid-binding protein 1	20.0
	405893	M22406		gb:Human Intestinal mucin mRNA, partial cds, clone SM	20.0
	406268			predicted exon	20.0
	403348			predicted exon	20.0
15	400970 414045	NM_002951	Hs.75722	predicted exon ribophorin II	20.0 20.0
10	427169	AA398823	Hs.97549	EST	20.0
	405586			predicted exon	20.0
	445834	AI913290	Hs.145532	ESTs, Weakly similar to Gag polyprotein [M.musculus	20.0
20	422525	AA758797	Hs.192807	ESTs .	20.0
20	425383 454590	D83407 AW809762	Hs.156007 Hs.222056	Down syndrome critical region gene 1-like 1	20.0 20.0
	411529	AA430348	Hs.288837	Homo sepiens cDNA FLJ11572 fis, clone HEMBA100 Homo sepiens cDNA FLJ12927 fis, clone NT2RP2004	20.0
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	20.0
25	403234			predicted exon	19.9
25	427267	Al201185	Hs.119164	ESTs	19.9
	400203	41 407057	Hs.23458	predicted exon	19.9
	449296 406704	AL137257 M21665	Hs.23458 Hs.929	Homo saplens mRNA; cDNA DKFZp434C1613 (from myosin, heavy polypeptide 7, cardiac muscle, beta	19.9 19.9
	423083	AA321774	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTEIN PH	19.9
30	422112	BE540240	Hs.111783	Lsm1 protein	19.9
_	413282	BE078159		gb:CM0-BT0615-140200-175-e06 BT0615 Homo saple	19.9
	453702	AA037637	Hs.42128	ESTs	19.9
	403065	414 40000		predicted exon	19.9
35	440633 456994	Al140686 AA383623	Hs.263320 Hs.293616	ESTs ESTs	19.9 19.9
55	458260	R41782	Hs.22279	ESTs	19.9
	452388	BE019696	Hs.29287	retinoblastoma-binding protein 8	19.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	19.9
40	441989	AA306207	Hs.285241	Homo saplens cDNA: FLJ22698 fis, clone HSI12044	19.9
40	418758	AW959311	Hs.87019	EST8	19.9
	406646 433053	M33600 BE301909	Hs.180255 Hs.279952	major histocompatibility complex, class II, DR beta 1 glutathione S-transferase subunit 13 homolog	19.8 19.8
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid ceramidase)	19.8
	452321	AW844498	Hs.289052	Homo saplens LENG8 mRNA, variant C, partial sequen	19.8
45	449713	AW027025	Hs.239262	EST8	19.8
	458827	AW970786	Hs.178470	Homo saplens cDNA: FLJ22662 fis, clone HSI08080	19.8
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	19.8
	441730	Al243276	Hs.149017	ESTS Months dimines to ACCOCTOR 1 B31665 2 D4 see	19.8 19.8
50	420701 403642	N42919	Hs.88630	ESTs, Weakly similar to AC007228 1 R31665 2 [H.sap predicted exon	19.8
50	408987	H85615		gb:yt03f11.r1 Soares retina N2b5HR Homo sapiens cD	19.8
	446712	AW204789	Hs.209828	ESTs	19.8
	403286			predicted exon	19.8
55	434439	AI022360	Hs.190583	ESTs	19.8
55	404087	BE067300		predicted exon gb:PM2-BT0349-161299-001-h10 BT0349 Homo saple	19.7 19.7
	455694 403287	DE007300		gu.Finz-610345-101255-001-1110 610345 Hollio sapie	19.7
	434633	Al189587	Hs.120915	ESTs	19.7
	408199	AA132637	Hs.15396	ESTs	19.7
60	420080	M94065	Hs.94925	dihydrocrotate dehydrogenase	19.7
	408852	AW291435	Hs.254961	ESTs	19.7
	403786 416839	H94900	Hs.17882	predicted exon ESTs	19.7 19.7
	434385	AA631946	Hs.259580	EST8	19.7
65	446845		Hs.156108	ESTs	19.7
••	425612		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:CM0-BN0103-180300-296-c04 BN0103 Homo sapi	19.7
	402520			predicted exon	19.6
	436098		Hs.9739	ESTs	19.6
70	438974	AF089816 AA339541	Hs.6454	chromosome 19 open reading frame 3 hypothetical protein FLJ22056	19.6 19.6
70	447751 451310		Hs.24956 Hs.26213	ESTs, Moderately similar to dJ447F3.3 [H.saplens]	19.6
	435961	BE293127	Hs.283722	GTT1 protein	19.6
	452937	BE410390	Hs.288940	five-span transmembrane protein M83	19.6
75	404850			predicted exon	19.6
75	438360		Hs.288193	hypothetical protein FLJ10375	19.6
	436508		Hs.121121	ESTS ablanta abanda adakum refinalad forullu mombor 2	19.6 19.6
	430486 407824		Hs.241551 Hs.9812	chloride channel, calcium activated, family member 2 ESTs	19.6
	406388		10.3012	predicted exon	19.6
80	430204		Hs.146137	ESTs, Weakly similar to putative [C.elegans]	19.5
_	457560	AI801934	Hs.163909	ESTs	19.5
	429521		Hs.50949	ESTs	19.5
	429758		Hs.246804	ESTs	19.5 19.5
	441473	AA934995	Hs.184846	ESTs. Wealthy similar to R28830 1 [H.saplens]	19.5

	444704	4.4774774			
	411724 450453	AA770559 AA009883	Hs.71618 Hs.50186	polymerase (RNA) II (DNA directed) polypeptide L (7. ESTs	19.5 19.5
	419687	A1638859	Hs.227699	ESTs, Weathly similar to Yhr217cp [S.cerevislae]	19.5
_	442162	AW294966	Hs.150649	ESTs	19.5
5	435056	AW023337	Hs.5422	glycoprotein MSB	19.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	19.5
	413825	BE299181	Hs.75564	CD151 antigen	19.4
	422687 435551	AW068823	Hs.119206	insulin-like growth factor binding protein 7	19.4
10	440069	AF212365 BE617892	Hs.5470 Hs.6895	IL-17B receptor actin related protein 2/3 complex, subunit 3 (21 kD)	19.4 19.4
	432277	AI669790	Hs.161825	ESTs	19.4
	428044	AA093322	Hs.182225	RNA binding motif protein 3	19.4
	456064	AA256213	Hs.72010	ESTs	19.4
1.5	424897	D63216	Hs.153684	frizzled-related protein	19.4
15	424673	AA345051	Hs.294092	ESTs	19.4
	403852			predicted exon	19.3
	405699 433096	AU076803	Hs.282975	predicted exon carboxylesterase 2 (Intestine, liver)	19.3 19.3
	400344	NM_012368	Hs.258574 .		19.3
20	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg), short basic	19.3
	400449			predicted exon	19.3
	453801	AL134751	Hs.23450	mRNA for FLJ00023 protein	19.3
	435849	BE305242	Hs.112442	ESTs, Weakly similar to CLDE_HUMAN CLAUDIN-	19.3
25	454181	AW177377	11- 77040	gb:CM4-CT0129-190899-007-e09 CT0129 Homo saple	19.3
23	414807 406326	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD) predicted exon	19.3 19.3
	421921	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	19.3
	416700	AW498958	Hs.79572	cathepsin D (lysosomal aspartyl protease)	19.2
	458857	AI627342	Hs.224601	ESTs	19.2
30	405501			predicted exon	19.2
	416601	R08652	Hs.20205	hemoglobin, beta pseudogene 1	19.2
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	19.2
	425590 428151	AI954686 AA422028	Hs.158321	beaded filament structural protein 2, phakinin gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapiens cDN	19.2 19.2
35	426420	BE383808	Hs.169829	KIAA1180 protein	19.2
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	19.2
	404601			predicted exon	19.2
	403861			predicted exon	19.2
40	448363	BE174595	Hs.366	6-pyruvoyitetrahydropterin synthase	19.2
40	406655	M21533	Hs.181244	major histocompatibility complex, class I, A	19.1
	435372 413154	AA809591	Hs.106486	ESTs, Highly similar to CIKG_HUMAN VOLTAGE-G	19.1 19.1
	443021	BE067870 AA368546	Hs.8904	gb:RCO-BT0362-021299-031-b06 BT0362 Homo saple lg superfamily protein	19.1
	412975	170956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,40, sulfated	19.1
45	412633	AF001691	Hs.74304	periplakin	19.1
	402071			predicted exon	19.1
	410387	A1277367	Hs.47094	ESTs	19.1
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin Hike)	19.1
50	407032	U73799		gb:Human dynactin mRNA, partial cds.	19.0 19.0
50	404034 456534	X91195	Hs.100623	predicted exon phospholipase C, beta 3, neighbor pseudogene	19.0
	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse homolog) 6	19.0
	426410	BE298446	Hs.180372	BCL2-like 1	19.0
	419618	AA528295		gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens cDNA c	19.0
55	457632	AW292151	Hs.112689	ESTs	19.0
	417138	AA193646	Hs.65771	Homo sapiens chromosome 19, BAC CIT-HSPC_204F	19.0
	417933	X02308	Hs.82962 Hs.246295	thymidylate synthetase ESTs	19.0 19.0
	458808 415860	AW134832 D56051	Hs.78888	diazepam binding inhibitor (GABA receptor modulator	18.9
60	440919	AW291274	Hs.262826	ESTs	18.9
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	18.9
	401747			predicted exon	18.9
	454209	AW179083	45104	gb:MR4-ST0065-270899-006-A07 ST0065 Homo sapi	18.8
65	417661	T84155 C14937	Hs.15464 Hs.11169	Homo saplens cDNA: FLJ21351 fis, clone COL02762 Gane 33/Mig-6	18.8 18.8
05	426499 404240	C14937	ns.11103	predicted exon	18.8
	439718	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homolog)	18.8
	401789			predicted exon	18.8
70	456952	AW445081	Hs.301469	ESTs	18.8
70	439739	AJ199391	Hs.124464	ESTs	18.8
	437974	T74445	Hs.5957	Homo saplens clone 24416 mRNA sequence	18.8
	427490 443482	Z95152 AW188093	Hs.178695 Hs.250385	mitogen-activated protein kinase 13 ESTs	18.8 18.8
	411420	BE390652	1040000	gb:601286820F1 NIH_MGC_44 Homo saptens cDNA	18.8
75	435196		Hs.188128	ESTs, Moderately similar to ALUB_HUMAN !!!! ALU	18.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain family 2	18.8
	413531	AL036958	Hs.75416	DAZ associated protein 2	18.7
	428981	BE313077	Hs.93135	EST ₈	18.7
80	421598		Hs.106061	RD RNA-binding protein	18.7
οU	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding protein brain protein i3	18.7 18.7
	406754 400661	AA477223	Hs.75922	predicted exon	18.7
	442638	AI088742	Hs.134713	ESTs .	18.7
	434169		Hs.179724	ESTs	18.7

	424126	AA335635	Hs.96917	ESTs	18,7
	408473	BE259039	Hs.129953	Ewing sarcoma breakpoint region 1	18.7
	401962			predicted exon	18.7
5	447326 459053	AW002252 AI807052	Hs.201395 Hs.210361	ESTs ESTs	18.7 18.7
,	403362	74007002	143,2,10001	predicted exon	18.7
	427697	T18997	Hs.180372	BCL2-like 1	18.7
	402061 433785	HB3363 BE044593	Hs.109571 Hs.112704	translocase of inner mitochondrial membrane 10 (yeast) ESTs	18.7 18.7
10	405423	DEVTTOSO	110.112704	predicted exon	18.6
-	429259	AA420450	Hs.292911	ESTs	18.6
	444071 410512	AI627808 AA085603	Hs.110524 Hs.250570	ESTs ESTs	18.6 18.6
	440376	AI024452	Hs.236816	ESTs	18.6
15	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotropic hormone)	18.6
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	18.6
	415602 407891	F12920 AA486620	Hs.165575 Hs.41135	ESTs endomucin-2	18.6 18.6
••	455910	Z43712	710,71100	gb:HSC1JA121 normalized infant brain cDNA Homo s	18.6
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg), short basic	18.6
	444246 428125	H93281 AA393071	Hs.10710 Hs.182579	hypothetical protein FLJ20417 leucine aminopeptidase	18.6 18.6
	406457	74030071	15.106015	predicted exon	18.5
25	446625	Al333070	Hs.156141	ESTs	18.5
25	423334 423103	AK000906 AA322029	Hs.127273	hypothetical protein FLI10044 gb:EST24685 Cerebellum II Homo sapiens cDNA 5' en	18.5 18.5
	443549	T89608	Hs.16601	ESTs	18.5
	419299	AJ311085	Hs.62406	Homo saplens cDNA: FLJ22573 fis, clone HSI02387	18.5
30	411942	AW877015	Un 440400	gb:QV2-PT0010-250300-096-f12 PT0010 Homo saplen	18.5 18.5
50	442440 454574	BE464435 AW809109	Hs.146180	ESTs, Weakly similar to non-receptor protein tyrosine k gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapie	18.5
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library	18.5
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic subunit of DNA p	18.5
35	421733 420603	AL119671 AB042636	Hs.1420 Hs.4775	fibroblast growth factor receptor 3 (achondroplasta, tha functophilin 3	18.5 18.4
33	401373	AD042000	(13.4113	predicted exon	18.4
	402292			predicted exon	18.4
	444118	AA458542	Hs.10326	coatomer protein complex, subunit epsilon	18.4 18.4
40	408310 411236	AW179023 AW833752		gb:PM3-ST0036-170899-001-e08 ST0036 Homo sapia gb:QV4-TT0008-130100-077-b07 TT0008 Homo sapie	18.4
	431405	A1470895	Hs.252574	ribosomal protein L10a	18.4
	441408	AI733249	Hs.126897	ESTs	18.4 18.4
	453994 444518	BE180964 Al160278	Hs.165590 Hs.146884	ribosomal protein S13 ESTs	18.4
45	402407	74.002.0	110.170001	predicted exon	18.4
	404270		1	predicted exon	18.4
	409103 415198	AF251237 AW009480	Hs.112208 Hs.943	XAGE-1 protein natural killer cell transcript 4	18.4 18.3
	430771	BE387244	Hs.2664	flavin containing monooxygenase 4	18.3
50	432636	AA340864	Hs.278562	claudin 7	18.3
	433504	NM_014874 W70022	Hs.3363	KIAA0214 gene product gb:zd51e10.r1 Soares_fetal_heart_NbHH19W Homo sa	18.3 18.3
	415606 401401	BE047878	Hs.99093	Homo sepiens chromosome 19, cosmid R28379	18.3
	420758	AW297536	Hs.33053	ESTs	18.3
55	457520	AA553495	Hs.162264	ESTs	18.3 18.3
	432323 404750	AK001409	Hs.274356	hypothetical protein FLJ10547 predicted exon	18.3
	450645	AL117441 .	Hs.25264	DKFZP434N126 protein	18.3
60	445160	Al299144	Hs.150797	ESTS	18.3 18.3
UU	418461 401809	BE242781	Hs.288037	Homo saplens cDNA FLJ12999 fis, clone NT2RP3000 predicted exon	18.3
	458121	S42416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from	18.3
	435106		Hs.193380	ESTs, Highly similar to AF174600 1 F-box protein Fbx	18.3
65	448398 428145		Hs.170838 Hs.182626	ESTs chromosome 22 open reading frame 5	18.3 18.2
05	445302		Hs.12488	hypothetical protein FLJ10675	18.2
	407352	H47860		gb:yp76h12.r1 Soares fetal liver spleen 1NFLS Homo s	18.2
	413190		Hs.40368 Hs.113912	adaptor-related protein complex 1, sigma 2 subunit ESTs	18.2 18.2
70	436371 400965		П5.113512	predicted exon	18.2
. •	433427	Al816449	Hs.171889	cholinephosphotransferase 1	18.2
	427504		Hs.191589	ESTs	18.2 18.2
	426759 423792		Hs.21213 Hs.245854	ESTs ESTs	18.2
75	406826		Hs.84298	CD74 antigen (invariant polypeptide of major histocom	18.1
	406659	AA663985	Hs.277477	major histocompatibility complex, class I, C	18.1
	437453 409276		Hs.181391 Hs.278429	hypothetical protein DKFZp761G2113 hepatocellular carcinoma-essociated antigen 59	18.1 18.1
•	449628		· Hs.197713	ESTs	18.1
80	421043	8E379455	Hs.89072	ESTs	18.1
	442344 448744		Hs.301212 Hs.9469	ESTs phosphoinositol 3-phosphate binding protein-1	18.1 18.1
	416062		Hs.74427	p53-induced protein	18.1
	414500		Hs.76285	DKFZP564B167 protein	18.1

	427272	NIM OUTOOR	Un 474440	ATD elitate house	40.4
	403964	NM_001096	Hs.174140	ATP citrate lyase predicted exon	18.1
	433217	AB040914	Hs.278628	KIAA1481 protein	18.1 18.1
	427902	AI809202	Hs.208343	ESTs, Weakly similar to cerebroside sulfotransferase [H	18.1
5	449586	AI863918	Hs.195078	ESTs	18.1
•	430826	U10061	Hs.248019	POU domain, class 4, transcription factor 3	18.1
	414195	BE263293	113.2.10013	gb:601144881F2 NIH_MGC_19 Homo sapiens cDNA	18.1
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	18.1
	411088	BE247593	Hs.145053	ESTs	18.1
10	419407	AW410377	Hs.41502	Homo saplens cDNA: FLJ21276 fis, clone COL01829	18.1
	407938	AA905097	Hs.85050	phospholamban	18.1
	449360	AJ640623	Hs.252720	ESTs	18.1
	417286	AA122237	Hs.81874	microsomal glutathione S-transferase 2	18.0
	405515			predicted exon	18.0
15	439319	AW016401	Hs.233476	ESTs	18.0
	419387	BE379356	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface antig	18.0
	414015	AA340987	Hs.75693	prolylcarboxypeptidase (anglotensinase C)	18.0
	447778	BE620592	Hs.71190	EST ₈	18.0
20	435523	T62849	Hs.11090	high affinity immunoglobulin epsilon receptor beta sub	18.0
20	429230	AF088991	Hs.198274	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	18.0
	457822	AA970001	Hs.150319	ESTs	18.0
	442424	AJ342715	Hs.129569	ESTs, Moderately similar to B34087 hypothetical prote	18.0
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	18.0
25	413477	AJ815825	Hs.48756	ESTs, Moderately similar to neuronal-STOP protein [M	18.0
23	405277 450192	AA263143	Hs.24596	predicted exon	18.0
	442191	W95186	Hs.8136	RAD51-interacting protein endothelial PAS domain protein 1	18.0 18.0
	429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively spliced product u	18.0
	406744	AA554082	Hs.279860	hypothetical protein FLJ20030	17.9
30	425205	NM_005854	Hs.155106	receptor (calcitonin) activity modifying protein 2	17.9
50	414387	AL043148	Hs.186257	ESTs	17.9
	411811	AW864370	100.0020.	gb:PM4-SN0016-100500-004-h09 SN0016 Homo saple	17.9
	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	17.9
	414333	BE274897		gb:601122959F1 NIH_MGC_20 Homo saptens cDNA	17.9
35	403747			predicted exon	17.9
	435542	AA687376	Hs.269533	ESTs	17.9
	403093			predicted exon	17.9
	412088	A1689496	Hs.108932	EST8	17.9
40	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	17.9
40	404763			predicted exon	17.9
	454633	AW811380		gb:lL3-ST0143-290999-019-D05 ST0143 Homo saplen	17.9
	440788	A1806594	Hs.128577	ESTs	17.9
	411800	N39342	Hs.5184	TH1 drosophila homolog	17.9
15	441361	BE263308	Hs.7797	TERF1 (TRF1)-Interacting nuclear factor 2	17.8
45	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted in velocardiof	17.8
	405333			predicted exon	17.8
	408297	R17710	Hs.113314	ESTs	17.8
	403036	********	11-00000	predicted exon	17.8
50	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	17.8
30	417091	AA193283	Hs.291990	ESTs	17.8
	440789 438397	AB007857	Hs.7416	KIAA0397 gene product	17.8
	435948	AA806478 AA702675	Hs.123206 Hs.114135	ESTs ESTs	17.8 17.8
	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	17.8
55	435969	W85773	Hs.191386	ESTs	17.8
55	427031	AA397601	Hs.125147	ESTs	17.8
	454505	AW801365	110.120141	gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapi	17.8
	403447	***************************************		predicted exon	17.8
	433297	AV658581	Hs.282633	ESTs	17.8
60	443326	BE156494	Hs.188478	ESTs	17.8
	448283	AI340462	Hs.182979	ribosomal protein L12	17.8
	458067	AA393603	Hs.36752	Homo sapiens cDNA: FLJ22834 fis, clone KAIA4314	17.8
	452359	BE167229	Hs.29206	Homo saplens clone 24659 mRNA sequence	17.8
CF	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo saplens cDN	17.8
65	450911	AA011586	Hs.272097	ESTs	17.7
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, receptor for, gamma	17.7
	407082	Z47055		gb:Human partial cDNA sequence, famesyl pyrophosph	17.7
	415271	X94232	Hs.78335	microtubule-associated protein, RP/EB family, member	17.7
70	417413	AA197072	Hs.86092	Human DNA sequence from done RP11-243J16 on chr	17.7
70	408937	AA210734	Hs.291386	ESTS share 27h05 at NGL CCAR Cout Name against aCNA	17.7
	433459	AA593498	Un 4/E/00	gb:nn27b05.s1 NCI_CGAP_Gas1 Homo saplens cDNA	17.7
	459536	AI254723	Hs.145496	ESTs della 6 fatty and decaturate	17.7
	428500 433463	AI815395 R41963	Hs.184641 Hs.4197	della-6 fatty acid desaturase ESTs	17.7 17.7
75	406537	1411303	1614.61	predicted exon	17.7
	410003	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937221) Homo	17.7
	440857	AA907808	Hs.135556	ESTs	17.7
	451072	AA013451	Hs.117929	ESTs	17.7
	418693	AI750878	Hs.87409	thrombospondin 1	17.7
80	443624	BE616129	Hs.9651	related RAS viral (r-ras) oncogene homolog	17.6
	422626	AA344932	Hs.118786	metallothionein 2A	17.6
	410758	AB037820	Hs.66159	KIAA1399 protein	17.6
	436621	AI266254	Hs.132929	ESTs	17.6
	453317	NM_002277	Hs.41696	keratin, hair, acidic,1	17.6
				•	

	456828	AF156889	Hs.148427	LIM homeobox protein 3	17.6
	421486	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.6
	428834	AW899713	Hs.10338	ESTs	17.6
5	451419 448413	R36309 Al745379	Hs.174369 Hs.42911	EST ESTs	17.6 17.6
•	424323	AA338791	Hs.146763	nascent-polypeptide-associated complex alpha polypept	17.6
	423943	AF163570	Hs.135756	polymerese (DNA-directed) kappa	17.6
	439423	BE536678	Hs.147099	ESTs	17.6
10	434025 408246	AF114264 N55669	Hs.216381 Hs.43946	Homo sapiens clone HH409 unknown mRNA L13 protein	17.6 17.6
	441579	AW468847	Hs.127194	ESTs	17.5
	420867	NM_0141B3	Hs.100002	HSPC162 protein	17.5
	453680	AL079647	Hs.14485	ESTs	17.5
15	400202 410768	AF038185	Hs.66187	predicted exon Homo saplens clone 23700 mRNA sequence	17.5 17.5
13	409932	Al376750	Hs.57600	adaptor-related protein complex 1, sigma 1 subunit	17.5
	425563	AF084199	Hs.299837	ESTs	17.5
	440475	Al807671	Hs.128343	ESTs	17.5
20	452767	AW014195	Hs.61472	ESTs, Weakly similar to unknown [S.cerevisiae]	17.5
20	410570 419600	AI133096 AA448958	Hs.64593 Hs.91481	ATP synthase, H+ transporting, mitochondrial F1F0, su NEU1 protein	17.4 17.4
	419588	Al347205	Hs.91375	Human clone 23614 mRNA sequence	17.4
	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase kinase 6	17.4
25	448928	A1350260	Hs.5384	Homo saplens cDNA FLJ11743 fis, clone HEMBA100	17.4
43	403924 419889	AA251600		predicted exon gb:zs10d12.rf NCI_CGAP_GCB1 Homo saplens cDNA	17.4 17.4
	405023	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.4
	426065	N32049		gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to	17.4
30	453199	Al336266	Hs.301854	Homo sapiens PRO0412 mRNA, complete cds	17.4
30	455132 442932	AWB57955 AA457211	Hs.8858	gb:PM0-CT0325-151299-002-A12 CT0325 Homo sapi bromodomein edjacent to zinc finger domain, 1A	17.4 17.4
	432065	AA401039	Hs.2903	protein phosphalase 4 (formerly X), catalytic subunit	17.3
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)	17.3
25	417935	R53697	Hs.170044	ESTs	17.3
35	430050	AA430993	Hs.227913	APIS-like 1	17.3
	446272 425996	BE268912 W67330	Hs.14601 Hs.81256	hematopoietic cell-specific Lyn substrate 1 S100 calcium-binding protein A4 (calcium protein, calv	17.3 17.3
	416964	D87467	Hs.80620	guanine nucleotide exchange factor for Rap1; M-Ras-re	17.3
40	437418	AI478954	Hs.59459	ESTS	17.3
40	447255	A1884908	Hs.158607	ESTs	17.3
	402203 417611	AW993983		predicted exon gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapie	17.3 17.3
	426560	AA381661	Hs.119878	EST8	17.3
4.5	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PLACE1010	17.3
45	445017	Al205493	Hs.176860	ESTs	17.3
	438658 442238	Al222068 AW135374	Hs.123571 Hs.270949	ESTs '	17.3 17.3
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002	17.3
	442609	AL020996	Hs.8518	selenoprotein N	17.2
50	416591	AA091976	Hs.79387	proteasome (prosome, macropain) 26S subunit, ATPase	17.2
	403674	A 4 2 4 0 5 0 4	11- 044507	predicted exon	17.2
	430514 411696	AA318501 AW857404	Hs.241587	megakaryocyte-enhanced gene transcript 1 protein gb:CM3-CT0313-291199-046-c11 CT0313 Homo saple	17.2 17.2
	434560	R13052	Hs.3964	Homo saplens clone 24877 mRNA sequence	17.2
55	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68kD	17.2
	414364	D38521	Hs.75935	KIAA0077 protein	17.2
	409119 425640	AA531133 U34051	Hs.4253 Hs.299204	G protein-coupled receptor 44 ESTs, Highly similar to CD5S_HUMAN CYCLIN-DE	17.2 17.2
	436044	BE247571	Hs.15627	Nit protein 2	17.2
60	401657			predicted exon	17.2
	449763	AI822112	Hs.118241	EST8	17.2
	409601 449636	AF237621 AI656608	Hs.80828 Hs.281328	keratin 1 (epidermolytic hyperkeratosis) ESTs	17.2 17.2
	444958	AW292643	Hs.167047	ESTs	17.2
65	429978	AA249027	Hs.241507	ribosomal protein S6	17.2
	453043	AW135440	Hs.224277	ESTs	17.2
	458640	AI284935 T41418		gbxk55g09.x1 NCI_CGAP_Co8 Homo sapiens cDNA gbxh1h3_19/1TV Outward Alu-primed hncDNA librar	17.1 17.1
	456329 414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	17.1
70	403662			predicted exon	17.1
	411651	AW855392		gb:CM3-CT0275-191099-024-e12 CT0275 Homo saple	17.1
	404097	D00046		predicted exon	17.1 17.1
	447252 430024		Hs.227730	gb:yn01e10.r1 Soares adult brain N2b4HB55Y Homo s integrin, alpha 6	17.1
75	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerst	17.1
	444558		Hs.165892	ESTs	17.1
	420869		Hs.123638	regulatory factor X, 1 (influences HLA class II expressi	17,1
	448812 431777		Hs.22140 Hs.105470	BM88 antigen found in inflammatory zone 1	17.0 17.0
80	422007		Hs.39168	ESTs	17.0
-	403051			predicted exon	17.0
	402427		15.00000	predicted exon	17.0
	417408 450598		Hs.86092 Hs.25199	Human DNA sequence from clone RP11-243J16 on chr hypothetical protein	17.0 17.0
	730350	101010	, 10.20 100	-Mk-manne kramm	

	421121 458488	AA459028 AL040565	Hs.86228 Hs.209544	TRIAD3 protein ESTs	17.0 17.0
	417158	AW965223	Hs.110062	ESTs, Weakly similar to ACR3_HUMAN 30 KD ADIP	17.0
5	439318	AW837046	Hs.6527	G protein-coupled receptor 56	17.0
3	428758 447572	AA433988 AI631546	Hs.98502 Hs.159732	Homo sapiens cDNA FLJ14303 fis, clone PLACE2000 ESTs	17.0 17.0
	434434	AA633516	Hs.157201	ESTs	17.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	17.0
10	408927 439093	AW295650 AA534163	Hs.255453 Hs.5476	ESTs serine protease inhibitor, Kazal type, 5	17.0 17.0
10	454466	AA984138	Hs.279895	Homo saplens mRNA for KIAA1578 protein, partial od	17.0
	426996	AW968934	Hs.173108	Homo saplens cDNA: FLJ21897 fis, clone HEP03447,	17.0
	436659 422731	Al217900	Hs.144464	ESTS	17.0
15	429294	AL138411 AA095971	Hs.198793	gb:DKFZp434A1229_r1 434 (synonym: htes3) Homo s KIAA0750 gene product	17.0 17.0
	432847	BE266941	Hs.279554	proteasome (prosome, macropain) 26S subunit, non-AT	16.9
	416977 406827	AW130242	Hs.293476	ESTs	16.9
	453758	AA971409 U83527	Hs.84298	CD74 antigen (invariant polypeptide of major histocom gb:HSU83527 Human fetal brain (M.Lovetl) Homo sap	16.9 16.9
20	431314	Al732204	Hs.105423	EST8	16.9
	423185	BE299590	Hs.125078	omithine decarboxylase antizyme 1	16.9
	435086 447383	AW975243 N24231	Hs.122596	ESTs gb:yx22a11.r1 Soares melanocyte 2NbHM Homo saple	16.9 16.9
0.5	456251	R13326	Hs.21303	ESTs ·	16.9
25	456327	H68741	Hs.38774	ESTs	16.9
	450594 428177	N31036 AA423967	Hs.178113	gb:yx51g04.r1 Soares melanocyte 2NbHM Homo saple ESTs, Moderately similar to kinesin like protein 9 [M.m.	16.9 16.9
	453250	Al346520	Hs.121619	chromosome 11 open reading frame 15	16.9
20	418294	AF061739	Hs.83954	protein associated with PRK1	16.9
30	446546 421100	BE167687 AW351839	Hs.156628 Hs.124660	ESTs Homo saplens cDNA: FLJ21763 fis, clone COLF6967	16.9 16.9
-	455993	BE179085	113.124000	gb:RC0-HT0613-140300-021-d06 HT0613 Homo sapie	16.9
	459375	BE251770		gb:601112470F1 NIH_MGC_16 Homo saplens cDNA	16.9
35	454803 445474	AW860148 Al240014	Hs.259558	gb:RC0-CT0379-290100-032-b10 CT0379 Homo sapis	16.9 16.9
55	443198	AI039813	ris.203000	ESTs gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo	16.9
	441557	AW452647	Hs.270482	ESTs	16.9
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glucose transporter),	16.9
40	442202 416913	BE272862 AW934714	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone HSi06009 gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapie	16.9 16.9
	419355		Hs.90061	progesterone binding protein	16.9
	452975	M85521	Hs.69469	dendritic cell protein	16.9
	432525 453718	Al796096 AL119317	Hs.109414 Hs.120360	ESTs phospholipase A2, group VI (cytosolic, calcium-indepe	16.8 16.8
45	437270	R18087	Hs.11282	ESTs, Weakly similar to cleft lip and palate transmemb	16.8
	408007	AW135965	Hs.246783	ESTs	16.8
	450954 402958	Al904740	Hs.25691	receptor (calcitonin) activity modifying protein 3 predicted exon	16.8 16.8
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H	16.8
50	410684	AA088500	Hs.170298	ESTs	16.8
	437669 447869	AJ358105 AW139113	Hs.123164 Hs.164307	ESTs, Weakly similar to match to ESTs AA667999 [H. ESTs	16.8 16.8
	458025	Al275406	NS. 104307	gb:ql63c10.x1 Soares_NhHMPu_S1 Homo sapiens cDN	16.8
	445614	AV660763	Hs.110675	apolipoprotein C-IV	16.8
55	454610	AW810224	11- 02/02	gb:MR4-ST0125-021199-017-e07 ST0125 Homo saple	16.8
	449303 422105	AK001495 Al929700	Hs.23467 Hs.111680	hypothetical protein FLJ10533 endosulfine alpha	16.8 16.8
	444788	AI871122	Hs.202821	ESTs	16.8
60	414057	AI815559	Hs.75730	signal recognition particle receptor ("docking protein")	16.8
UU	408822 433379	AW500715 AA586368	Hs.57079 Hs.190232	Homo sapiens CDNA FLJ13267 tis, clone OVARC1000 ESTs	16.8 16.8
	441552	AA937975		gb:oc08e12.s1 NCL_CGAP_GCB1 Homo sapiens cDN	16.8
	403582			predicted exon	16.8
65	433871 439509	W02410 AF086332	Hs.205555 Hs.58314	ESTs ESTs	16.8 16.8
05	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.8
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	16.8
	401465 448913	AA194422	Hs.22564	predicted exon myosin VI	16.8 16.8
70	410261	AF145713	Hs.61490	schwannomin interacting protein 1	16.8
	421199	BE244219	Hs.102497	paxilin	16.7
	450489	A1697990	Hs.224375	ESTs	16.7
	410186 447224	AW602528 BE617125		gb:RC5-BT0562-260100-011-A02 BT0562 Homo sapi gb:601441664F1 NIH_MGC_65 Homo sapiens cDNA	16.7 16.7
75	403010			predicted exon	16.7
	404881	11015111	., 45555	predicted exon	16.7
	445572 419440		Hs.189654 Hs.90419	ESTs KIAA0882 protein	16.7 16.7
00	443406		Hs.143316	ESTs	16.7
80	457901	AW207023	Hs.250497	ESTs, Highly similar to dJ745C22.1 [H.saplens]	16.7
	448364 407239		Hs.16561 Hs.67846	HSPC141 protein leukocyte immunoglobulin-like receptor, subfamily 8 (16.6 16.6
	401847			predicted exon	16.6
	429523	AK000788	Hs.205280	Homo sapiens cONA FLJ20781 fls, clone COL04235	16.6
				100	

	432845	AJ989751	Hs.150378	ESTs	16.6
	400246			predicted exon	16.6
	404971			predicted exon	16.6
	422954	AW998605	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP like prot	16.6
5	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	16.6
•	432201	AI538613	Hs.135657	ESTs	16.6
	456993	AL134577	Hs.200302	ESTs	16.6
	456525				16.6
	444060	AW468397	Hs.100000	S100 catcium-binding protein A8 (catgranulin A)	
10		AA340277	Hs.10248	Homo saplens cDNA FLJ20167 fis, clone COL09512	16.6
10	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
	448199	AI953278	Hs.170557	ESTs	16.6
	443422	R10288	Hs.301529	ESTs	16.6
	401117			predicted exon	16.6
	400613			predicted exon	16.6
15	431214	AA294921	Hs.250811	v-ral simian leukernia viral oncogane homolog B (ras re	16.6
	431649	AL133077	Hs.266746	Homo saplens cDNA: FLJ22615 fls, clone HSi05118	16.5
	421335	X99977	Hs.103505	ARS component B	16.5
	427154	AL137262	Hs.288991	Homo sapiens cDNA: FLJ22523 fis, clone HRC12507	16.5
	401010	7107202	110.200001	predicted exon	16.5
20	436678	BE512828	Hs.5273	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30k	16.5
20		DE312020	M3.0275		
	401589			predicted exon	16.5
	402538			predicted exon	16.5
	430478	NM_014349	Hs.241535	TNF-inducible protein CG12-1	16.5
25	437623	D63880	Hs.5719	chromosome condensation-related SMC-associated pro	16.5
25	401244			predicted exon	16.5
	415167	AA160784	Hs.26410	ESTs	16.5
	438291	BE514605	Hs.289092	Homo saplens cDNA: FLJ22380 fls, clone HRC07453,	16.5
	405183			predicted exon	16.5
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	16.5
30	456691	Al023428	Hs.205696	ESTs	16.5
-	418332	R34976	Hs.78293	ESTs	16.5
	446052	AA358760	1 10.7 01.00	gb:EST67699 Fetal lung II Homo sapiens cDNA 5' end	16.5
			Un 457/07		
	444859	AW449137	Hs.157487	ESTs .	16.5
25	437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yea	16.5
35	400891			predicted exon	16.5
	448372	AW445166	Hs.170802	ESTs	16.5
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens cDNA 5' en	16.5
	459253	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (from c	16.5
	420746	AW195932	Hs.197488	ESTs	16.4
40	414717	BE271039	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	16.4
	400727			predicted exon	16.4
	422691	NM_003365	Hs.119251	ubiquinol-cytochrome c reductase core protein I	16.4
	405639	1111/2000000	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	predicted exon	16.4
	414444	BE298594		gb:601119754F1 NIH_MGC_17 Homo saplens cDNA	16.4
45			Un 7000E		16.4
₩.	456146	AL034349	Hs.79005	protein tyrosine phosphalase, receptor type, K	
	414610	BE388044		gb:601283747F1 NIH_MGC_44 Homo sapiens cDNA	16.4
	414267	AL078459	Hs.289109	dimethylarginine dimethylaminohydrolase 1	16.4
	401268			predicted exon	16.4
~~	403613			predicted exon	16.4
50	414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens cDNA	16.4
	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	16.4
	452114	N22687	Hs.8236	ESTs	16.4
	404638			predicted exon	16.4
	404600	•		predicted exon	16.3
55	448855	AF070574	Hs.22316	Homo saplens clone 24819 mRNA sequence	16.3
		AP070374 AW277078	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	16.3
	406629				
	450957	BE515202	Hs.21497	Homo saplens mRNA for FLJ00042 protein, partial cds	16.3
	449966	H60542	Hs.37848	ESTs	16.3
60	402585			predicted exon	16.3
60	436008	A1078428	Hs.58785	ESTs	16.3
	40.1492			predicted exon	16.3
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140kD, antigen C	16.3
	405088			predicted exon	16.3
	437345	BE259522	Hs.5556	NADH dehydrogenase (ubiquinone) 1, alpha/beta subco	16.3
65	432280	BE440142	Hs.2943	signal recognition particle 19kD	16.3
05	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	16.3
	428801	AW277121	Hs.254881	ESTs	16.3
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	16.3
70	452998	BE019681	Hs.6019	Homo saplens cDNA: FLJ21288 fis, clone COL01927	16.3
70	439938	AI147392	Hs.124607	ESTs	16.3
	418844	M52982	Hs.1200	arachidonate 12-lipoxygenase	16.3
	.446081	AA972412	Hs.13755	f-box and WD-40 domain protein 2	16.3
	443534	Al076123		gb:oy92e04.x1 Soares_fetal_liver_spleen_INFLS_S1 H	16.3
	459510	AA076706		gb:7801802 Chromosome 7 Fetal Brain cDNA Library	16.3
75	450517	AI523755	Hs.59236	ESTs, Wealty similar to B35049 ankyrin 1, erythrocyte	16.3
-	451938	Al354355	Hs.16697	down-regulator of transcription 1, TBP-binding (negativ	16.3
	454478	AW805749		gb:QV1-UM0105-180400-162-f10 UM0105 Homo sap	16.2
	407214	AA412048	Hs.279574	CGI-39 protein; cell death-regulatory protein GRIM19	16.2
			- marwit	predicted exon	16.2
80	406580		Ue 200774		
30	409452		Hs.289271	cytochrome c-1	16.2
	416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	16.2
	458710			gb:AV660856 GLC Homo saplens cDNA clone GLCG	16.2
	450657		Hs.25277	hypothetical protein FLJ21065	16.2
	 404230 			predicted exon	16.2
				100	

	439471	W69839	Hs.58033	ESTs	16.2
	400848		11- 400000	predicted exon	16.2
	428797	AA496205	Hs.193700	Homo saplens mRNA; cDNA DKFZp586I0324 (from c	16.2
5	416272	AA178882	Un 442042	gb:zp38b09.r1 Stratagene muscle 937209 Homo sapiens	16.2
,	444465 431257	AI206592	Hs.143843	ESTs	16.2 16.2
	447775	AF039597 BE179318		gb:Homo saptens Ku86 autoantigen related protein 1 (K gb:RC1-HT0615-290300-021-g05 HT0615 Homo saple	16.2
	403833	DE113310		predicted exon	16.2
	444140	AV648089	Hs.282383	ESTs	16.2
10	446102	AW168067	Hs.252956	ESTs	16.2
	416475	T70298	,	gb:yd26g02.s1 Soares fetal liver spleen 1NFLS Homo s	16.2
	430783	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	16.2
	414070	AW963783		gb:EST375856 MAGE resequences, MAGH Homo sap	16.2
	444283	Al138971	Hs.154636	ESTs	16.2
15	405599	X92715	Hs.3057	zinc finger protein 74 (Cos52)	16.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo saplen	16.2
	409417	AA156247	Hs.295908	ESTs, Wealdy similar to ALU7_HUMAN ALU SUBFA	16.2
	435380	AA679001	Hs.192221	ESTs	16.2
••	405752	A1285598	Hs.217493	annexin A2	16.2
20	406096	F12200	Hs.5811	chromosome 21 open reading frame 59	16.2
	417551	Al816291	Hs.82273	hypothetical protein	16.2
	441252	AW360901	Hs.183047	ESTs, Weakly similar to unnamed protein product [H.s	16.2
	419608	AL037237	Hs.91586	transmembrane 9 superfamily member 1	16.1
25	438894	Al630819	Hs.300431	ESTs	16.1
25	451287	AK002158	Hs.26194	hypothetical grotein FLJ11296	16.1
	412499	AW956916	Hs.11238	KIAA0622 protein; Drosophila "multiple asters" (Mast	16.1
	433355	AI808235		gb:wf44e01.x1 Soares_NFL_T_GBC_S1 Homo saplen	16.1
	416818	AI986408	Hs.204766	ESTs, Weakly similar to B48013 proline-rich proteogly	16.1
30	438765	A1031888	Hs.132594	ESTs .	16.1
30	424470	BE244261	Hs.5615	nuclear RNA export factor 1	16.1
	416194	H27114	Hs.301212	ESTs	16.1 16.1
	446702	R44518	Hs.143496	ESTs sorbitol dehydrogenase	16.1
	414222 443122	AL135173 AI806656	Hs.878 Hs.209022	ESTs, Weakly similar to Pro-Pol-dUTPase polyprotein	16.1
35	448648	BE614345	Hs.159089	ESTs	16.1
55	456394	W28506	118, 133003	gb:48f1 Human retina cDNA randomly primed sublibra	16.1
	445887	AI263105	Hs.145597	ESTs	16.1
	412332	AW937661	Hs.288324	Homo sapians cDNA FLJ13283 fis, clone OVARC1001	16.1
	403912	7111001001	10.200021	predicted exon	16.1
40	441446	R66269	Hs.28714	ESTs	16.1
••	403153			predicted exon	16.0
	444907	AW772596	Hs.148586	ESTs	16.0
	421946	R99629	Hs.109773	hypothetical protein FLJ20625	16.0
	437513	AW410681	Hs.5648	proteasome (prosome, macropain) 268 subunit, non-AT	16.0
45	407752	AA573581	Hs.13328	ESTs	16.0
	447953	AI804218	Hs.209614	Homo saplens cDNA: FLJ22343 fis, clone HRC06043	16.0
	425708	AK001342	Hs.14570	Homo sapiens cDNA: FLJ22530 fis, clone HRC12866	16.0
	421449	AA713491	Hs.291501	ESTs	16.0
~~	418323	NM_002118	Hs.1162	major histocompatibility complex, class II, DM beta	16.0
50	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo saplens cDNA	16.0
	422716	A1702835	Hs.124475	ESTs	16.0
	443958	BE241880	Hs.10029	cathepsin C	16.0
	417908	AA207221		gb:zq55h04.s1 Stratagene neuroepithelium (937231) Ho	16.0
EE	438542	AA810131	Hs.123317	ESTs	16.0
55	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor, alpha polypeptid	16.0
	456825	H67220	Hs.146406	nitrilase 1	16.0
	431360	NM_000427	Hs.251680	loricrin	16.0
	414266	BE267834	U- 420700	gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA c	16.0
60	440571 426075	AA904461 AW513691	Hs.130798 Hs.270149	ESTs ESTs	16.0 16.0
00	413488	BE144017	Hs.184693	transcription elongation factor B (Sill), polypeptide 1 (1	16.0
	446767	Al380107	Hs.158954	ESTs	16.0
	418008	W56044	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone HEP16248	16.0
	404239		, 1000	predicted exon	16.0
65	458401	AW236939	Hs.172154	ESTs	16.0
	412955	BE241849	Hs.75082	ras homolog gene family, member G (rho G)	15.9
	423072	A1792946	Hs.123116	solute carrier family 12 (sodium/polassium/chloride tran	15.9
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor 2, subunit 2 (beta	15.9
	449023	AI623261	Hs.248875	ESTs	15.9
70	435729		Hs.275017	EST	15.9
	438575		Hs.146550	myosin, heavy polypeptide 9, non-muscle	15.9
	413047	H02209		gb:yj38c09.r1 Soares placenta Nb2HP Homo sapiens cD	15.9
	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	15.9
75	446863	AW614370	Hs.254620	ESTs	15.9
75	448564		Hs.21453	Homo sapiens mRNA for Inositol 1,4,5-trisphosphate 3	15.9
	455640			gb:QV3-BT0296-010300-111-e04 BT0296 Homo saple	15.9
	404345		Hs.159156	protocadherin 11	15.9
	418512		Hs.89981	diacylglycerol kinase, zeta (104kD)	15.9
90	411551		.,	gb:IL3-CT0220-170200-067-C11 CT0220 Homo sapien	15.9
80	446726		Hs.209209	Homo sapiens cDNA FLJ11629 fis, done HEMBA100	15.9
	410748		Hs.136005		15.9
	449618		Hs.14366	Homo saplens cDNA FUJ12819 fis, clone NT2RP2002	15.9
	429697		Hs.24605	ESTs turnor protein 63 kDa with strong homology to p53	15.9 15.9
	424012	AW368377	Hs.137569	mine breezin on una um sand minimalà m baa	10.5

	403151			predicted exon	15.8
	452363	AI582743	Hs.94953	ESTs, Highly similar to C1QC_HUMAN COMPLEME	15.8
	425971	AF135024	Hs.165296	kallikrein 13	15.8
5	432826	X75363	Hs.250770	kalikrein 15	15.8
)	431972 400269	Al805145	Hs.191711	ESTs predicted exon	15.8 15.8
	404703	Al904493	Hs.99890	polymerase (DNA directed), delta 1, catalytic subunit (1	15.8
	449335	AW150717	Hs.296176	STAT induced STAT inhibitor 3	15.8
10	418443	NM_005239	Hs.85146	v-ets avian erythrobiastosis virus E26 oncogene homolo	15.8
10	445773 433782	H73456 AF090945	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (from gb:Homo sapiens clone HQ0670	15.8 15.8
	406473	A 030343		predicted exon	15.8
	420831	AA280824	Hs.190035	ESTs	15.8
1.5	402939			predicted exon	15.8
15	405196	A14H 20442		predicted exon	15.8 15.8
	452947 414170	AW130413 AA335996	Hs.3743	gb:xf50f04.x1 NCI_CGAP_Gas4 Homo saplens cDNA matrix metalloproteinase 24 (membrane-inserted)	15.8
	437133	AB018319	Hs.5460	KIAA0776 protein	15.8
20	458356	Al024855	Hs.131575	EST8	15.B
20	407857	A1928445	Hs.92254	hypothetical protein FLJ20163	15.8
	405687 415189	L34657	Hs.78146	predicted exon platelet/endothelial cell adhesion molecule (CD31 antig	15.8 15.8
	408662	AW247699	Hs.105897	ESTs	15.7
0.5	448338	A1492857		gb:th72h08.x1 Soares_NhHMPu_S1 Homo sapiens cDN	15.7
25	402694	*******	11. 005075	predicted exon	15.7
	430224 458792	AW675175 N56666	Hs.235975	hypothetical protein DKFZp434D0412 gb:yw75e02.r1 Soares_placenta_8to9weeks_2NbHP8to	15.7 15.7
	402944	1430000		predicted exon	15.7
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor 5A	15.7
30	408661	AW247625		gb:2820094.5prtme NIH_MGC_7 Homo saplens cDNA	15.7
	423238	AA323569	Hs.280482	ESTs	15.7
	421517 429865	AB018352 AB023217	Hs.105399 Hs.225968	KIAA0809 protein KIAA1000 protein	15.7 15.7
	440815	AW071945	Hs.7436	pulative acyltransferase	15.7
35	400634			predicted exon	15.7
	451034	AL050341	Hs.25846	zinc metalloproteinase, STE24 (yeast, homolog)	15.7
	457571	Al375726 BE281124	Hs.279918 Hs.288013	hypothetical protein similar to yeast BET3 (S. cerevisize)	15.7 15.7
	450105 407464	AJ276396	NS.200013	gb:Homo sapiens mRNA for matrix extracellular phosp	15.7
40	439465	AF086285		gb:Homo sapiens full length Insert cDNA clone ZD47B	15.7
	451837	T92157	Hs.16970	ESTs	15.7
	435313 402738	A1769400	Hs.189729	ESTs	15.7 15.7
	432986	AA650114		predicted exon gb:ns92h09.s1 NCI_CGAP_Pr3 Homo saplens cDNA c	15.7
45	457666	AW470302	Hs.129663	ESTs	15.7
	401269			predicted exon	15.7
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a ligand)	15.7
	418846 448891	AI821602 AI587332	Hs.115127 Hs.209115	ESTs ESTs	15.6 15.6
50	445930	AF055009	Hs.13456	Homo saplens clone 24747 mRNA sequence	15.6
	421254	AK001724	Hs.102950	coat protein gamma-cop	15.6
	447073	AW204821	Hs.157726	EST8	15.6
	445438 432126	AB014578 AA865239	Hs.12707 Hs.55144	KIAA0678 protein ESTs	15.6 15.6
55	424091		Hs.139263	calcium channel, voltage-dependent, alpha 1F subunit	15.6
	440832		Hs.128224	ESTs	15.6
	449228		Hs.148590	ESTs, Weekly similar to AF208846 1 BM-004 [H.saple	15.6
	434253	A1393345	Hs.116215	EST8	15.8 15.6
60	459270 454425	AL039604 AW300927	Hs.27192	gb:DKFZp434E2211_1 434 (synonym: htes3) Homo s hypothetical protein dJ1057B20.2	15.6
•	412055	AA099907	Hs.271806	ESTs	15.6
	400837			predicted exon	15.6
	458866		Hs.288042	Homo sapiens cDNA FLJ14299 fis, clone PLACE1010	15.6 15.6
65	417124 414376	BE122762 BE393856	Hs.25338 Hs.66915	ESTs ESTs, Wealdy similar to 16.7Kd protein (H.saplens)	15.6
05	418636	AW749855	110.00010	gb:QV4-BT0534-281299-053-c05 BT0534 Homo saple	15.6
	454128	AL031259	Hs.41639	programmed cell death 2	15.6
	441074	AW500001	Hs.4783	Homo sapiens cDNA: FLJ22035 fis, clone HEP08838	15.6 15.6
70	451742 403687	177609	Hs.117970	ankyrin 2, neuronal predicted exon	15.6
	431838	Al097229	Hs.217484	ESTs	15.6
	402855			predicted exon	15.6
	449635		Hs.232150	ESTs EST:	15.6 15.6
75	434392 444301		Hs.268051 Hs.10760	ESTs hypothetical protein FLJ20129	15.6
, 5	414973		120.10100	gb:C19089 Human placenta cDNA (TFujiwara) Homo	15.5
	428374	AW405156	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	15.5
	415745		Hs.150790	ESTs	15.5
80	432532 417112		Hs.162246	ESTs gb:zr41b09.s1 Soares_NhHMPu_S1 Homo saplens cDN	15.5 15.5
50	417112		Hs.98485	gap junction protein, beta 4 (connexin 30.3)	15.5
	453110		Hs.225160	Homo saplens cDNA FLJ13102 fis, clone NT2RP3002	15.5
	458606	AJ239397		gb:AJ239397 Uni-ZAP XR retinal pigment epithelium H	15.5
	436989	AA741028	Hs.256155	ESTs	15.5

	407396	AF011757		sh-Home conione BACC hinding protein (B12) mBNA	15.5
	449684	Al659166	Hs.207144	gb:Homo sapiens RAGE binding protein (P12) mRNA, ESTs	15.5
	454666	AW812994		gb:RC3-ST0186-230300-019-g02 ST0186 Homo saplen	15.5
•	430492	U15197	Hs.300803	Human histo-blood group ABO protein mRNA, partial	15.5
5	439460	AA836220	Hs.13774	ESTS	15.5
	449231 453060	BE410360 AW294092	Hs.21594	gb:601302340F1 NTH_MGC_21 Homo saplens cDNA ESTs	15.5 15.5
	416961	BE391476	Hs.80617	ribosomal protein S16	15.5
10	439988	AA860119	Hs.255976	ESTs	15.5
10	400917	1404040		predicted exon	15.5
	424585 431029	AA464840 BE392725	Hs.248571	gb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Homo Homo saptens PAC clone RP5-1163J12 from 7q21.2-q3	15.5 15.5
	441680	AW444598	Hs.7940	RAP1, GTP-GDP dissociation stimulator 1	15.5
	437830	AB020658	Hs.5867	KIAA0851 protein	15.5
15	409479	BE163800	Hs.136912	ESTs	15.5
	409885 459090	AW503068 AA443323	Hs.107812	gb:UI-HF-BP0p-aje-g-10-0-UI.r1 NIH_MGC_51 Homo ESTs, Weakly similar to SPOP [H.sapiens]	15.4 15.4
	429324	AA488101	Hs.199245	inactivation escape 1	15.4
	403766	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		predicted exon	15.4
20	413970	U59309	Hs.75653	fumarate hydratase	15.4
	456674	BE266120	Hs.269358	ESTs	15.4 15.4
	417931 430125	W95642 U46418	Hs.82961 Hs.233950	trefoil factor 3 (intestinal) serine protease inhibitor, Kunitz type 1	15.4
	452154	AW953265	Hs.271277	hypothetical protein from EUROIMAGE 363668	15.4
25	422984	W28614	Hs.75984	chorionic somatomammotropin hormone 2	15.4
	408649	BE242232	Hs.26045	protein tyrosine phosphalase, receptor type, A	15.4
	417497 404666	AW402482	Hs.82212	CD53 anligen predicted exon	15.4 15.4
	456847	Al360456	Hs.37776	ESTs	15.4
30	426995	AA400646	Hs.221988	ESTs	15.4
	445350	AF052112	Hs.12540	lysophospholipase I	15.4
	450214 449733	BE439763 R74546	Hs.227571 Hs.29438	regulator of G-protein signalling 4 Homo saptens cDNA FLJ12094 fis, clone HEMBB100	15.4 15.4
	411660	AW855718	115.23400	gb:RC1-CT0279-070100-021-a06 CT0279 Homo saple	15.4
35	442653	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
	447552	AI394125	Hs.160413	ESTs	15.4
	448712	W01046	Hs.181634	Homo saplens cDNA: FLJ23602 fis, clone LNG15735	15.4 15.4
	420180 440099	A1004035 AL080058	Hs.25191 Hs.6909	ESTs OKFZP564G202 protein	15.4
40	427550	BE242818	Hs.179606	nuclear RNA helicase, DECD variant of DEAD box fam	15.4
	432894	AW167668	Hs.279772	brain specific protein	15.3
	412113	AW161274	Hs.74427	p53-induced protein	15.3
	431614	A1189827 AW410053	Hs.13406	gb:qd19d07.x1 Soares_placenta_8to9weeks_2NbHP8to syntaxin 18	15.3 15.3
45	445870 424347	AA723883	Hs.145513	Homo saplens mRNA; cDNA DKFZp434L0435 (from	15.3
	425132	AW250114		gb:2821134.5prime NIH_MGC_7 Homo saplens cDNA	15.3
	439756	AL359651	Hs.283852	Homo saplens mRNA full length insert cDNA clone EU	15.3
	432946 406130	U60899	Hs.279854	mannosidase, alpha, class 28, member 1 predicted exon	15.3 15.3
50	453359	AA448787	Hs.24872	ESTs, Weakly similar to aortic carboxypeptidase-like p	15.3
	405491			predicted exon	15.3
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	15.3
	446826	AK000626	Hs.16230 Hs.7750	hypothetical protein FLJ20619 hypothetical protein AL133206	15.3 15.3
55	441211 418711	AW946155 AW247977	Hs.87595	translocase of inner mitochondrial membrane 22 (yeast)	15.3
	457301		110101000	gb:nc67e03.s1 NCI_CGAP_Pr1 Homo saplens cDNA c	15.3
	449999	Al679421	Hs.231098	ESTs, Highly similar to ALU4_HUMAN ALU SUBFA	15.3
	439090 416586	H65724 D44643	Hs.271663 Hs.14144	ESTs secreted modular calcium-binding protein 1	15.3 15.3
60	411940	AW876686	115.14144	gb:CM4-PT0031-180200-507-e05 PT0031 Homo saple	15.3
	407639	AW205369	Hs.252936	ESTs	15.3
	458012	AI424899	Hs.188211	ESTs	15.3 15.3
	426490 408741		Hs.170087 Hs.646	aryl hydrocarbon receptor carboxypeptidase A3 (mast cell)	15.3
65	437371		Hs.5570	hypothetical protein FLJ10006	15.3
	437134		Hs.42915	ARP2 (actin-related protein 2, yeast) homolog	15.3
	441890		Hs.128075	ESTS	15.3
	409442 407078		Hs.169248	cytochrome c gb:H.saptens isoform 1 gene for L-type calcium channe	15.3 15.2
70	436553		Hs.181125	Immunoglobulin lambda locus	15.2
	443177		Hs.202	benzodiazaplne receptor (peripheral)	15.2
	448771		Hs.296244	SNARE protein	15.2
	436837 423623	AI968248 AB011117	Hs.187869 Hs.129943	ESTs KIAA0545 protein	15.2 15.2
75	422651		Hs.118926	DKFZP586K0919 protein	15.2
	403221		Hs.119500	karyopherin alpha 4 (Importin alpha 3)	15.2
	431620	AA126109	Hs.264981	2-5 oligoadenylate synthetase 2	15.2
	404794		Hs.89538	cholesteryl ester transfer protein, plasma ESTs	15.2 15.2
80	412944 450817		Hs.197143 Hs.29698	ESTS ESTS	15.2
	418666		Hs.155119		15.2
	451636	AW173270	Hs.140444		15.2
	426302		Hs.275163	non-metastatic cells 2, protein (NM238) expressed in gb:PM0-UM0018-120400-002-h01 UM0018 Homo sep	15.2 15.2
	454485	AW795322		go:rwo-owoo 16-120400-002-101 0woo 16 Hotto Sap	10.2
				1'12	

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	440617	AA894880	Hs.181181	ESTs	15.2
	449718	AA459480	Hs.23956	hypothetical protein FLJ20502	15.2
	405227 431006	BE152871		predicted exon gb:CM1-HT0333-101299-064-d12 HT0333 Homo sapi	15.2 15.2
5		AW058594	Hs.133878	ESTs, Weakly similar to AF151889 1 CGI-131 protein	15.2
	438828		Hs.6434	hypothetical protein DKFZp761F2014	15.2
	407634 436857	AW016569 AA732647	Hs.301280	ESTs, Highly similar to AF241831 1 intracellular hyalu gbmz89d01.s1 NCL_CGAP_GC81 Homo sapiens cDN	15.2 15.2
		Y10129	Hs.258742	myosin-binding protein C, cardiac	15.1
10		NM_006289	Hs.18420	KIAA1027 protein	15.1
		AA723297	Hs.127138	ESTs	15.1
		BE618609	Hs.279591	Homo saptens clone 25056 mRNA sequence	15.1
		AL353957 AW083791	Hs.284181	hypothetical protein OKFZp434P0531	15.1 15.1
15		AA993138	Hs.21263 Hs.142287	Homo saplens cDNA FLJ13152 fis, clone NT2RP3003 ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CL	15.1
10		BE387420	Hs.241531	pelin	15.1
		AW291276	Hs.285532	ESTs	15.1
		. AB017548	Hs.160100	Homo saplens gene for Septapterin Reductase, partial c	15.1
20		AI884911	Hs.32989	receptor (calcitonin) activity modifying protein 1	15.1
20	447246	AW449032	Hs.170257	ESTs predicted exon	15.1 15.1
		AA018893	Hs.3727	unr-interacting protein	15.1
		Al695549	Hs.183868	glucuronidase, beta	15.1
0.5		AI809587	Hs.148782	ESTs ·	15.1
25	425972		Hs.165433	ESTs, Highly similar to T17342 hypothetical protein D	15.1
	426062		Hs.44013	ESTS	15.1
	451234 429565	AI914901 AB020719	Hs.24052 Hs.207802	ESTs KIAA0912 protein	15.1 15.1 ·
	418092		Hs.106604	ESTs	15.1
30		Al650541	Hs.115298	ESTs	15.1
	425023		Hs.154210	endothelial differentiation, sphingolipid G-protein-coup	15.1
	445213		Hs.170784	ESTs .	15.1
	418102		Hs.26608	ESTS	15.0
35	450082		Hs.245893 Hs.16089	ESTs CCI 136 protein	15.0 15.0
55	446749 406124	NW_010003	FIS. 10009	CGI-136 protein predicted exon	15.0
	457408	AL137507	Hs.255348	Homo saplens mRNA; cONA DKFZp761P211 (from c	15.0
	410051		Hs.218182	ESTs, Weakly similar to dJ1042K10.2 [H.sapiens]	15.0
40	440965		Hs.169859	ESTs .	15.0
40	440190	AW752597	LI- 02422	gb:lL3-CT0214-161299-045-806 CT0214 Homo sepien	15.0 15.0
	417437 454249	U52682 AW249008	Hs.82132	interferon regulatory factor 4 gb:2821048.5prime NIH_MGC_7 Homo saplens cDNA	15.0
	432276		Hs.274255	somatostatin receptor-interacting protein	15.0
	401116	,		predicted exon	15.0
45		AA164516	Hs.136309	CGI-61 protein	15.0
	451661		Hs.26777	KIAA0843 protein	15.0
	450983		Hs.25740	ERO1 (S. cerevisiae)-like	15.0
	446187 404122	AK001241	Hs.14229	hypothetical protein FLJ10379 predicted exon	15.0 15.0
50	411299	BE409857	Hs.69499	hypothetical protein	15.0
-	403077	DC-100001	1 10.00	predicted exon	15.0
	438000	A1825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	15.0
	447118	AB014599	Hs.17411	KIAA0699 protein	15.0
55	417878		Hs.82845	Human clone 23815 mRNA sequence	15.0 15.0
33	444079 458234		Hs.23606 Hs.127196	ESTs ESTs	15.0
	434208		Hs.127648	hypothetical protein PRO2176	15.0
	423136		Hs.124147	ESTs	15.0
60	403177			predicted exon	15.0
60		AI857269	Hs.227351	ESTs	15.0
		AW957442	Hs.252766 Hs.155335		15.0 15.0
	423430	AJ381837	ris. 100000	2018	13.0
	TABLE	38:			
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		mber: Gene dust			
	Accessi	on: Genbank acc	ession number	3	
	Pkey	CAT Number	Accessi	-n	
70	· 408310			23 AW179010	
, •	408647	1071855_1		31 AW273207	
	408651	1073036_1		25 AW249214	
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13	409545 409828			82 AW629821 I37 AW501295 AW501212	
	409865			208 AW502366 AW502148	
	409885			068 AW503789	
00	410003		AA0794	87 AA128547 AA128291 AA079587 AA079600	
80	410186	1182096_1	AW602	528 BE073859 Z38412	
	410626		BE4077		2 0E146313 AMR12106 AMRETED3 AMRICO14 DECOTEDS
	411004		AW813	242 BE146089 AW813195 AW813173 AW813206 BE14595 D72 AW813375 AW813385 AW813372 AW813436 AW8161	3 BE146212 AW813196 AW854582 AW813241 BEU61582 48 AW813475 AW816107 AW813398 AW813479 AW814475 AW813317
	411014 411028			1/2 AW\$133/5 AW\$13365 AW\$133/2 AW\$13436 AW\$1614 703 AW\$13839	1100 DAY CHANDRA ELECTORY REPORTED IN INCIDITAL PRINCIPAL
	711020	1823707_1	711013	•	
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AW855392 AW855559 AW855423
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           Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402489-495
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10	405537	7711478	Plus	32904-33017
	406571	7711622	Minus	65634-65912,66116-66596
	406580	7711838	Minus	96654-97640

15 TABLE 4A lists about 131 genes up-regulated in ovarian cancer compared to normal ovaries that are likely to be extracefular or cell-surface proteins. These were selected as for Table 3A, except that the ratio was greater than or equal to 10, and the predicted protein contained a PFAM domain that is indictive of extracefular localization.

TABLE 4A: ABOUT131 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL OVARY Pkpy: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Tide: Unigene Title
PFAM domains

20

ratio: turnor vs. normal overy

25	1000. 1211	DI 15. NOI MAI 010	u y	*		
	Pkey	Ex. Acon	UGID	Title	PFAM	ratio
	403077			predicted exon	fn3	15.0
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TP	Kunitz_BPTI	14.9
20	403089			predicted exon	fn3	14.9
30	457148	AF091035	Hs.184627	KIAA0118 protein	erf;res	14.8
	431176	Al026984	Hs.293662	ESTs	taminin_EGF;taminin_B;	14.8
	434293	NM_004445	Hs.3796	EphB6	fn3;pklnase;EPH_lbd	14.8
	408482	NM_000676	Hs.45743	edenosine A2b receptor	7lm_1	14.6
25	428695	Al355647	Hs.189999	purinergic receptor (family A group 5)	7tm_1	14.5
35	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) ho	EGF	14.4
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxy	sugar_tr,MCT	14.3
	422125	NM_003459	Hs.111967	solute carrier family 30 (zinc transporte	Cation_efflux	14.2
	407483	NM_012368	41-467040	(NONE)	7tm_1	14.2
40	446689 410184	AW594695	Hs.167046	ESTs 45	7(m_1	14.1
40		AW503667	Hs.59545	ring finger protein 15	zf-C3HC4;SPRY;zf-B_box	14.0
	423217 405448	NM_000094 Al015709	Hs.1640 Hs.172089	collagen, type VII, alpha 1 (epidermoly Homo saplens mRNA; cDNA DKFZp5	fn3;vwa trypsin;sushi;CUB	14.0 14.0
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II		14.0
	406692	L36607	ns.23333	gb:Homo saplens (clone 22) pregnancy	ig ig	13.9
45	425549	U64863	Hs.158297	programmed cell death 1	ig Ig	13.8
10	452755	AW138937	Hs.213436	ESTs	cystatin	13.8
	427637	AK000816	Hs.179986	flotilin 1	Band_7	13.7
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	7tm_1	13.7
	405024		110.100000	predicted exon	TGF-beta;TGFb_propeptide	13.7
50	405285			predicted exon	A2M;A2M_N	13.7
	412116	AW402166	Hs.784	Epstein-Barr virus Induced gene 2 (lym	7tm_1	13.7
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascu	cadherin;Cadherin_C_lerm	13.6
	420511	AF052692	Hs.98485	gap junction protein, beta 4 (connexin 3	connexin	13.5
	448638	R17122	Hs.21639	nuclear protein, marker for differentiat	ig	13.4
55	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF:DSL	13.4
	439285	AL133916	Hs.298998	ESTs	ig:pkinase:LRRNT;LRRCT	13.4
	424283	AA338246	Hs.301678	ESTs	E1-E2_ATPase;Hydrolase	13.3
	436233	A1742878	Hs.124116	ESTs	lg .	13.3
	443859	NM_013409	Hs.9914	follistatin	kazal	13.2
60	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (IL8	13.2
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologo	IL8	13.2
	400242			predicted exon	Ephrin .	13.0
	429057	AF156557	Hs.194816	slomatin-like protein 1	Band_7;SCP2	12.9
CE	438294	A1693753	Hs.143004	ESTs	E1-E2_ATPase;Hydrolase	12.9
65	458493	AV849408	Hs.282418	ESTs	RYDR_ITPR	12.8
	444181	AB033063	Hs.10491	KIAA1237 protein	fn3;lg;PH;RhoGEF	12.8
	422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	cadherin	12.7
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	serpin	12.7
70	407000	U12139	11- 45440	gb:Human alpha1(XI) collagen (COL1	TSPN;Collagen;COLFI	12.6
70	417064	W02903	Hs.15440	ESTs	lectin_c	12.6
	439389	AA318940	Hs.56004	ESTs	hamopexin;Peptidase_M10	12.6
	407786	AA687538	Hs.38972	tetraspan 1	transmembrane4	12.5
	410498	AA355749	ti. 400007	gb:EST64459 Jurkat T-cells VI Homo	8a_permeases	12.5
75	422487	AJ010901	Hs.198267 Hs.115263	mucin 4, tracheobronchial	wd EGF	12.5
13	422330 402425	D30783	FIS. 1 1 32 93	epiregulin		12.5 12.4
	414875	H42679	Hs.77522	predicted exon major histocompatibility complex, clas	ion_trans	12.4
	424239		Hs.143526	dopamine receptor D5	ig 71-m 4	12.2
	442622	M67439 NM_000435	Hs.8546	Notch (Drosophila) homolog 3	7tm_1 EGF;ank;notch	12.2
80	405368	1116_000433	18.0540	predicted exon	7tm_1	12.2
00	402406			predicted exon	Gal-bind_lectin	12.1
	426514	BE616633	Hs.301122	bane morphogenetic protein 7 (osteoge	TGF-beta;TGFb_propeptide	12.1
	406811	U82979	Hs.67846	teukocyte kmmunoglobulin-like recepto	ig	12.0
	416441	BE407197	10.070	. gb:601301552F1 NIH_MGC_21 Homo	SDF	12.0
	410441	DC-101 131		· Bernataaran · · · · · · · · · · · · · · · · · · ·	75 1	12.0

	100004	100/00/2		10144404		(.n. i.nner	44.6
	433221 442915	AB040917 AA852875	Hs.97860 Hs.8850	KIAA1484 protein		fn3;ig;LRRCT dlsintegrin;Reprolysin;	11.9 11.9
	423613	AF036035	Hs.129910	a disintegrin and metalloproteinase dom hyaluronoglucosaminidase 3		ig;Sema;Acelyltransf	11.9
_	411213	AA676939	Hs.69285	neuropilin 1		CUB;MANt;F5_F8_type_C	11.9
5	425483	AF231022	Hs.301273	Homo septens protocadherin Fat.2 (FA		EGF;cadherin;laminin_G	11.8
	421258	AA286731		gb:zs53d08.r1 NCL_CGAP_GCB1 Hom		7tm_3	11.8
	423795	AW849759	11-440-73	gb:IL3-CT0218-240200-077-C04 CT0		arf,ras	11.7
	422424 443296	AI186431 AI765286	Hs.116577	prostate differentiation factor gb:wi73b05.x1 NCI_CGAP_Kid12 Ho		TGF-beta ig	11.7 11.7
10	448999	AF179274	Hs.22791	transmembrane protein with EGF-like		kazal	11.7
. •	414878	AA341040	Hs.77541	ADP-ribosylation factor 5		art;ras	11:5
	429344	R94038	Hs.199538	inhibin, beta C		TGF-beta	11.5
	402114			predicted exon		laminin_EGF;laminin_G	11.5
16	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (IL8	11.5
15	430263	D12614	Hs.36	lyphotoxin alpha (TNF superfamily, m		TNF Bostidada CO	11.4 11.4
	400464 456841	AA875863	Hs.152345	predicted exon pollovirus receptor-related 1 (herpesvir		Pepildase_S9 Ig	11.4
•	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kal		laminin_EGF;laminin_B	11.4
	418043	AW377752	Hs.83341	Haspiens mRNA for tyrosine kinase re		fn3;ig;pkinase	11.3
20	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrog		Na_H_Exchanger	11.3
	446051	BE048061	Hs.153315	ESTs		Reprolysin; disintegrin	11.3
	439710	AF086543	11- 70000	gb:Homo saplens full length insert cDN		Xlink	11.3
	416602	NM_006159 AA279530	Hs.79389 Hs.83968	nel (chicken)-like 2		vwc;TSPN integrin_B	11.3 11.3
25	418299 425721	AC002115	Hs.159309	Integrin, betå 2 (antigen CD18 (p95), ly uroplakin 1A,		transmembrane4;COX6B;Ets	11.2
	409757	NM_001898	Hs.123114	cystatin SN		cystatin	11,2
	430630	AW269920	Hs.2621	cystatin A (stefin A)		7tm_3;ANF_receptor	11.2
	429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perieca		laminin_EGF;ig;ldi_recept_a	11.1
20	427289	A1097346	Hs.174203	solute carrier family 1 (glutamate/neutr		SDF	11.1
30	401248	AB028989	Hs.88500	milogen-activated protein kinase 8 inte		wa;wd;TlL	11.1
	412627 420104	BE391959 U09825	Hs.74276 Hs.1287	chloride intracellular channel 1 zinc finger protein 173		G-patch;ig;MutS_C zf-C3HC4;SPRY;zf-B_box	11.1 11.1
	405275	AB028989	Hs.88500	mitogen-activated protein kinase 8 inte		vwa;vwd;TiL	11.1
	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily		7tm_1	11.1
35	446745	AW118189	Hs.156400	ESTs		wwa	11.1
	441834	AL138034	Hs.7979	KIAA0736 gene product		sugar_tr	11.0
	450986	BE241845	Hs.25744	Novel human gene mapping to chomos		PH;RhoGAP;Gal-blnd_lectin	11.0
	416118	N52773	Hs.167721	ESTs		hemopexin;Peptidase_M10	11.0
40	443071 431247	AL080021 AL021578	Hs.8986 Hs.278489	complement component 1, q subcompo matrilin 4		C1q;Collagen EGF;vwa	10.9 10.9
40	431449	M55994	Hs.256278	tumor necrosis factor receptor superfam		TNFR_c6	10.9
	457044	S73899	Hs.2131	arginine vasopressin receptor 1A		7tm_1	10.9
	416319	Al815601	Hs.79197	CD83 antigen (activated B lymphocyte		lg _	10.8
4.5	402172			predicted exon		lg	10.7
45	424218	AF031824	Hs.143212	cystatin F (leukocystatin)		cystatin	10.6
	409208	Y00093	Hs.51077	integrin, alpha X (antigen CD11C (p15		vwa	10.6
	426330	M77235	Hs.169331	sodium channel, voltage-gated, type V,		lon_trans;IQ transmembrane4	10.6 10.6
	439758 412429	AA845235 AV650262	Hs.124470 Hs.75765	ESTs GRO2 oncogene		IL8	10.6
50	449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 11		ABC_tran;ABC_membrane	10.6
	432408	N39127	Hs.76391	myxovirus (Influenza) resistance 1, hom		ion_trans;K_tetra	10.6 ·
	406672	M26041	Hs.198253	major histocompatibility complex, clas		ig;MHC_II_alpha	10.5
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like		kazal;thyrogiobulin_1	10.5
55	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence		fn3;wap	10.5 10.5
33	425009	X58288 BE409301	Hs.154151 Hs.134012	protein tyrosine phosphatase, receptor t C1q-related factor		fn3;ig;Y_phosphatase;MAM GTP_EFTU;EFG_C	10.5
	423869 430209	AF177941	Hs.235368	Pro-(alpha)3(V) collagen		Collagen; COLFI; TSPN	10.4
	400834	14 111011	110.20000	predicted exon		IRK	10.4
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61		Cys_knot;tsp_1;vwc;IGFBP	10.4
60	403691			predicted exon		tsp_1;Reprolysin;	10.4
	430776	AJ011021	Hs.247905	potassium voltage-gated channel, subfa		ion_trans	10.3
	432342	AL036128	Hs.274404 Hs.75511	plasminogen activator, tissue connective tissue growth factor		EGF;fn1;kringle;trypsin Cys_knot;tsp_1;vwc	10.3 10.3
	413731 423309	BE243845 BE006775	Hs.126782	sushi-repeat protein		sushi:HYR	10.3
65	431728	NM_007351		multimerin		EGF;C1q	10.3
00	450245	AA007536	Hs.271767	ESTs, Moderately similar to ALU1_HU		lg .	10.2
	446983	AA157484	Hs.97199	complement component C1q receptor		EGF;Xlink	10.2
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		death;ank;ZU5	10.1
70	400253			predicted exon		7tm_1	10.0
70	406694	M94891	Hs.225932	pregnancy specific bela-1-glycoprotein		ig EGF	10.0 10.0
	418793 410664	AW382987 NM_006033	Hs.88474 Hs.65370	prostaglandin-endoperoxide synthase 1 lipase, endothelial		Ribosomal_L22	10.0
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo		pkinase;ig	10.0
				A constant to the constant to		•	
75	TABLE 4						
		nique Eos probe		mber			
		ber: Gene dus		•			
	Accessio	n: Genbank acc	ession numbers	3			
80	Cha.	CATAL	r Accession				
ov.	Pkey 410498	CAT Numbe 120611_1		A085520 AW966333 AA340319 BE170936			
	416441	159480_1		A182474 AA180369 BE275628 BE276131			
	421258	200725_1		A287621 AW188228 AW137774			
	423795	232093_1	AW849759	AW849758 T89549 AA331069			
					133		

439710 47550_1 AF066543 W96291 W96225 443296 56539_2 Al765286 AW297086 BE568658 TABLE 4C: Ref: Valque number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402489-495 5 Strand: Indicates DNA strand from which exons were predicted NL position: Indicates nucleotide positions of predicted exons 10 Pkey 400464 400834 Ref 9929670 8705192 Nt_position 22074-22214 121963-122288 Strand Plus Plus 402114 8318586 Plus 71578-71715 8575911 3970929 9796347 8954241 15 402172 Minus 143378-143671 10872-11123,12932-13048 50224-50395 146923-147222,147326-147628 171964-172239 80280-88463 402406 Plus 402425 Minus 403077 Plus 403089 8954241 Plus 20 403691 7387384 Minus 405024 7107727 Plus 55744-55903,57080-57170,61478-61560 46055-47188 88500-88697 405285 6139075 Minus

TABLE 5A lists about 685 genes down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 3A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal ovary).

TABLE 5A: 68S DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

30 Pkey: Primekey Ex. Acon: Exemplar Accession UGID: UniGene ID Title: UniGene Title

405368

25

25

ratio: ration normal overy vs tumor

2104517

Plus

35		•			
	Pkey	Ex, Acon	UGID	Title	ratio
	421013	M62397	Hs.1345	mutated in colorectal cancers	14.8
	439360	AA448488	Hs.55346	ESTs, Weakly similar to Z141_HUMAN ZINC FINGE	12.8
	407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, member 2	12.6
40	424851	AA676441	Hs.119059	ESTs	11.6
	455056	AW853057		gb:RC1-CT0249-170200-025-h04 CT0249 Homo saple	11.5
	420727	H75701	Hs.99886	complement component 4-binding protein, beta	11.3
	451617	C01056	Hs.168000	ESTs	10.0
4.5	401308			predicted exon	9.9
45	440987	AA911705	Hs.130229	ESTs	9.7
	409725	T40760	Hs.90459	EST	9.7
	415752	BE314524	Hs.78776	putative transmembrane protein	9.7
	437690	AAB04362	Hs.180544	ESTs	9.6 .
	437787	Al908263	Hs.291625	ESTs	• 9.5
50	459054	AW798466	Hs.82396	2,5-oligoadenylate synthetase 1	9.2
	435330	R16769	Hs.185689	ESTs	9.2
	436642	AA724430	Hs.127960	ESTs	9.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2) Homo sa	9.1
	451683	Al808964	Hs.207673	ESTs	9.1
55	401464	AF039241	Hs.9028	histone deacetylase 5	9.0
	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Hom	8.7
	410758	8E535988		gb:601062418F1 NIH_MGC_10 Homo sepiens cDNA	8.7
	412637	AA115097	Hs.261313	ESTs	8.4
	419166	AA234638	Hs.293584	ESTs	8.3
60	423739	AA398155	Hs.97600	ESTs	8.1
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	8.1
	416211	R14625		gb:yg45c03.r1 Soares infant brain 1NIB Homo saplens	8.0
	443131	A1033833	Hs.132689	ESTs	7.9
15	415866	T10115	Hs.92423	KIAA1566 protein	7.9
65	410130	AI912097	Hs.163208	ESTs	7.9
	439426	Al131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE	7.8
	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	7.7
	419015	T79262	Hs.14463	ESTs	7.6
70	441573	BE563966	Hs.6529	ESTs	7.5
70	419386	AA236867	Hs.143868	ESTs	7.5
	430562	D78260	Hs.285097	ESTs	7.5
	434738	AA836265		gb::::d17e02.s1 NCI_CGAP_GCB1 Homo saplens cDNA	7.4
	403283			predicted exon	7.4
76	415861	Z43123	Hs.144513	ESTs	7.4
75	412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo saple	7.4
	441247	AW118681	Hs.128051	ESTs	7.4
	442865	N57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c-	7.3
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapia	7.3
00	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo saptens cDNA	7.3
80	421418	AA805639		gb:ob88g05.s1 NCI_CGAP_GC81 Homo saplens cDN	. 7.2
	413597	AW302885	Hs.117183	ESTs	7.2
	454102	AW752363		gb:RCO-CT0201-270999-011-f03 CT0201 Homo sapien	7.1
	445487	AI806287	Hs.201217	ESTs	7.1
	457604	AJ004397	Hs.130558	ESTs, Weakly similar to similar to O-sialoglycoprotein	7.1

	400040			8-1-1	
	400942 407596	R86913		pradicted exon object 1 Segment and Business 1 MELS Home ex	6.9 6.9
	422046	AI638562		gb:yq30f05.r1 Soares fetal liver spicen 1NFLS Homo sa gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA c	6.9
_	441284	AA927676	Hs.196542	ESTs	6.9
5	446224	AW450551	Hs.13308	EST ₈	6.9
	424943	AU077260	Hs.153924	death-associated protein kinase 1	6.9
	453967	AW009077	Hs.232947	ESTs	6.9
	448583	AA167642	Hs.14632	ESTs	6.8
10	431877 411337	AA521204 AW837349	'Hs.105507	ESTs gb:QV2-LT0038-270300-108-d12 LT0038 Homo saple	6.8 6.8
10	410596	AA374186		gb:EST86290 HSC172 cells I Homo sapiens cDNA 5' e	6.8
	417762	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937233) Homo	6.7
	405364			predicted exon	6.7
	452238	F01811	Hs.187931	ESTs, Moderately similar to S22703 voltage-gated pota	6.7
15	415288	R15794	Hs.141027	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	6.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cds.	6.7
	439126	AF085984		gb:Homo sapiens full length insert cDNA clone YT99F	6.6
	452453 431800	AJ902519 AW452768	Hs.162045	gb:QV-BT009-101198-051 BT009 Homo saplens cDNA ESTs	6.6 6.5
20	426380	A1291267	Hs.149990	ESTs, Weakly similar to unnamed protein product (H.sa	6.5
	449529	Al990559	Hs.232033	ESTs	6.4
	437755	AW204256	Hs.291887	ESTs	6.4
	448307	AJ480289	Hs.211026	ESTs	6.4
0.5	439586	AA922936	Hs.110039	ESTs	6.4
25	420051	N35696	Hs.44745	ESTs	6.4
	425806	AI522299	Hs.173369	EST6	6.4
	433923 408159	A1823453 H63977	Hs.146625 Hs.118526	ESTs .	6.4 6.3
	434844	AF157116	Hs.301355	hypothetical protein LOC56757	6.3
30	430197	AA468888	Hs.187697	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	6.3
	440332	Al218517	Hs.188051	ESTs	6.3
	450061	AI797034	Hs.201115	ESTs ·	6.3
	454994	AW850176		gb:IL3-CT0219-271099-022-H04 CT0219 Homo sapien	6.3
25	402105	112000	11 400405	predicted exan	6.3
35	409090	W56067	Hs.103105	ESTs	6.2 6.2
	405752 408074	R20723	Hs.124764	predicted exon ESTs	6.2
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	6.1
	416310	T81421	Hs.221396	ESTs	6.1
40	421976	AL138443	Hs.23450	mRNA for FLJ00023 protein	6.1
	429755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	6.0
	448732	BE614063		gb:601503993F1 NIH_MGC_71 Homo sapiens cDNA	6.0
	453909	AW004045	Hs.203365	ESTs	6.0
45	431178	AA493884	Hs.218008	Homo saplens cDNA: FLJ21440 fis, clone COL04389	6.0 6.0
40	449671	AW959755 W01715	Hs.288896 Hs.102958	Homo sapiens cDNA FLJ12977 fis, clone NT2RP20062 ESTs, Weakly similar to Lpg6p [S.cerevisiae]	6.0
	421349 453282	AK000043	Hs.32922	hypothetical protein FLJ20036	5.9
	420618	AA278781	Hs.280698	ESTs	5.9
	412480	BE142364		gb:CMO-HT0143-270999-062-d12 HT0143 Homo sapi	5.9
50	449858	AW205979	Hs.196065	ESTs	5.9
	429884	AL049925	Hs.225984	DKFZP547G0910 protein	5.9
	416453	H56968	Hs.114593	ESTs	5.9
	459497	AA825742 AA759293	Hs.87517 Hs.112692	ESTS ESTS	5.9 5.9
55	433773 458942	AA739293 AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin a	5.9
33	436054	AJ076262	Hs.119813	ESTs	5.9
	410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF H	5.8
	403277			predicted exon	5.8
C 0	444302	Al140115	Hs.225130	ESTs	5.8
60	439834	AJ754576	Hs.124523	ESTs	5.8
	404020	AW381251	Nº 4VEV	predicted exon pleckstrin homology, Sec7 and coiled/coil domains 1(cy	5.8 5.7
	454338 430922	AW373747	Hs.1050 Hs.183337	ESTs	5.7 5.7
	420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	5.7
65	428498	AA429575	Hs.243032	ESTs	5.7
	445597	H65649		gb:yr72d10.r1 Soares fetal liver spleen 1NFLS Homo sa	5.7
	411543	AW851248		gb:iL3-CT0220-160200-056-F01 CT0220 Homo saplen	5.7
	408354	AJ382803	Hs.159235	ESTs	5.7
70	444431	AW513324	Hs.42280	ESTs	5.7 5.7
70	406605	AF039241	U- 0030	predicted exon histone deacetylase 5	5. <i>f</i> 5.6
	405541 458090	AP039241 AI282149	Hs.9028 Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD	5.6
	454529	Z45439	Hs.270425	ESTs	5.6
	445832	Al261545		gb:qz30a07.x1 NCI_CGAP_Kid11 Homo sapiens cONA	5.6
75	441223	AI475067	Hs.132499	ESTs	5.6
	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	5.6
	443650	A1698330	Hs.151444	ESTs	5.6
	403714	A) 497449	D= 40144	predicted exon	5.6 5.6
80	444165 458914	AL137443 BE327696	Hs.10441 Hs.280922	hypothetical protein FLJ11236 ESTs	5.6 5.6
50	420620	AA278807	Hs.173343	EST8	5.5
	458228	AA934995	Hs.184846	ESTs, Weakly similar to R28830 1 [H.sapiens]	5.5
	448067	R68568	Hs.183373	src homology 3 domain-containing protein HIP-55	5.5
	427000	Al187420	Hs.145221	ESTs	5.5

	450054	4400000		1 .00.104 .4.0	
	452351 459359	AA025647 N99545		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W Homo sa	5.5 5.5
	408385	AF055634	Hs.44553	gb:za40a05.r1 Soares fetal liver spieen 1NFLS Homo sa unc5 (C.elegans homolog) c	5.5
	450938	AW753734	Hs.277215	ESTs	5.5
5	431888	H99557	Hs.2864	early endosome antigen 1, 162kD	5.4
	459418	W96550	Hs.26418	ESTs	5.4
	416718	R83017	Hs.204828	ESTs	5.4
	413235	H16442	Hs.127376	KIAA0266 gene product	5.4
10	439063	AF085922	Hs.113968	ESTs	5.4
10	446361 458253	Al291234 AW296952	Hs.282241 Hs.196802	ESTs ·	5.4 5.4
	433682	AA642418	Hs.17381	ESTs	5.4 5.4
	455790	BE090690	114.11.001	gb:RC1-BT0720-280300-011-g02 BT0720 Homo sapie	5.4
	445755	AW294870	Hs.223672	ESTs	5.3
15	436513	AJ278110	Hs.125507	DEAD-box protein	. 5.3
	416671	N94087	Hs.26073	ESTs, Moderately similar to HG14_HUMAN NONHIS	5.3
	440231	AW015420	Hs.163323	ESTs	5.3
	429866	AA460104	Hs.99540	ESTs	5.3
20	437779	AA345232	Hs.21227	ESTs	5.3
20	424029	AB014594	Hs.137579	KIAA0694 gene product	5.3
	425614 430653	AJ334983 AW902062	Hs.156256 Hs.30280	ESTs ESTs	5.3 5.2
	408855	T83061	Hs.279604	desmin	5.2
	410454	AW749041	115.27 5004	gb:RC3-BT0319-100100-012-c05 BT0319 Homo sapie	5.2
25	438116	AI904105	Hs.122016	ESTs	5.2
	409138	W73159	Hs.58290	ESTs	5.2
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-specific)	5.2
	440212	AW300959	Hs.126216	ESTs, Wealty similar to good similarity to E. coti hypo	5.2
20	404108			predicted exon	5.2
30	456253	T12198		gb:A588F Heart Homo saplens cDNA clone A588, mRN	5.2
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.1
	444013	T08531	Hs.44404	hypothetical protein PRO1488	5.1
	454071	AI041793	Hs.42502	ESTs	5.1 5.1
35	419761 451250	M17373 AA491275	Hs.93177 Hs.236940	interferon, beta 1, fibroblast Homo sapiens cDNA FLJ12542 fis, clone NT2RM4000	5.1
55	405290	PM31213	F18.230340	predicted exon	5.1
	454487	AW796342		gb:PM2-UM0027-230200-002-h02 UM0027 Homo sap	5.1
	444131	AI806600	Hs.207119	EST, Weakly similar to Intrinsic factor-B12 receptor pr	5.1
	441679	BE502267	Hs.65996	ESTs	5.1
40	450077	AA523752	Hs.120855	ESTs	5.1
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	5.1
	445140	AI650599	Hs.197913	ESTs	5.1
	421126	M74587	Hs.102122	insulin-like growth factor binding protein 1	5.1
45	447037	Al357568	Hs.157612	ESTS	5.1 5.0
43	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Homo sapiens gb:Homo sapiens cDNA FLJ10222 fis, clone HEMBB1	5.0
	436196 442772	AK001084 AW503680	Hs.300513	ESTs, Weakly similar to T1587.2 [C.elegans]	5.0
	444138	A1701572	Hs.151153	ESTs	5.0
	458589	AV654623	Hs.288141	Homo sapiens cDNA FLJ13016 fis, clone NT2RP30006	5.0
50	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chromos	5.0
	441318	AI078234	Hs.176130	ESTs	5.0
	407490	S79281		gb:pancreatic ribonuclease [human, mRNA Recombinan	4.9
	438224	AA933999		gb:on91f04.s1 Soares_NFL_T_GBC_S1 Homo saplens	4.9
	451638	AW798466	Hs.82396	2,5-oligoadenylate synthetase 1	4.9
55	457356	AA489621	Hs.191670	ESTs	4.9
	430679	R44428	Hs.22801	EST8	4.9
	445747	AJ820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	4.9 4.9
	409036	T88693	Hs.226410	ESTs ESTs	4.9
60	433382 401287	T64293	Hs.291453	predicted exon	4.9
00	424188	AW954552	Hs.142634	zinc finger protein	4.9
	404868			predicted exon	4.9
	410152	AW593104	Hs.23681	ESTs	4.9
	444997	AI204451	Hs.146196	ESTs	4.9
65	431075	BE267477		gb:601189542F2 NIH_MGC_7 Homo saptens cDNA cl	4.8
	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolog 6	4.8
	414337	BE386606		gb:601273980F1 NIH_MGC_20 Homo saplens cDNA	4.8
	410336	BE391510	Hs.18498	Homo saptens cDNA FLJ12277 fis, clone MAMMA10	4.8
70	445283	AW515763	Hs.246872	ESTs	4.8 4.8
70	434792 433403	AA649253 AF040247	Hs.132458	ESTs gb:Homo saplens erythroid differentiation-related factor	. 4.8
	454940	AV846202		ab:QV0-CT0179-011299-061-410 CT0179 Homo sapie	4.8
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo sapi	4.8
	416437	N48990	Hs.37204	ESTs	4.8
75	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo saplans cDNA	4.8
-	434977	AI734233	Hs.226142	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	4.8
	416192	NM_005038	Hs.998	peroxisome proliferative activated receptor, alpha	4.8
	459218	AA812633	Hs.10845	ESTs	4.8
00	402109			predicted exon	4.8
80	444490	Al151080	Hs.146830	ESTs	4.8
	432632	AW973801	Hs.134656	ESTs	4.8 4.8
	438683	AA813982	Hs.291842	ESTs	4.8 4.8
	404044 449882	A1672277	Hs.199475	predicted exon ESTs	4.8
	443002	MUI CLI I	16.155415	w	7.0

	419002	178625	Hs.268594	ESTs	4.7
	425582 416086	AL157686 H18252	Hs.293737	ESTs ST	4.7
	441133	AA918191	Hs.227263 Hs.194457	ESTS ESTS	4.7 4.7
5	446323	AI288274	Hs.149868	ESTs	. 4.7
	440347	AI125590	Hs.142864	ESTs	4.7
	439481 456388	AF086294 W28557	Hs.125844	ESTs gb:48d8 Human retina cDNA randomly primed sublibra	4.6 4.6
	441864	R34177	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SU	4.6
10	445910	R93483	Hs.260273	ESTs	4.6
	403531	A1220400	11- 040704	predicted exon	4.6
	429773 422563	AI332482 BE299342	Hs.218791 Hs.19348	proteoglycan 4, (megakaryocyte stimulating factor, artic Homo saplens cDNA FLJ13119 fis, clone NT2RP30026	4.6 4.6
	422890	243784	Hs.78713	solute carrier family 25 (mitochondrial carrier; phospha	4.6
15	453663	AL048807	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	4.6
	447839	N72050	Hs.164144	ESTs ESTs	4.5
	415612 433371	F12893 T25451	Hs.13301	gb:PTH1188 HTCDL1 Homo sapiens cDNA 5/3' simila	4.5 4.5
••	410667	AW936099		gb:QV0-DT0020-210100-095-d04 DT0020 Homo saple	4.5
20	410890	AW809575		gb:MR4-ST0121-060200-002-a12 ST0121 Homo saple	4.5
	404451	A10070E3	U- 55002	predicted exon	4.5
	441705 439597	AI087052 W79579	Hs.55993 Hs.58552	ESTs ESTs	4.5 4.5
	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.5
25	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) ho	4.5
	456278	BE300369	Hs.42643	ESTs, Weakly similar to KIAA1016 protein [H.saplens	4.5
	424719 439542	H90452 AW297571	Hs.17646	gb:yv01c03.r1 Soares fetal liver spleen 1NFLS Homo sa ESTs	4.5 4.5
	444433	AV649844	Hs.282436	ESTs	. 4.5
30	438831	BE263273	Hs.301128	ESTs	4.5
	410065	AW812744	11- 04040	gb:RC3-ST0186-181099-012-c09 ST0186 Homo saplen	4.5
	453895 458250	AA039843 AI807339	Hs.61948 Hs.152174	ESTs ESTs, Weakly similar to 2140_HUMAN ZINC FINGE	4.5 4.5
	423403	AA325483	113.1132114	gb:EST28475 Cerebellum II Horno sapiens cDNA 5' en	4.5
35	454679	AW813110		gb:CM4-ST0189-051099-021-05 ST0189 Homo sapien	4.5
	445368	Al221631	Hs.166788	ESTs	4.5
	401004 425837	AF007567	Hs,159609	predicted exon insulin receptor substrate 4	4.5 4.5
	420497	AW206285	Hs.253548	ESTs	4.5
40	449438	AA927317	Hs.176719	EST8	4.5
	429409	AI694817	Hs.155980	ESTs	4.5
	447959 407340	A1452784 AA810168	Hs.270270 Hs.232119	ESTs ESTs	4.4 4.4
	424326	NM_014479	Hs.145296	disintegrin protesse	4.4
45	443479	AF027219	Hs.9443	zinc finger protein 202	4.4
	443246	T75157	Hs.285516	ESTs, Weakly similar to hypothetical protein [H.sapien	4.4
	414475 432075	BE302955 AW972934	Hs.119598	ribosomal prolein L3 gb:EST385030 MAGE resequences, MAGM Homo sap	4.4 4.4
	417906	R24769	Hs.23725	ESTs	4.4
50	406518	W28077	Hs.79389	nei (chicken)-like 2	4.4
	441460 450549	A1962478 T49427	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU	4.4
	426528	AA380828	Hs.181244	major histocompatibility complex, class I, A gb:EST93827 Activated T-cells VII Homo saptens cDN	4.4
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo sepi	4.4
55	408479	BE047329	Hs.144483	ESTs	4.3
	448536	AI557139	Hs.129179	Homo saplens cDNA FLJ13581 fis, clone PLACE10090	4.3
	411280 440790	N50617 AW593050	Hs.128580	gb:yy89h02.r1 Soares_multiple_sclerosis_2NbHMSP H ESTs	4.3
	458301	AF003834		gb:AF003834 Clontech Hi1149x Homo sapiens cDNA	4.3
60	442277	AW448914	Hs.202391	ESTs	4.3
	449463 433426	A1657038 H69125	Hs.196109 Hs.133525	ESTs ESTs	4.3 4.3
	410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT2RM4002	4.3
	423040	AA320749	Hs.209464	KIAA1604 protein	4.3
65	432430	AW079984	Hs.262480	ESTs	4.3
	432072 452213	N62937 AL110237	Hs.269109 Hs.28425	ESTs Homo sapiens mRNA; cDNA DKFZp566D224 (from c	4.3 4.3
	403635	ALI 10231	113.20423	aredicted exan	4.3
=0	441919	AI553802	Hs.128121	ESTs	4.3
70	416717	H79559	Hs.297726	ESTs	4.3
	430995 429269	NM_005092 AA449013	Hs.248197 Hs.99203	turnor necrosis factor (ligand) superfamily, member 18 ESTs	4.2 4.2
	415840	R15955	Hs.21758	ESTs	4.2
25	451300	AA017066	Hs.237686	EST	4.2
75	445366	Al221511	Hs.298662	ESTs	4.2
	424194 459105	8E245833 NM_014517	Hs.169854 Hs.28423	hypothetical protein SP192 upstream binding protein 1 (LBP-1a)	4.2 4.2
	455387	BE069037	113.20423	gb:QV3-8T0379-161299-040-e12 BT0379 Homo saple	4.2
00	410507	AA355288	Hs.271408	ESTs	4.2
80	453823	AL137967	11-00-04	gb:DKFZp761D2315_r1 761 (synonym: harny2) Homo	4.2
	450966 432694	AA017245 AW991585	Hs.32794 Hs.276755	ESTs ESTs, Wealty similar to F53B1.2 (C.elegans)	4.2 4.2
	455108	AW856866		gb:RC0-CT0299-291199-031-G02 CT0299 Homo saple	4.2
	443609	AV650231	Hs.282941	ESTS	4.2
				105	

	427469 417178	AA403084 N51636	Hs.269347	ESTs obyyv87b01.s1 Soares_multiple_sciencsis_2NbHMSP H	4.2 4.2
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDNA clone EU	4.2
_	431982	AW419296	Hs.105754	ESTs	4.1
5	442641	AI890955	Hs.262983	ESTs	4.1
	422128	AW881145		gb:QV0-OT0033-010400-182-e07 OT0033 Homo saple	4.1
	449156	AF103907 Al033098	Hs.171353 Hs.132777	prostate cancer antigen 3 ESTs	4.1 4.1
	419668 418236	AW994005	Hs.172572	hypothetical protein FLJ20093	4.1
10	432663	AI984317	Hs.122589	ESTs	4.1
	448313	BE622486	Hs.121688	Homo saplens cDNA FLJ13463 fis, clone PLACE10034	4.1
	411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo saple	4.1
	440652	AI216751	Hs.143977	ESTs	4.1 4.1
15	416608 420405	R11499 AA743396	Hs.189716 Hs.189023	ESTs ESTs	4.1
13	405717	77(140000	113.103023	predicted exon	4.1
	435267	N23797	Hs.110114	ESTs ·	4.1
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr virus) recepto	4.1
~^	403560	AI929721	Hs.5120	dynein, cytoplasmic, light polypeptide	4.1
20	449162	Al632740	Hs.10476	ESTS	4.1
	459157	A1904385		gb:CM-BT054-080399-054 BT054 Homo saptens cDN gb:nn65e09.s1 NCI_CGAP_Lar1 Homo saptens cDNA	4.1 4.1
	432474 455388	AA584042 AW936234		gb:QV0-DT0020-090200-108-g05 DT0020 Homo saple	4.0
	426456	AA580748	Hs.130658	ESTs .	4.0
25	438597	AA811662	Hs.171497	ESTs	4.0
	437934	AW880871	Hs.77496	small nuclear ribonucleoprotein polypeptide G	4.0
	459385	BE380047	407040	gb:601159362F2 NIH_MGC_53 Homo sapiens cDNA	4.0
	436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3UTR, sequence 2 gb:UI-HF-BNO-akb-d-07-0-UI.r1 NIH_MGC_50 Homo	4.0 4.0
30	457740 437385	AW500458 AA757055	Hs.164060	ESTs ,	4.0
50	444530	AV650124	Hs.282435	ESTs	4.0
	408066	AA046914		gb:zf47h10.r1 Soares retina N2b4HR Homo sapiens cD	4.0
	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo sapie	4.0
25	433582	BE548749	Hs.148016	ESTS	4.0 4.0
35	438637 414571	BE500941	Hs.126730 Hs.22868	ESTs, Weakly similar to KIAA1214 protein [H.sapiens protein tyrosine phosphatase, non-receptor type 11	4.0
	446190	BE410746 Al279299	Hs.256564	EST8	4.0
	443542	Al927065	Hs.146040	ESTs	4.0
	430444	AW296421	Hs.121035	ESTs	4.0
40	454573	BE146471		gb:QV0-HT0216-011199-043-c09 HT0216 Homo saple	4.0
	409846	AW501748		gb:UI-HF-BR0p-sim-b-12-0-UI.r1 NIH_MGC_52 Hom	4.0
	456141	A1751357	Hs.288741	Homo saplens cDNA: FLJ22256 fis, clone HRC02860	4.0 4.0
	456140 441685	AA169515 Al459261	Hs.6006 Hs.144481	ESTs ESTs	4.0
45	416677	T83470	16.177701	gb:yd46g08.r1 Soares fetal liver spleen 1NFLS Homo s	4.0
	401740			predicted exon	4.0
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	4.0
	442594	AW272467	Hs.254655	Untitled	3.9
50	426294	AA374185		gb:EST86289 HSC172 cells I Homo saplens cDNA 5' e gb:PM4-PT0019-131299-008-E04 PT0019 Homo saple	3.9 3.9
30	411922 452320	AW876260 AA042873	Hs.160412	go: PM4-P10015-131235-000-E04 P10015 Hullo Sapis ESTs	3.9
	432320	AW972822	Hs.169248	cytochrame c	3.9
	409892	AW956113	110.1002.10	gb:EST368183 MAGE resequences, MAGD Homo sap	3.9
	418132	T92670	Hs.117421	ESTs	3.9
55	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (937208) Homo sap	3.9
	400196		11- 4040 -	predicted exon	3.9 3.9
	416900	M59964	Hs.1048 ** Hs.270	KIT Itgand pleckstrin homology, Sec7 and coiled/coil domains, bind	3.9
	445444 435957	AA380876 N39015	Hs.190368	ESTs	3.9
60	442299	AW467791	Hs.155561	ESTs	3.9
	419499	AA808136	Hs.177698	ESTs	3.9
	438403	AA806607	Hs.292206	ESTs	3.9
	449386	AA001308	Hs.193213	ESTS	3.9 3.9
65	443283 406481	BE568610		gb:601342622F1 NIH_MGC_53 Homo saplens cDNA predicted exon	3.9
05	453530	AW021633		ob:df26c02.v1 Morton Fetal Cochlea Homo sapiens cDN	3.9
	415558	AA885143	Hs.125719	ESTs	3.9
	416874	H98752	Hs.42568	ESTs	3.9
~^	454885	AW836922		gb:QV1-LT0038-150200-074-h06 LT0036 Homo saple	3.9
70	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA clon	3.9 3.9
	440962	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Secypa Complete Co	3.9
	419401 406562	AW804563		gb:QV4-UM0094-160300-135-d06 UM0094 Homo sap predicted exon	3.8
	405690	BE409855	Hs.808	heterogeneous nuclear ribonucleoprotein F	3.8
75	435282	AA677428	Hs.189731	EST8	3.8
-	402451			predicted exon	3.8
	451577	N69101	Hs.32703	ESTs	3.8
	457141	AA521410	Hs.41371	ESTs ESTs	3.8 3.8
80	407817 412613	H92553 AA653507	Hs.40400 Hs.285711	ESTs Homo sapiens cDNA FLJ13089 fis, clone NT2RP30021	3.8
UV	412013	L42563	Hs.1165	ATPase, H+/K+ transporting, nongestric, alpha polypep	3.8
	446357	AW161533	Hs.300866	ESTs	3.8
	407448	AJ001865		gb:Homo Saplens mRNA, partial cDNA sequence for h	3.8
	456383	AJ148037		gb:qg61e01.r1 Soares_testis_NHT Homo saptens cDNA	3.8

	444651	W58469	Hs.103120	EST8	3.8
	455067	AW854538	,	gb:RC3-CT0255-200100-024-b02 CT0255 Homo saple	3.8
	442657	BE502631	Hs.130645	ESTs	3.8
5	429142 429274	AA835639 Al379772	Hs,104972 Hs.99206	ESTs ESTs	3.8 3.8
•	437774	AW978199	Hs.291648	ESTs .	3.8
	427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME31P [H.s	3.8
	405671 413627	BE182082	Hs.246973	predicted exon ESTs	3.8 3.8
10	438858	R37529	Hs.269924	ESTs	3.8
	416612	H70565	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:yr97c04.r1 Soares fetal liver spleen 1NFLS Homo sa	3.8
	423045	AW967472	Hs.301511	ESTs, Highly similar to KPT2_HUMAN SERINE/THR	3.8
	453361	AA035197 AA747549	Hs.107375 Hs.259122	ESTs ESTs	3.7 3.7
15	437243 437987	AW450202	Hs.122963	ESTs	3.7
	408781	BE148621	Hs.254602	EST8	3.7
	455895	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo saple	3.7
	431492 413247	AW612343 AW963969		gb:hg97c10.x1 NCI_CGAP_Kld11 Homo saplens cDN gb:EST376042 MAGE resequences, MAGH Homo sap	3.7 3.7
20	422866	NM_002410	Hs.121502	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-g	3.7
	431828	AA572994		gb:nm33f12.s1 NCI_CGAP_Lip2 Homo saplens cDNA	3.7
	438872	R64197	Hs.23589	ESTs	3.7 3.7
	438673 416624	AI824717 H69044	Hs.123443	ESTs gb:yr77h05.s1 Soares fetal liver spieen 1NFLS Homo sa	3.7
25	401963	1103011		predicted exon	3.7
	402867			predicted exon	3.7
	408315	AW179148	13- 04004	gb:MR4-ST0067-200899-002-807 ST0067 Homo sapia	3.7 3.7
	418320 447199	D86981 Al939421	Hs.84084 Hs.160900	amyloid beta precursor protein (cytoplasmic tail)-bindin ESTs	3.7
30	422590	AA312758	Hs.193945	Homo sapiens cDNA FLJ13962 fls, clone Y79AA10012	3.7
	451996	AW514021	Hs.245510	ESTs	3.7
	412463	AW953444	Hs.78672	laminin, alpha 4	3.7 3.7
	440928 441951	AL046575 W31002	Hs.130198 Hs.128195	ESTs ESTs	3.7
35	440705	AA904244	Hs.153205	ESTs	3.7
	434231	AF119901	Hs.250568	hypothetical protein PRO2831	3.7
	411039	AL135674	Hs.163348	ESTs gb:PM0-BT0340-231199-001-b07 BT0340 Homo saple	3.7 3.7
	413137 417970	BE066915 AA309234	Hs.57760	Homo saplens cDNA: FLJ23119 (is, clone LNG07978	3.7
40	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDNA clone EU	3.7
	459595	AL040421		gb:DKFZp434B0714_r1 434 (synonym: htes3) Homo s	3.7
	443601	A1078554	Hs.15682	ESTs	3.7 3.6
	404041 406122			predicted exon predicted exon	3.6
45	404582			predicted exon	3.6
	455786	BE090077		gb:RC6-BT0710-300300-021-F02 BT0710 Homo saple	3.6
	411899	AA370573	11- 407770	gb:EST82238 Prostate gland I Homo saplens cDNA 5' e	3.6 3.6
	426758 421776	AL036430 AW301994	Hs.197772 Hs.108183	ESTs candidate tumor suppressor p33 ING1 homolog	3.6
50	430169	AA468531	Hs.189047	ESTs	3.6
	407695	A1808007	Hs.66450	ESTs	3.6
	454564	AW807573 X52509	Hs.161640	gb:MR1-ST0088-021299-004-g01 ST0088 Homo saple tyrosine aminotransferase	3.6 3.6
	425902 439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN ALU SU	3.6
55	429066	AA868555	Hs.178222	ESTs	3.6
	428690	Al948490	Hs.98765	ESTs	3.6
	437302	AA837146	Hs.180275 Hs.176154	ESTs	3.6 3.6
	443973 453993	A1580083 AW615224	Hs.252839	ESTs	3.6
60	413623	AA825721	Hs.246973	ESTs	3.6
	409196	NM_001874	Hs.169765	carboxypeptidase M	3.6
	424916	AW867440	Hs.23096	ESTs ret linger protein	3.6 3.6
	424769 400080	H06469	Hs.142653	predicted exon	3.6
65	421521	AI638760	Hs.161795	ESTs	3.6
	405549			predicted exon	3.6
	446114	AI275715	Hs.145926	ESTS	3.6 3.6
	441392 424025	AW451831 AI701852	Hs.222119 Hs.301296	ESTs, Weakly similar to K1CQ_HUMAN KERATIN, T ESTs	3.5
70	448527	A1525606	1.5.501200	gb:PT1.3_03_G05.r tumor1 Homo saplens cDNA 5', mR	3.5
	437063	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I) binding prot	3.5
	449880	A1673006	Hs.231948	ESTs, Weakly similar to ALUB_HUMAN IIII ALU CL ob:tt49a12x1 NCL_CGAP_GC6 Homo saptens cDNA c	3.5 3.5
	449311 442999	AI657014 AW662889	Hs.132395	go:tt43a12x1 NO_COAP_GCO Romo sapiens color c	3.5
75	416238	W90448	1 10.102033	gb:zh78c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.5
. •	423209	BE278528	Hs.106823	H.saplens gene from PAC 4266, similar to syntaxin 7	3.5
	409854	AW501833	11. 600455	gb:UI-HF-BR0p-ejo-d-01-0-UI.r1 NIH_MGC_52 Hom	3.5 3.5
	414941	C14865 AW751661	Hs.182159 Hs.65919	ESTs ESTs	3.5
80	456337 415296	F05086	113.00313	gb:HSC01A011 normalized infant brain cDNA Homo s	3.5
	423338	AB007961	Hs.127338	KIAA0492 protein	3.5
	415618			gb:HSC3GG091 normalized infant brain cDNA Homo s	3.5 3.5
	405583 435601		Hs.283077	predicted exon centrosomal P4.1-associated protein; uncharacterized bo	3.5
	40000 I	1.003	1 10.2000//	The state of the s	

	450007	4404464	11-045100	ECT.	3.5
	450867	AA011454	Hs.245122	ESTs ESTs	3.5
	431339	AA508294	Hs.257266 Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	3.5
	441959	AJ733388 AW970603		Homo saplens cDNA FLJ11661 fls, clone HEMBA100	3.5
5	431343 434317	A1674095	Hs.300941 Hs.116323	ESTs	3.5
,	414741	R51321	Hs.25780	Homo saplens cDNA FLJ12252 fis, done MAMMA10	3.5
	439707	AW297702	Hs.102915	ESTs	3.5
	443178	AI631241	Hs.47312	ESTs	3.5
	400397	AJ270770	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	3.5
10	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo saple	3.5
	434362	W27081	Hs.295446	ËSTs	3.5
	409211	AA078835		gb:zm94h04.s1 Stratagene colon HT29 (937221) Homo	3.5
	414390	BE281040		gb:601156234F1 NIH_MGC_21 Homo saptens cDNA	3.5
	457142	AI924353	Hs.290969	EST	3.5
15	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	3.5
	453363	A1989776	Hs.232623	ESTS	3.5
	418913	BE046745		gb:hn39b06.x1 NCI_CGAP_RDF2 Homo septens cDN	3.4
	440016	AW118114	Hs.137057	ESTs	3.4 3.4
20	405096		11. 440000	predicted exon	3.4
20	435072	AW592176	Hs.116932	ESTs	3.4
	438535	L09078	U- 42747C	gb:Homo saptens mRNA fragment KIAA1051 protein	3.4
	424001	W67883	Hs.137476 Hs.183858	transcriptional intermediary factor 1	3.4
	428361	NM_015905 AA370706	Hs.11252	ESTs, Weakly similar to Weak similarity with the Ysy6	3.4
25	410587 454543	AW806895	113.11232	gb:QV4-ST0923-160400-172-c06 ST0023 Homo sapien	3.4
23	419515	S81944	Hs.90791	gamma-aminobutyric acid (GABA) A receptor, alpha 6	3.4
	410280	AA083558	Hs.261286	ESTS	3.4
	425714	AW963278	10.201200	gb:EST375351 MAGE resequences, MAGH Homo sap	3.4
	416895	AW961600		gb:EST373672 MAGE resequences, MAGG Homo sap	3.4
30	427935	AW503687	Hs.119424	ESTs. Wealdy similar to unnamed protein product [H.sa	3.4
50	411673	BE064863		gb:RC1-BT0313-110300-015-f08 BT0313 Homo saplen	3.4
	453339	AW992599	Hs.252797	ESTs	3.4
	424696	BE439547	Hs.151903	Homo sapiens clone 24705 mRNA sequence	3.4
	436242	AK002187		gb:Homo sapiens cDNA FLJ11325 fis, clone PLACE10	3.4
35	442837	Al022082	Hs.50492	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone HRC01333	3.4
	433936	A1208072	Hs.123459	ESTs	3.4
40	458177	A1744995	Hs.267072	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.4 3.4
40	401896			predicted exon	3.4 3.4
	406237		11 0040	predicted exon	3.4
	457688	AL110157	Hs.3843	Homo saplens mRNA; cDNA DKFZp586F2224 (from	3.4
	456914	AW363582	Hs.75323	prohibilin Horno saplens cDNA: FLJ23546 fis, clone LNG08361	3.4
45	421916	R34441	Hs.101007 Hs.269069	ESTs	3.4
40	419321	N48146	Hs.19904	cystathionase (cystathionine gamma-lyase)	3.4
	447876	AV654978	NS. 13304	predicted exon	3.4
	406197 443005	AJ027184	Hs.200918	EST8	3.4
	450078	Al681743	113.2000.0	gb:bx38g10.x1 NCI_CGAP_Lu24 Homo saplens cDNA	3.4
50	431301	AA502384	Hs.151529	ESTs	3.4
30	430202	T85775	,	gb:yd60g02.r1 Soares fetal liver spleen 1NFLS Homo s	3.4
	428559	H24338	Hs.27041	ESTs	3.4
	455731	BE072188		gb:QV4-BT0536-211299-055-b09 BT0536 Homo saple	3.4
	420735	AW297440	Hs.88653	ESTs	3.4
55	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A receptor, alpha 4	3.3
	405836			predicted exon	3.3
	449178	A1633748	Hs.197597	ESTs	3.3
	453265	U61232	Hs.32675	tubulin-specific chaperone e	3.3 3.3
<i>c</i> 0	430700	AA768902	Hs.247812	H2A histone family, member K, pseudogene	3.3
60	424496	A1733451	Hs.129212	ESTs	3.3
	446963	A1862668	Hs.176333	ESTS	3.3
	422879	A1241409	Hs.188092 Hs.5415	ESTs ESTs	3.3
	419831	AW448930	113.0410	gb:zh86c06.r1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.3
65	449570 406255	AA001793		predicted exon	3.3
UJ	412319	AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo saple	3.3
	401350			predicted exon	3.3
	439098	AF085955		gb:Homo sapiens full length insert cDNA clone YR86G	3.3
	450589	AI701505	Hs.202526	EST8	3.3
70	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral related oncogene, n	3.3
	430689	A1695595	Hs.293219	ESTs	3.3
	454753	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo saple	3.3
	444479	AA194980	Hs.30818	Homo septens cDNA FLJ13581 fis, clone PLACE20000	3.3 3.3
76	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo saple	3.3
75	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens cDNA 5 end,	3.3
	457107	AA418246	Hs.185796	ESTs, Weakly similar to b34l8.1 [H.saplens]	3.3
	421480	NM_01615		erythrocyte transmembrane protein	3.3
	444289	BE267060		myxovirus (influenza) resistance 1, homolog of murine	3.3
00	417725	R25257	Hs.21503	ESTs qb:DKFZp434N247_r1 434 (synonym: htes3) Homo sa	3.3
80	453631	AL046418	Un 04027	gp:UKF2p434N247_f1 434 (synonym: ntess) nomb sa hypothetical protein FLJ23053	3.3
	450692	H50603	Hs.94037	cbzc35e06.r1 Soares_senescent_fibroblasts_NbHSF H	3.3
	413357 415327	W47611 H22769	Hs.1861	membrane protein, palmitoyfated 1 (55kD)	3.3
	415327 457569				· 3.3
	401003			· · · · · · · · · · · · · · · · · · ·	

			•		
	448501	R61666	Hs.293690	ESTs	3.3
	436526	AW993633	Hs.287681	Homo saplens cDNA: FLJ21685 ffs, clone COL09372	3.3
	440589	BE397763	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (from	3.3
E	418768	T39310	Hs.1139	cold shock domain protein A	3.3 3.3
5	426768	AW303337	Hs.270411	ESTs	3.3
	400394	AF040257	Hs.283818	Homo septens TNF receptor homolog mRNA, partial cd	3.3
	433565	AA599763	Hs.112520	ESTs gb:EST39621 Epididymus Homo sapiens cDNA 5' end,	3.3
	424093	AA335025	U. 02722		3.3
10	449552 431892	AA001742 AA521315	Hs.83722 Hs.194424	ESTs ESTs	3.3
ŢŲ		AA321313	NS. 134424	predicted exon	3.3
	405512 446990	Al354717	Hs.223908	ESTs	3.3
	457729	AI821863	Hs.293467	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	3.2
	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	3.2
15	456420	AW401361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit,	3.2
13	403497	7111-101001		predicted exon	3.2
	427145	R52635	Hs.25935	ESTs	3.2
	406454			predicted exon	3.2
	441033	BE562555		gb:601335867F1 NIH_MGC_44 Homo saplens cDNA	3.2
20	408444	AW661839	Hs.253204	ESTs	3.2
	434739	AA804487	Hs.144130	ESTs	3.2
	437060	AA745591	Hs.292063	ESTs	3.2
	423092	BE274837	Hs.123637	putative homeodomain transcription factor	3.2
	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-associated glycopr	3.2
25	443362	AI053464	Hs.166505	ESTs -	3.2
	437500	AL390150		gb:Homo saplens mRNA; cDNA DKFZp547L156 (from	3.2
	425458	H89317	Hs.182889	ESTs	3.2
	439171	AA831133	Hs.294128	ESTs	3.2
	407647	AW860158		gb:RC0-CT0379-290100-032-b04 CT0379 Homo saple	3.2
30	435608	AW183971	Hs.250896	ESTs	3.2
	426743	AA383833	Hs.245022	ESTs	3.2 3.2
	457525	AW973800		gb:EST385901 MAGE resequences, MAGM Homo sap	3.2
	413800	Al129238	Hs.192235	ESTS	3.2
25	414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapians cDNA	3.2
35	455565	BE000537	11 4 4 4 4 4 4 4 4	gb:RC3-BN0072-240200-011-d07 BN0072 Homo saple	3.2
	410061	T91029	Hs.15069	ESTs	3.2
	450666	T99968	Hs.18799	ESTs	3.2
	458529	AV652120	Hs.213232	ESTs .	3.2
40	424751	AA769482	Hs.296320	ESTs ESTs	3.2
40	442225	AI306597	Hs.129192	gb:RC3-ST0186-250200-018-c05 ST0186 Homo saplen	3.2
	410990	AW812929	Ne senero	ESTs	3.2
	435644 405347	AA700867	Hs.269659	predicted exon	3.2
	441202	AI632143	Hs.135853	ESTs	3.2
45	446694	AV659942	Hs.258132	ESTS	3.2
70	454652	AW812088	115.230102	gb:RC4-ST0173-191099-032-e07 ST0173 Homo saplen	3.2
	418985	AI042330	Hs.87128	ESTs, Weakly similar to similar to YBS4 YEAST [C.el	3.2
	430118	Al377255	Hs.183287	ESTs	3.2
	430691	C14187	Hs.103538	ESTs	3.2
50	416313	H47206	Hs.194109	ESTs, Weakly similar to ALUB_HUMAN IIII ALU CL	3.2
	446122	Al362790	Hs.181801	ESTs	3.2
	453725	W28543		gb:48c5 Human retina cDNA randomly primed sublibra	3.2
	453954	AW118336	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	3.2
	428166	AA423849	Hs.79530	M5-14 protein	3.2
55	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone CAS05917	3.2
	401871			predicted exon	3.2
	442160	AJ337127	Hs.156325	ESTs	3.2
	404708			predicted exon	3.1
	412588	AW993055	Hs.44024	ESTs	3.1
60	431976	AA719001	Hs.291065	ESTs	3.1
	408884	AW891024	Hs.281172	ESTs	3.1
	433811	AW975015	Hs.123138	ESTs	3.1 3.1
	431691	A1208511	Hs.292510	ESTs	3.1
66	418719	AW975590	Hs.161707	ESTs	3.1
65	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67 PR01777 [H	3.1
	435699	Al911488	Hs.213724	ESTs	3.1
	459344	AW499533	Hs.257976	ESTS ESTS	3.1
	431729	AW004714 AW975687	Hs.162033 Hs.292979	ESTS	3.1
70	436771		Hs.59395	Homo sapiens clone IMAGE:112574 mRNA sequence	3.1
70	434480 459547	AW956268 AI400579	Hs.225186	EST	3.1
	427962	AA946582	Hs.133546	Homo saplens cDNA: FLJ21120 fis, clone CAS05691	3.1
	403743		110,1000-10	oredicted exon	3.1
	413560	BE148411		gb:MR0-HT0241-131299-002-f04 HT0241 Homo saple	3.1
75	454372	H96643	Hs.283565	FOS-like antigen-1	3.1
15	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	3.1
	428839	AI767756	Hs.82302	ESTs	3.1
	407110		Hs.95078	ESTs	3.1
	436133	T77531	Hs.191124	ESTs	3.1
80	418872		Hs.270263	ESTs	3.1
	404418			predicted exon	3.1
	446877		Hs.270720		3.1
	429053		Hs.194114	ESTs .	3.1
	425189			. gb:ym26c07.r1 Soares infant brain 1NIB Homo saplens	3.1

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	404134			predicted exon	3.1
	441404	A1638880	Hs.126895	ESTs	3.1
	400076			predicted exon	3.1
_	411876	AW981336	Hs.69705	ESTs, Wealthy stimitar to KIAA0443 [H.saptens]	3.1
5	451048	AA013349	Hs.60602	ESTs	3.1 3.1
	447021	Al356564	Hs.161406	ESTs predicted exon	3.0
	404083 415833	H05175	Hs.107510	ESTs	3.0
	402142	noons	15.107510	predicted exon	3.0
10	415820	R53720	Hs.189745	ESTs	3.0
10	441140	AW016534	Hs.226994	ESTs	3.0
	449376	AA001278	Hs.59905	ESTs	3.0
	457593	Al738815	Hs.117323	ESTs .	3.0
	411542	AW850767		gb:iL3-CT0220-031199-025-A05 CT0220 Homo saplen	3.0
15	403375			predicted exon	3.0
	449561	Al022240	Hs.17924	ESTs	3.0
	406241			predicted exon	3.0
	420306	AA258318	Hs.219226	ESTs .	3.0
00	413161	BE068130		gb:CM2-BT0368-171299-056-a01 BT0368 Homo saple	3.0
20	448221	BE622615		gb:601440775T1 NIH_MGC_72 Homo saplens cDNA	3.0 3.0
	415920	Z45684		gb:HSCZRD121 normalized infant brain cDNA Homo	3.0
	459135	A1902802		gb:RC-BT015-311298-026 BT015 Homo sapiens cDNA	3.0
	425357	AA355842	•	gb:EST64303 Jurkat T-cells VI Homo saplens cDNA 5'	3.0
25	454724	AA091228	U- 204624	gb:cchn2152.seq.F Human fetal heart, Lambda ZAP Ex	3.0
23	429395	AK002071	Hs.201624 Hs.270479	hypothetical protein FLJ 11209 ESTs	3.0
	427607	AA406119 AA4400070	Hs.14822	ESTs	3.0
	443598 437948	AW499970 AA772920	ns. 14022	gb:ae73c09.s1 Stratagene schizo brain S11 Homo sapien	3.0
	418105	AW937488	Hs.178000	ESTs	3.0
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	426593	AW958560		gb:EST370630 MAGE resequences, MAGE Homo sapl	3.0 3.0
	431899	AA521381	Hs.187726	ESTs	3.0
	422406	AF025441	Hs.116206	Opa-Interacting protein 5	3.0
15	448178	AI479482	Hs.170789	ESTs predicted exon .	3.0
45	404227	A 4 0 0 0 0 70	Hs.126006	ESTs	3.0
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	459459	AA460445	113.200040	gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_9w Homo	3.0
50	403403	74400443		Borroom, Inc. good of Transfer of the Control of th	
50	TABLE 5	A:			•
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		ber. Gene dust			
			ession numbers		
55					
	Pkey	CAT Number			
	407596	1003489_1	R86913 F	86901 H25352 R01370 H43764 AW044451 W21298	4000 Alamonoro Alamonoro
	407647	1007366_1		8 AW862385 AW860159 AW862386 AW862341 AW821869 AW82	1053 AYY002000 AYY002030
C 0	408066	103849_1		4 AA057231 H38371	•
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, 0	410758	1219899 1	BE53598	8 AW801777	•
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00	411543		AW8512	48 AW851425 AW850805 AW851021 AW850905	20 DEDECTO DE 163636 AMPRECESS DE 166070 DESCACET
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	411899		AA3705	73 BE160501 BE160500 BE160498 BE160502 BE160497 N724247 60 AW876269 AW876340 AW876146 AW876323 AW876320 AW8	76171 AW876421 AW876227 AW876243
	411922			60 AW8/6269 AW8/6540 AW8/6146 AW8/6525 AW8/6520 AW8 103 AW936907 AW936908 AW936914	
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AW846202 AW846530 AW846560 AW846536 AW846458 AW846470 AW846466 AW846192 AW846479 AW8465260 AW846200 AW846139
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           Ref. Sequence source. The 7 digit numbers in this column are Genbank identifier (Gi) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495

Strand: Indicates DNA strand from which exons were predicted
35
           Nt_position: Indicates nucleotide positions of predicted exons
           Pkey
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                                       Strand
                                                     Nt position
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                         7229982
                                                     62580-62772
                                                     42287-42431
169019-169649
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                                       Minus
           40130R
                         9212516
                                       Plus
                                                     14471-14623
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                                       Plus
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                                                     58158-59585
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5 ·	406255	7417729	Ptus	2959-3200	
	406364	9256114	Minus	50715-50833	
	406454	9588380	Minus	91746-91958	
	406481	9864741	Minus	91439-91579	
	406562	7711584	Plus	37316-37426	
10	406605	8272666	Minus	23275-23493,23723-23903	

TABLE 6A lists about 68 genes highly down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 5A, except the "average" ovarian cancer level was set to the maximum value amongst various ovarian cancers and the "average" normal ovary level was set to the minimum value from various non-malignant ovary specimens, and the ratio was greater than or equal to 2.5 (i.e. 2.5-fold down-regulated in the highest tumor vs. the lowest normal ovary). This has the overall effect of increasing stringency, and reducing the number of false-positives. 15

TABLE 6A: ABOUT 68 HIGHLY DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey
Ex. Acon: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title 20

ratio: ration of normal ovary vs. tumor

25	Pkey	Ex. Acon	UGID	Title -,	ratio
	424851	AA676441	Hs.119059	ESTs	7.9
	437690	AA804362	Hs.180544	ESTs	4.7
	433682	AA842418	Hs.17381	ESTs	4.1
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cds.	4.1
30	437787	A1908263	Hs.291625	ESTs	4.0
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	4.0
	440987	AA911705	Hs.130229	ESTs	3.8
	443131	AI033833	Hs.1326B9	ESTs	3.8
	431075	BE267477		gb:601189542F2 NIH_MGC_7 Homo saplens cDNA do	3.6
35	412637	AA115097	Hs.261313	ESTs	3.6
•	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	3.5
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	3.5
	430653	AW902062	Hs.30280	ESTs	3.4
	401308	**********		predicted exon	3,4
40	410758	BE535988		gb:601062418F1 NIH_MGC_10 Homo septens cDNA c	3.4
	421418	AA806639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo saptens cDNA	3.4
	450061	A1797034	Hs.201115	ESTs	3.3
	409725	T40760	Hs.90459	EST	3.3
	434738	AA836265	110.00100	gb:od17e02.s1 NCI_CGAP_GCB1 Homo saplens cDNA	3.3
45	431644	AW972822	Hs.169248	cytochrome c	3.3
	450938	AW753734	Hs.277215	ESTs	3.2
	420497	AW206285	Hs.253548	ESTs	3.2
	439426	AI131502	Hs.143135	ESTs, Wealty similar to FAFY_HUMAN PROBABLE C	3.2
	407596	R86913	123,140100	gb:yq30f05.r1 Soares fetal liver spleen 1NFLS Homo sap	3.2
50	448683	AA167642	Hs.14632	ESTs	3.2
50	431982	AW419296	Hs.105754	ESTs	3.1
	452320	AA042873	Hs.160412	ESTs	3.1
	419401	AW804663	15.100112	gb:QV4-UM0094-160300-135-d06 UM0094 Homo sapim	3.1
	402105	711001003		predicted exon	3.1
55	444997	AI204451	Hs.146196	ESTs	3.1
55	403283	ALCOHOI	119.170100	predicted exon	3.0
	455388	AW936234		gb:QVO-DT0020-090200-106-g05 DT0020 Homo sapie	3.0
	428559	H24338	Hs.27041	ESTs	2.9
	419002	178625	Hs.268594	ESTs	2.9
60	404858	170020	HS.200094	predicted exon	2.9
UU		W56067	Hs.103105	ESTs	2.9
	409090	YOUGGVV	ns.103103	predicted exon	2.9
	406605 441202	AI632143	Hs.135853	ESTs	2.5
			ns.133033	gb:ts50a10.x1 NCI_CGAP_Ut1 Homo saptens cDNA d	2.8
65	422046 442865	A1638562	Un 114E41		2.8
UJ		N57659	Hs.114541	ESTs, Weakly similar to nauronal thread protein AD7c-N	2.8
	444431	AW513324	Hs.42280	ESTS	2.8
	426294	AA374185		gb:EST86289.HSC172 cells I Homo sapiens cDNA 5' en	2.8
	412480	BE142364	Un 40000E	gb:CM0-HT0143-270999-062-d12 HT0143 Homo sapie	28
70	449858	AW205979	Hs.196065	ESTs	27
70	401464	AF039241	Hs.9028	histone deacetylase 5	27
	439126	AF085984		gb:Homo saplens full length insert cDNA clone YT99F0	
	403277	41004740		predicted exon	27
	450078	A1681743	11. 50040	gb:bx38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	27
75	458090	Al282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD D	2.7
13	420620	AA278807	Hs.173343	EST8	2.7
	459054	AW798466	Hs.82396	2,5'-oligoadenylate synthetase 1	2.6
	421379	Y15221	Hs.103982	small inducible cytokine subfamily 8 (Cys-X-Cys), mem	2.6
	454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled/coil domains 1(cyt	2.6
00	454529	Z45439	Hs.270425	ESTs	2.6
80	446877	A1559472	Hs.270720	ESTs	2.6
	412588	AW993055	Hs.44024	ESTs	2.6
	449862	AI672277	Hs.199475	ESTs	2.6
	446694	AV659942	Hs.258132	ESTs	2.6
	424029	AB014594	Hs.137579 ,	KIAA0694 gene product	2.6

```
454102
                         AW752363
                                                          gb:RC0-CT0201-270999-011-f03 CT0201 Homo sapien
           430922
                         AW373747
                                         Hs.183337
                                                          EST8
           420289
                         N55394
                                         Hs.96398
                                                          8-oxoguanine DNA glycosylase
                                                                                                                                          2.5
2.5
2.5
2.5
           410495
                         N95428
                                                          gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF Ho
  5
           412319
                         AW936903
                                                          gb:RC1-DT0029-030200-012-d02 DT0029 Homo saplen
                                                         gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapten
gb:qz30a07.x1 NCL_CGAP_Kid11 Homo saptens cDNA
discs, large (Drosophila) homolog 2 (chapsyn-110)
           409699
                         BE154650
           445832
                         A1261545
                                                                                                                                          2.5
2.5
           429755
                         NM_001364
                                         Hs.215839
           445755
                         AW294870
                                         Hs.223672
                                                          ESTs
10
           TABLE 6B:
           Pkey: Unique Eos probeset identifier number
           CAT number: Gene cluster number
           Accession: Genbank accession numbers
15
                         CAT Number
           Pkey
           407596
                         1003489_1
                                             R86913 R86901 H25352 R01370 H43764 AW044451 W21298
           409899
                         1149033_1
                                             BE154650 BE154785 AW468343 BE154816 BE154667
           410495
                         1205826_1
                                             N95428 W24040 AW751366 H81987
BE535988 AW801777
20
                         1219899_1
           410758
                                             AW936903 AW936907 AW936908 AW936914
           412319
                         1288602_1
                         129929_1
184454_1
           412480
                                             BE142364 BE142341 AA112025
                                             AW804663 AW805017 AA236969
AA806639 AA291008 AA836274 AW978806
AI638562 T16929 H13401 F07773 R55836
           419401
           421418
                         202288 1
25
           422046
                         210744_1
           426294
                         263994_1
                                             AA374185 AW956180 H38344
                                             BE267477 AA491488 AW836723
AA836265 AA648266 AW974440
AF085984 H95905 H95906
           431075
                         327638_1
           434738
                         392562 1
                         46887_1
           439126
30
                         651925_1
                                             Al261545 N59134 AW875371 AW875247
           445832
           450078
                         823882_1
                                             Al681743 AW897287 AW897205 AW897284
           454102
                         1011603_1
                                             AW752363 BE147120 N22640
           455388
                         1287904_1
                                             AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
35
            Pkey: Unique number corresponding to an Eos probeset
           Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted
40
           Nt_position: Indicates nucleotide positions of predicted exons
           401308
                         9212516
                                                      169019-169649
                                        Plus
                                                      22856-24055
           402105
                         8131588
                                       Minus
           403277
                         8072597
                                       Minus
                                                      27494-27642
45
           403283
                         8076905
                                                      71124-71996
                                       Minus
           404868
                         9454593
                                                      39954-40430
                                        Ptus
           406605
                         8272656
                                       Minus
                                                      23275-23493,23723-23903
50
           Table 7A lists about 770 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01
           GeneChip array such that the ratio of "average" ovarian cancer to "average" normal edult tissues was greater than or equal to 2.5. The "average" ovarian cancer level was set to
           the 2nd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 7th highest amongst various non-malignant tissues. In order to remove
           gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.
55
           TABLE 7A: ABOUT 770 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
           Pkey: Primekey
           Ex. Accn: Exemplar Accession
           UG ID: UniGene ID
60
           Title: UniGene Title
           ratio: ration tumor vs. normal tissues
                        Ex. Acon
                                        UG ID
           Pkey
                                                          Title
                                                                                                                          ratio
            109680
                        F09255
                                        Hs.4993
                                                                                                                          23.2
                                                          ESTs
65
            119743
                       W70242
                                        Hs.58086
                                                          ESTs
                                                                                                                          22.0
                       AA283006
            132528
                                        Hs.50758
                                                          chromosome-associated polypeptide C
                                                                                                                          22.0
                        X51630
                                                          Wilms tumor 1
steroidogenic acute regulatory protein
5-hydroxytryptamine (serotonin) receptor 3A
            129571
                                        Hs.1145
                                                                                                                          20.0
                                        Hs.3132
            102151
                        U17280
                                                                                                                          19.6
            130941
                        D49394
                                        Hs.2142
                                                                                                                           17.5
70
                       AA164819
U65011
            132624
                                        Hs.53631
                                                          ESTs
                                                                                                                           15.9
                                                          preferentially expressed antigen in melanoma 
protein kinase C: lota
            102610
                                        Hs.30743
                                                                                                                           15.4
                        L33881
            101249
                                        Hs.1904
                                                                                                                          14.5
                        AA460530
                                        Hs.256579
                                                          EST8
                                                                                                                          14.5
            122802
                                                          cyclin E1
            135242
                        M74093
                                        Hs.9700
                                                                                                                           13.8
75
            101804
                        M86699
                                        Hs.169840
                                                          TTK protein kinase
                                                                                                                           12.2
                        AA479726
            123005
                                        Hs.105577
                                                          ESTs
                                                                                                                           12.0
```

11.5

11.4

10.9

10.9

10.8

10.5

10.3

10.1

114965

115536

132191

121853

115881

119780

104301

132632

80

AA250737

AA347193

AA449431

AA425887

AA435577

W72987

D45332

N59764

Hs.72472

Hs.62180

Hs.158688

Hs.98502

Hs.184942

Hs. 191381

Hs.6783

Hs.5398

ESTs

ESTs

ESTs

ESTs

KIAA0741 gene product

G protein-coupled receptor 64

guanine-monophosphate synthetase

ESTs; Weakly similar to hypothetical protein

				•	
	105298	AA233459	Hs.26369	ESTs	9.7
	108857 113168	AA133250 T53592	Hs.62180 Hs.161586	ESTs EST	9.1 9.0
_	115892	AA435946	Hs.50831	ESTs	8.9
5	125666	AA199856	Hs.118811	ESTs	8.9
	102200 108055	U21551 AA043562	Hs.157205 Hs.62637	branched chain aminotransferase 1; cytosolic ESTs	8.8 8.6
	132572	AA448297	Hs.237825	signal recognition particle 72kD	8.6
10	115909	AA436666	Hs.59761	ESTs	8.5
10	109166	AA179845	Hs.73625	RAB6 Interacting; kinesin-like (rabkinesin6)	8.3
	121779 102915	AA422036 X07820	Hs.98367 Hs.2258	ESTs matrix metalloproteinase 10 (strometysin 2)	8.3 8.0
	105317	AA233926	Hs.23635	ESTs	7.8
1.0	125250	W87465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	7.8
15	126960	AA317900	Hs.161756	ESTs	7.8 7.7
	122969 130376	AA478539 R40873	Hs.104336 Hs.155174	ESTs KIAA0432 gene product	7.7
	123339	AA504253	Hs.101515	ESTs	7.7
20	134972	M19720	Hs.169252	Human L-myc protein gene; complete cds	7.6
20	111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c (S.cerevi	7.5 7.5
	123689 123494	AA609556 AA599786	Hs.256562 Hs.112110	ESTs ESTs	7.4
	131985	AA434329	Hs.36563	ESTs	7.4
0.5	106738	AA470145	Hs.25130	ESTs .	7.4
25	108768	AA127741	Hs.61345	ESTS	7.3 7.2
	106474 123308	AA450212 AA496211	Hs.42484 Hs.103538	Homo sapiens mRNA; cDNA DKFZp584C053 (from cl ESTs	7.2
	106124	AA423987	Hs.7567	ESTs	7.2
20	111345	N89820	Hs.14559	ESTs	7.1
30	105200	AA195399	Hs.24641	ESTs .	7.1 7.1
	116416 118846	AA609219 N80567	Hs.39982 Hs.50895	ESTs ESTs	7.1
	133434	AA278852	Hs.250786	ESTs	7.1
25	120472	AA251875	Hs.104472	ESTs; Wealdy similar to Gag-Pol polyprotein [6.9
35	115291	AA279943	Hs.122579	ESTs	6.9 6.9
	111185 108778	N67551 AA128548	Hs.12844 Hs.90847	EGF-like-domain; multiple 6 general transcription factor IIIC; polypeptid	6.9
	132939	U76189	Hs.61152	exostoses (multiple)-like 2	6.9
40	134520	N21407	Hs.257325	ESTs	6.9
40	114724	AA131701	Hs.256287	ESTs; Highly similar to SPERM SURFACE PROTEIN Homo sapiens mRNA; cDNA DKFZp586K1318 (from c	6.8 6.8
	116296 102136	AA489033 U15552	Hs.62601 Hs.85769	acidic 82 kDa protein mRNA	6.7
	132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7 (35kD	6.5
45	109648	F04600	Hs.7154	ESTs	6.4
45	116401	AA599963	Hs.59698	ESTs	6.4 6.4
	127563 104252	AI367707 AF002246	Hs.150587 Hs.210863	ESTs cell adhesion molecule with homology to L1CAM	6.4
	120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	6.2
	131978	D80008	Hs.36232	KIAA0186 gene product	6.2
50	134621	L02547	Hs.172865	cleavage stimulation factor; 3' pre-RNA; subu	6.2 6.2
	120571 102627	AA280738 U66561	Hs.128679 Hs.158174	ESTs zinc finger protein 184 (Kruppet-like)	6.1
	100661	HG2874-HT3		Ribosomal Protein L39 Homolog	6.1
	118204	N59859	Hs.48443	ESTs	6.0
55	131386	AA096412	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	6.0 5.9
	129097 131228	S50223 AA279157	Hs.24485	HKR-T1=Kruppel-like zinc finger protein (huma chondroitin sulfate proteoglycan 6 (bamacan)	5.9
	106369	AA443828	Hs.25324	ESTs	5.9
	108255	AA063157	Hs.172608	ESTs	5.8
60	125370	AA256743	Hs.151791	KIAA0092 gene product	5.8 5.8
	130010 131945	N52966 M87339	Hs.142838 Hs.35120	ESTs replication factor C (activator 1) 4 (37kD)	5.7
	116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.7
	102221	U24576		LIM domain only 4	5.6
65	130757	R00641	Hs.18925	ESTs; Wealdy similar to cDNA EST yk339a7.5 co	5.6
	131278 101383	U81523 M14113	Hs.25195 Hs.79345	endometrial bleeding associated factor (left- coagulation factor Ville; procoagulant compon	5.6 6.5
	131836	AA610086	Hs.32990	DKFZP566F084 protein	5.5
~^	129628	U26727	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	5.5
70	106523	AA453441	Hs.31511	ESTs	5.5 5.5
	111772 101255	R28287 L34600	Hs.237146 Hs.149894	ESTs mitochondrial translational initiation factor	5.5 5.5
	106895	AA489665	Hs.25245	ESTs	5.5
~-	104943	AA065217	Hs.169874	ESTs	5.5
75	129229	AA211941	Hs.109543	polyadenylate binding protein-interacting pro	5.4
	102305 106553	U33286 AA454967	Hs.90073 Hs.5887	chromosome segregation 1 (yeast homolog)-like ESTs; Highly similar to RNA binding molif pro	5.4 5.4
	112305	R54822	Hs.26244	ESTs	5.3
•	123972	C14782	Hs.70337	immunoglobulin superfamily; member 4	5.3
80	102676	U72514	Hs.12045	putative protein	5.3
	106459	AA449741 AA025104	Hs.4029	glioma-amplified sequence-41 ESTs	5.2 5.2
	107865 121121	AA399371	Hs.61252 Hs.189095	ESTs; Weakly similar to zinc finger protein S	5.2
	127162	N76398	Hs.21187	ESTs	5.2

	131646	AA171895	Hs.30057	Homo saplens clone 24749 and 24750 mRNA seque	5.2
	121770	AA421714	Hs.11469	KIAA0896 protein	5.2
	122512	AA449311	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	5.1 5.1
5	105870 100341	AA399623 D63506	Hs.23505 Hs.8813	ESTs syntaxin binding protein 3	5.1
•	116848	H65187	Hs.39001	ESTs	5.1
	120821	AA347419	Hs.96870	Homo sapiens mRNA full length insert cDNA do	5.1
	130690	AA084286	Hs.139033	paternally expressed gene 3	5.1 5.1
10	122661 123169	AA454936 AA488892	Hs.245541 Hs.104472	ESTs ESTs; Wealdy similar to Gag-Pol potyprotein [5.1
	108810	AA130596	Hs.71331	ESTs; Wealty similar to POTENT HEAT-STABLE PR	5.0
	110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	5.0
	120619	AA284372	Hs.111471	ESTs	5.0
15	122792 129912	AA460225 AA047344	Hs.99519 Hs.107213	ESTs ESTs; Highly similar to NY-REN-6 antigen [H.s	5.0 5.0
13	102823	U90914	Hs.5057	carboxypeptidase D	4.9
	129890	M13699	Hs.111461	ceruloplasmin (ferroxidase)	4.9
	101084	L05425		Homo saplens autoantigen mRNA; complete cds	4.9
20	134859	D87716	Hs.90315	KIAA0007 protein	4.9 4.9
20	115955 105516	AA446121 AA257971	Hs.44198 Hs.21214	Homo saplens BAC clone RG054D04 from 7q31 ESTs	4.9
	114932	AA242751	Hs.16218	KIAA0903 protein	4.9
	106672	AA461300	Hs.30643	ESTs	4.8
25	105126	AA424006	Hs.22972	ESTs; Moderately similar to H5AR (M.musculus)	4.8
25	110695	H93463	Hs.124777	ESTS	4.8 4.8
	102025 133282	U03911 U52960	Hs.78934 Hs.250855	mutS (E. coli) homolog 2 (colon cancer; nonpo SRB7 (suppressor of RNA polymerase B; yeast)	4.8
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	4.7
	120695	AA291468		ESTs	4.7
30	128651	AA446990	Hs.103135	ESTs	4.7
	103152	X66533	Hs.77890	guanylate cyclase 1; soluble; beta 3	4.7 4.7
	108699 115094	AA121514 AA255921	Hs.70832 Hs.88095	ESTs ESTs	4.7
	121429	AA406293	Hs.193498	ESTs	4.7
35	123203	AA489671	Hs.89709	glutamate-cysteine ligase (gamma-glutamylcyst	4.7
	126802	AA947601	Hs.97058	ESTs	4.7
	130527	C17384	Hs.184227	F-box protein 21	4.7 4.7
	134470 100449	X54942 D87470	Hs.83758 Hs.75400	CDC28 protein kinase 2 KIAA0280 protein	4.7
40	110970	N51374	Hs.96870	Homo sapiens mRNA full length Insert cDNA clo	4.7
	115901	AA436403	Hs.86909	ESTs; Moderately similar to Frizzled-6 (H.sap	4.7
	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	4.6
	116195	AA465148	Hs.72402	ESTs Chalasson interceding transportived as with Clu	4.6 4.6
45	132122 108990	U65092 AA152296	Hs.40403 Hs.72045	Cbp/p300-interacting transactivator; with Glu ESTs	4.6
1.5	109055	AA160529	Hs.48524	ESTs	4.6
	115937	AA443269	Hs.30991	KIAA0957 protein	4.6
	133520	X74331	Hs.74519	primase; polypeptide 2A (58kD)	4.6
50	131200 121369	AA609427 AA405657	Hs.210706 Hs.128791	ESTs; Moderately similar to IIII ALU SUBFAMIL Human DNA sequence from clone 967N21 on chrom	4.6 4.5
50	132880	AA444369	Hs.177537	ESTs	4.5
	127386	AI457411	Hs.106728	EST8	4.5
	120067	W93592	Hs.47343	ESTs	4.5
55	122986 135286	AA479063	Hs.102947 Hs.97849	ESTs ESTs	4.5 4.5
55	130155	AA401269 L33404	Hs.151254	kaliikrein 7 (chymobyptic; stratum corneum)	4.5
	106103	AA421104	Hs.12094	ESTs	4.5
	102654	U68494	Hs.24385	Human hbc647 mRNA sequence	4.4
60	107876	AA025315	Hs.61184	Novel human gene mapping to chomosome X	4.4 4.4
oo	109454 125960	AA232255 D63307	Hs.46912 Hs.145968	ESTs ESTs	4.4
	126892	A1160190	Hs.76127	hect (homologous to the E6-AP (UBE3A) carboxy	4.4
	100269	D38550	Hs.1189	E2F transcription factor 3	4.4
65	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	4.3
65	100502	HG1496-HT		Adrenal-Specific Protein Pg2	4.3 4.3
	105542 109787	AA261858 F10610	Hs.8241 Hs.34853	ESTs; Weakly similar to heat shock protein hs inhibitor of DNA binding 4; dominant negative	4.3
	110759	N21671	Hs.19025	ESTs	4.3
5 0	129970	AA478975	Hs.200434	ESTs	4.3
70	134666	AA482319	Hs.8752	putative type il membrane protein	4.3
	117693	N40939	Hs.44162 Hs.7222	ESTs; Wealdy similar to cDNA EST yk342h12.5 c ESTs	4.3 4.3
	111008 120977	N53388 AA398155	Hs.97600	ESTs	4.2
	105808	AA393808	Hs.21490	KIAA0438 gene product	4.2
75	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [4.2
	100893	HG4557-HT		Small Nuclear Ribonucleoprotein U1, 1snrp	4.2
	107176	AA621762	Hs.7576	ESTs ESTs	4.2 4.2
	118976 130703	N93629 N63295	Hs.93391 Hs.18103	ESTs	4.2
80	106540	AA454607	Hs.38114	ESTs; Weakly similar to coded for by C. elega	4.2
	119367	T78324	Hs.90905	ESTS	4.2
	133833	D21262	Hs.75337	nucleolar phosphoprotein p130	4.2 4.2
	105520 114264	AA258068 Z40074	Hs.33085 Hs.27595	WD repeat domain 3 ESTs	4.2
	114404	270014	113.21 030		71.1

	131046	X02530	Hs.2248	IP10; 'small inducible cytokine subfamily 8 (4.1
	105220	AA210695	Hs.17212	ESTs	4.1
	103111 125640	X63187 R37700	Hs.2719 Hs.208261	epididymis-specific; whey-ecidic protein type ESTs	4.1 4.1
5	110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING	4.1
	118092	N54915	Hs.82719	Homo sapiens mRNA; cDNA DKFZp585F1822 (from c	4.1
	134891 112364	F03517 R59312	Hs.90787 Hs.197642	ESTs ESTs; Weakly shullar to DNA-DIRECTED RNA POLY	4.1 4.1
	120699	AA291716	Hs.97258	ESTs	4.1
10	106272	AA432074	Hs.32538	ESTs	4.1
	112041 131689	R43300 AA599653	Hs.22929 Hs.30696	ESTs transcription factor-like 5 (basic helix-loop	4.1 4.1
	116134	AA460246	Hs.50441	ESTs; Highly similar to CGI-04 protein (H.sap	4.1
15	107638	AA00952B	Hs.42743	ESTs; Weakly similar to predicted using Genef	4.0
13	131941 106154	D62657 AA425304	Hs.35086 Hs.6994	ubiquitin-specific protesse 1 ESTs	4.0 4.0
	105546	AA262032	Hs.26089	ESTs; Weakly similar to 6209.a [D.melanogaste	4.0
	106319	AA436606	Hs.7392	ESTs; Weakly similar to Gu protein (H.sapiens	4.0
20	121816 122851	AA424814 AA463627	Hs.187509 Hs.99598	ESTS ESTs	4.0 4.0
	123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevi	4.0
	128643	N40212	Hs.102958	ESTS	4.0 4.0
	129011 130895	S72869 AA609828	Hs.107932 Hs.21015	DNA segment; single copy; probe pH4 (transfor ESTs; Highty similar to tetracycline transpor	4.0
25	132323	AA436102	Hs.256559	ESTs	4.0
	134255	J05032	Hs.80758 Hs.6456	aspartyl-LRNA synthetase chaperonin containing TCP1; subunit 2 (beta)	4.0 4.0
	102827 102123	U91327 U14518	Hs.1594	centromere protein A (17kD)	4.0
20	102813	U90651	Hs.151461	embryonic ectoderm development protein	3.9
30	113970 107145	W86748 AA621108	Hs.8109 Hs.173001	ESTs ESTs	3.9 3.9
	114212	Z39338	Hs.21201	DKFZP566B0846 protein	3.9
	106614	AA458934	Hs.179912	ESTs	3.9
35	132742	AA490862	Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans] ESTs; Highly similar to similar to mago nashi	3.9 3.9
33	120948 129337	AA397822 R63542	Hs.104650 Hs.110488	KIAA0990 protein	3.9
	103835	AA172215	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	3.9
	133330	U42360	Hs.71119	Putative prostate cancer tumor suppressor	3.9 3.9
40	133928 133640	N34096 D83004	Hs.7766 Hs.75355	ubiquitin-conjugating enzyme E2E 1 (homologou ubiquitin-conjugating enzyme E2N (homologous	3.9
	133350	AA135468	Hs.71573	ESTs	3.9
	115623	AA401475	Hs.39733	postsynaptic protein CRIPT	3.9 3.9
	101973 102669	S82597 U71207	Hs.80120 Hs.29279	UDP-N-acetyl-alpha-D-galactosamina:polypeptid eyes absent (Drosophila) homolog 2	3.9
45	134248	AA292677	Hs.80624	ESTs	3.9
	102380	U40434	Hs.155981	mesothelin	3.9 3.8
	116157 106691	AA461063 AA463453	Hs.44298 Hs.23259	ESTs; Highly similar to HSPC011 [H.sapiens] ESTs; Weakly similar to ACTIN; CYTOPLASMIC 2	3.8
	115844	AA430124	Hs.234607	ESTs	3.8
50	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.cerevi	3.8 3.8
	106498 134405	AA452141 J04177	Hs.7171 Hs.82772	ESTs collagen; type XI; alpha 1	3.8
	106260	AA431448	Hs.5250	ESTs; Wealdy similar to BACR37P7.g [D.melanog	3.8
55	109864	H02554	Hs.30323	ESTs ESTs	3.8 3.8
22	124648 134719	N91948 L07515	Hs.125034 Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.8
	113702	T97307	Hs.161720	ESTs; Moderately similar to IIII ALU SUBFAMIL	3.8
	128639	N91246	Hs.102897	ESTs ESTs	3.8 3.7
60	111299 129351	N73808 AA167268	Hs.24936 Hs.62349	Human ras inhibitor mRNA; 3' end	3.7
	119741	W70205	Hs.43670	kinesin family member 3A	3.7
	105012 128734	AA116036 AA343629	Hs.9329 Hs.104570	chromosome 20 open reading frame 1 katlikrein 8 (neuropsin/ovasin)	3.7 3.7
	130567	L07493	Hs.1608	replication protein A3 (14kD)	3.7
65	114253	Z39909	Hs.14831	ESTs	3.7
	103169 111269	X68560 N70711	Hs.44450 Hs.18885	Sp3 transcription factor ESTs; Highly similar to CGI-116 protein (H.sa	3.7 3.7
	112876	T03488	Hs.4842	ESTs	3.7
70	118261	N62780	Hs.94122	ESTs	3.7
70	130385 129300	AA126474 C20976	Hs.155223 Hs.110165	stanniocalcin 2 ESTs; Highty similar lo ribosomal protein 1.26	3.7 3.7
	134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	3.7
	106968	AA504631	Hs.26813	ESTs; Weakly similar to hypothetical 43.2 kDa	3.7
75	100906 100418	HG4716-HT D86978	5158 Hs.84790	Guanosine 5'-Monophosphate Synthase KIAA0225 protein	3.7 3.7
, 5	101484	M24594	Hs.20315	Interferon-induced protein 56	3.7
	102547	U57911	Hs.46638	chromosome 11 open reading frame 8	3.7
	103587 130600	Z29083 AA478601	Hs.82128 Hs.258737	5T4 oncofetal trophoblast glycoprotein ESTs	3.7 3.7
80	128733	AA328993	Hs.104558	ESTs	3.7
	134375	AA412720	Hs.82389	ESTs; Highly similar to CGI-118 protein [H.sa	3.7
	134098 101188	X06323 L20320	Hs.79086 Hs.184298	ribosomal protein; milochondrial; L3 cyclin-dependent kinase 7 (homolog of Xenopus	3.6 3.6
	132149	T10822	Hs.4095	ESTs	3.6

	116200	AA465358	Hs.118793	ESTs; Highly similar to p621 [H.saplens]	3.6
	121920	AA428300	Hs.161841	ESTs	3.6
	128609 101078	AA234365 L04510	Hs.102456 Hs.792	survival of motor neuron protein interacting ADP-ribosylation factor domain protein 1; 64k	3.6 3.6
5	108693	AA121289	Hs.49597	ESTs; Highly similar to relinoic acid-induced	3.6
-	109139	AA176121	Hs.59757	zinc finger protein 281	3.6
	111870	R37778	Hs.18685	ESTs; Weakly similar to hypothetical protein	3.6 3.6
	113848 127947	W60080 AJ432475	Hs.27099 Hs.146327	DKFZP564J0863 protein ESTs	3.6
10	128056	Al379480	Hs.125449	ESTs; Weakly similar to MaxiK channel beta 2	3.6
	129914	U22377	Hs.13321	rearranged L-myc fusion sequence	3.6
	132148	AA283988 S83308	Hs.4094 Hs.87224	ESTs SRY (sex-determining region Y)-box 5	3.6 3.6
	134644 115047	AA252627	Hs.22554	homeo box 85	3.6
15	102398	U42359		Human N33 protein form 1 (N33) gene, exon 1 a	3.6
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	3.6
	105545 101483	AA262030 M24486	Hs.5152 Hs.76768	ESTs; Weakly similar to katanin p80 subunit i procollagen-proline; 2-oxoglutarate 4-dioxyge	3.6 3.6
	105709	AA291268	Hs.26761	DKFZP586L0724 protein	3.6
20	122636	AA454103	Hs.110031	ESTs	3.6
	124792	R44357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL:T01421	3.6 3.5
	103621 105427	Z47727 AA251330	Hs.150675 Hs.28248	polymerase (RNA) II (DNA directed) polypeptid ESTs	3.5
	121553	AA412488	Hs.48820	ESTs `	3.5
25	115167	AA258421	Hs.43728	hypothetical protein	3.5
	134570	U66615	Hs.172280	SWI/SNF related; matrix associated; actin dep	3.5 3.5
	110787 131621	N24716 - U77665	Hs.12244 Hs.139120	ESTs; Weakly similar to C44B9.1 [C.elegans] ribonuclease P (30kD)	3.5
	132813	N72116	Hs.57435	solute carrier family 11 (proton-coupled diva	3.5
30	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMP	3.5
	131965	W90146	Hs.35962	ESTs	3.5 3.5
	115221 116093	AA262942 AA456020	Hs.79741 Hs.50848	ESTs ESTs; Weakly similar to KIAA0862 protein (H.s	3.5
	123507	AA600176	Hs.112345	ESTs	3.5
35	129801	F11087	Hs.239666	ESTs	3.5
	115084	AA255566	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	3.5 3.5
	123442 115061	AA598803 AA253217	Hs.111498 Hs.41271	ESTs ESTs	3.5
	100146	D13645	Hs.2471	KIAA0020 gene product	3.5
40	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	3.5
	115360	AA281950	Hs.5057	carboxypeptidase D reproduction 8	3.5 3.4
	130261 100824	D83767 HG4058-HT4	Hs.153678 1328	Oncogene Ami1-Evi-1, Fusion Activated	3.4
	102287	U31814	Hs.3352	histone deacetylase 2	3.4
45	102788	U86602	Hs.74407	nucleolar protein p40	3.4
	118836	N79820	Hs.50854	ESTs	3.4 3.4
	102423 106300	U44754 AA435840	Hs.179312 Hs.19114	smail nuclear RNA activating complex; polypep high-mobility group (nonhistone chromosomal)	3.4
	106156	AA425354	Hs.4210	ESTs	3.4
50	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.4
	107868 108187	AA025234 AA056538	Hs.61260 Hs.27842	ESTs ESTs; Wealdy similar to similar to 1-acyl-gly	3.4 3.4
	116123	AA459282	Hs.43756	ESTs	3.4
	119501	W37721	Hs.151363	ESTs	3.4
55	129121	AA127459	Hs.108788	ESTs; Wealdy similar to zeste [D.melanogaster	3.4
	131638 132962	D87120 N34893	Hs.29882 Hs.6153	predicted osteoblast protein ESTs; Highly similar to CGI-48 protein [H.sap	3.4 3.4
	133767	D63875	Hs.173288	KIAA0155 gene product	3.4
	111823	R35253	Hs.24944	ESTs	3.4
60	134372	D63877	Hs.82324	KIAA0157 protein	3.4
	130938 115169	AAU13250 AA258427	Hs.21398 Hs.58427	ESTs; Moderately similar to PUTATIVE GLUCOSAM ESTs	3.4 3.4
	123978	C20653	Hs.170278	ESTs	3.4
	108807	AA129968	Hs.49376	ESTs; Weakly similar to PROTEIN PHOSPHATASE P	3.4
65	132581	R42266	Hs.52256	ESTs; Weakly similar to beta-TrCP protein E3R	3.4 3.4
	134654 105730	W23625 AA292701	Hs.8739 Hs.5364	ESTs; Weakly similar to ORF YGR200c [S.cerevl OKFZP5641052 protein	3.4
	111295	N73275	Hs.21275	ESTs; Weakly similar to ubiquitin-conjugating	3.3
70	102009	U02680	Hs.82643	protein tyrosine kinase 9	3.3
70	114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.s estrogen receptor 1	3.3 3.3
	130604 100103	X03635 AF007875	Hs.1657 Hs.5085	dolichyl-phosphate mannosyltransferase polype	3.3
	121748	AA421171	Hs.234545	ESTs	3.3 3.3
75	106698	AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	
75	134353	S77154	Hs.82120	nuclear receptor subfamily 4; group A; member	3.3 3.3
	134154 133142	AA211320 F03321	Hs.79404 Hs.65874	neuron-specific protein ESTs	3.3
	124461	N50641	Hs.80285	Homo saplens mRNA; cDNA DKFZp586C1723 (from c	3.3
00	104903	AA055534	Hs.124134	ESTs	3.3
80	106772	AA478106	Hs.12692	ESTs; Wealdy similar to protein phosphatase-1	3.3
	109704	F09687 N64267	Hs.12876 Hs.10177	ESTs ESTs	3.3 3.3
	111131 115019	AA251906	Hs.48473	ESTs	3.3
	116019	AA450312	Hs.237480	Homo sapiens mRNA; cDNA DKFZp434E102 (from cl	3.3

150

	118528	N67889	Hs.49397	ESTs	3.3
	124027	F03625	Hs.107537	ESTs	3.3
	131699	R68657	Hs.90421	ESTs; Moderately similar to IIII ALU SUBFAMIL	3.3
5	111044	N55443	Hs.23625	ESTs	3.3
3	103768 131882	AA089997 N49091	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEMBRANE	3.3 3.3
	123673	AA609471	Hs.3385 Hs.112712	ESTs; Highly similar to CGI-134 protein (H.sa ESTs	3.3
	132936	AB002305	Hs.6111	KIAA0307 gene product	3.3
	103023	X53793	Hs.117950	multifunctional polypeptide similar to SAICAR	3.3
10	120572	AA280794	Hs.258787	ESTs	3.3
	132384	AA479933	Hs.46967	Human DNA sequence from clone 157A19 on chrom	3.3
	105658	AA282914	Hs.10176	ESTs	3.2
	105086 118695	AA147719 N71781	Hs.159441 Hs.50081	ESTs Homo sapiens mRNA full length insert cDNA do	3.2 3.2
15	112092	R44538	Hs.140889	ESTs	3.2
	125154	W38419	Hs.24936	ESTs	3.2
	108040	AA041551	Hs.48644	ESTs	3.2
	133453	M68941	Hs.73826	protein tyrosine phosphatase; non-receptor ty	3.2
20	124006	D60302	Hs.108977	ESTs	3.2
20	116083	AA455653	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROT	3.2
	106753 102621	AA476944 U66075	Hs.7331 Hs.50924	ESTs GATA-binding protein 6	3.2 3.2
	1033330	X85373	Hs.77496	small nuclear ribonucleoprotein polypeptide G	3.2
	128926	AA481403	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [H.s	3.2
25	101167	L15309	Hs.193677	zinc finger-protein 141 (clone pHZ-44)	3.2
	104055	AA393755	Hs.117211	ESTs: Highly similar to CGI-62 protein [H.sap	3.2
	112917	T10196	Hs.4263	ESTs; Weakly similar to Iprediction	3.2
	120358	AA213459	Hs.100932	transcription factor 17	3.2
30	121857	AA426017 AA434257	Hs.62694	ESTs; Highly similar to DNA-REPAIR PROTEIN CO ESTs; Moderately similar to !!!! ALU SUBFAMIL	3.2 3.2
50	122124 132231	H99131	Hs.186679 Hs.42635	ESTs Moderately Sittled to IIII ALO SOBFAMIL	3.2
	134272	X76040	Hs.223014	protease; serine; 15	3.2
	115860	AA431719	Hs.61809	ESTs	3.2
	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.melano	3.2
35	134125	R38102	Hs.50421	KIAA0203 gene product	3.2
	129160	AA131252	Hs.109007	ESTS	3.2
	121710	AA419011	Hs.96744	DKFZP586D0823 protein	3.2 3.2
	102242 104956	U27185 AA074880	Hs.32943 Hs.120975	relinoic acid receptor responder (tazarolene ESTs; Weakly similar to hypothetical protein	3.2
40	113047	T25867	Hs.7549	ESTs	3.2
	115017	AA251880	Hs.179982	tumor protein p53-binding protein	3.2
	133780	M14219	Hs.76152	decorin	3.1
	129453	AA421213	Hs.111632	Lsm3 protein	3.1
45	130353	X86018	Hs.172210	MUF1 protein	3.1
43	106036 102234	AA412505 U26312	Hs.10653 Hs.8123	EST8	3.1 3.1
	106133	AA424346	Hs.107573	chromobox homolog 3 (Drosophila HP1 gamma) sialyltransferase	3.1
	116803	H47357	110.101010	ESTs; Moderately similar to weak similarity t	3.1
	106721	AA465194	Hs.6670	ESTs	3.1
50	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [H.sa	3.1
	133228	N90029	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA;	3.1
	104733	AA019498	Hs.23071	ESTs	3.1 3.1
	103879 103038	AA228148 X54941	Hs.50252 Hs.77550	ESTs; Weakly similar to putative [C.elegans] CDC28 protein kinase 1	3.1
55	135154	AA126433	Hs.173242	sorting nexin 4	3.1
	114860	AA235112	Hs.106227	ESTs; Moderately similar to similar to murine	3.1
	102437	U46569	Hs.221986	aquaporin 5	3.1
	100352	D64159		Homo sapiens mRNA for 3-7 gene product, parti	3.1
60	103631	Z48570	11- 07040	H.saplens Sp17 gene	3.1
UU	104238 108613	AB002364 AA100967	Hs.27916 Hs.69165	a disintegrin-like and metalloprotease (repro ESTs	3.1 3.1
	115915	AA436884	Hs.48926	ESTs	3.1
	120640	AA286945	Hs.163933	ESTs	3.1
	124068	H03099	Hs.101619	ESTs	3.1
65	130375	U91931	Hs.155172	adaptor-related protein complex 3; beta 1 sub	3.1
	131632	AA443671	Hs.29826	ESTs	3.1
	131523	H88801	Hs.201676	M phase phosphoprotein 10 (U3 small nucleolar	3.1
	115827	AA427890	Hs.44426	ESTs; Weakly similar to PHOSPHOLIPID HYDROPER	3.1 3.1
70	108828 112198	AA131584 R49483	Hs.71435 Hs.22159	DKFZP56400463 protein ESTs; Weakly similar to ZINC FINGER PROTEIN H	3.1
, ,	123960	AA621785	Hs.170008	methylmatonate-semialdehyde dehydrogenase	3.1
	131538	Z29331	Hs.28505	ubiquitin-conjugating enzyma E2H (homologous	3.1
	105616	AA280670	Hs.24968	ESTs	3.1
75	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (zeta	3.1
75	100280	D42085	Hs.155314	KIAA0095 gene product	3.1
	132744	X54326	Hs.55921	glutamyt-prolyt-IRNA synthetase proteasome (prosome; macropaln) subunit; alph	3.1 3.1
	103105 106984	X61970 AA521201	Hs.76913 Hs.7129	ESTs	3.1
_	105127	AA158132	Hs.11817	ESTs; Wealdy similar to contains similarity t	3.1
80	102302	U33052	Hs.69171	protein kinase C-like 2	3.1
	117708	N45114	Hs.46476	ESTs	3.1
	111314	N74574	Hs.33922	H.saplens novel gene from PAC 117P20; chromos	3.0
	132902	AA490969	Hs.168147	ESTS	3.0 3.0
	130356	X84373	Hs.155017	nuclear receptor interacting protein 1	3.0

	128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown (H.sapiens)	3.0
	108746	AA126974	Hs.43388	ESTS	3.0
	127236	Al341818	Hs.98658	budding uninhibited by benzimidazolas 1 (yeas	3.0
5	114208 107071	Z39301 AA609053	Hs.7859 Hs.35198	ESTs ESTs	3.0 3.0
_	104957	AA074919	Hs.10026	ESTs; Wealtly similar to ORF YJL063c [S.cerevi	3.0
	124073	H05394	Hs.127376	KIAA0266 gene product	3.0
	130869 101232	AA128100 L28997	Hs.2057 Hs.242894	uridine monophosphate synthetase (orotate pho ADP-ribosylation factor-like 1	3.0 3.0
10	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapiens]	3.0
	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate	3.0
	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	3.0 3.0
	100405 101335	D86425 L49054	Hs.82733	nidogen 2 Homo sapiens t(3;5)(q25.1;p34) fusion gene NP	3.0
15	108761	AA127514	Hs.61603	ESTs	3.0
	111346	N89829	Hs.13259	ESTs	3.0
	114988 116008	AA251089 AA449338	Hs.94576 Hs.48589	ESTs; Wealdy similar to phosducin; retinal (H ESTs; Wealdy similar to finger protein HZF6;	3.0 3.0
	116545	D20313	Hs.74899	ESTs	3.0
20	117873	N49957	Hs.46624	ESTs	3.0
	121463 128625	AA411745 AA242816	Hs.239681 Hs.102652	ESTs; Weakly similar to KIAA0554 protein [H.s ESTs; Weakly similar to KIAA0437 [H.saplens]	3.0 3.0
	131185	M25753	Hs.23960	cyclin B1	3.0
25	134380	D38073	Hs.179565	minichromosome maintenance deficient (S. cere	3.0
25	105740	AA293206	Hs.10852	EST8	3.0 3.0
	130919 134423	AA291710 W96151	Hs.21276 Hs.83006	collagen; type IV; alpha 3 (Goodpasture antig ESTs; Highly similar to CGI-139 protein [H.sa	3.0
	104896	AA054228	Hs.23165	ESTs	3.0
20	134407	X72964	Hs.82794	caltractin (20kD calcium-binding protein)	3.0 3.0
30	106378 112283	AA445994 R53545	Hs.21331 Hs.20952	ESTs Homo sapiens clone 24411 mRNA sequence	3.0
	109018	AA156960	Hs.114992	ESTs	3.0
	114239	Z39742	Hs.222478	ESTs	3.0
35	114969	AA250775 AA608752	Hs.87747 Hs.71969	ESTs Homo sapiens mRNA; cDNA DKFZp564P0823 (from c	3.0 3.0
23	116408 115286	AA279803	Hs.82204	ESTs	2.9
	105809	AA393827	Hs.20104	ESTs ·	2.9
	113811	W44928	Hs.4878	ESTs	2.9 2.9
40	107248 134489	D59894 U09284	Hs.34782 Hs.112378	ESTs LIM and senescent cell antigen-like domains 1	2.9
	134064	D87685	Hs.78893	KIAA0244 protein	2.9
	127370	A1024352	Hs.70337	immunoglobulin superfamily; member 4	2.9 2.9
	113277 132783	T65797 N74897	Hs.11774 Hs.5683	protein (peptidyl-protyl cis/trans Isomerase) DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.9
45	109010	AA156460	Hs.44229	dual specificity phosphalase 12	2.9
	130095	F01831	Hs.14838	ESTs	2.9
	106618	AA459249	Hs.8715	ESTs; Wealdy similar to Similarity with snall H.sapiens mRNA for Ptg-12 protein	2.9 2.9
	103427 133980	X97303 D00760	Hs.181309	proteasome (prosome; macropain) subunit; alph	2.9
50	111353	N90430	Hs.6616	ESTs	2.9
	105344	AA235303	Hs.8645	ESTs	2.9 2.9
	134498 117910	M63180 N50828	Hs.84131 Hs.12940	threonyl-IRNA synthetase zinc-lingers and homeoboxes 1	2.9
	118903	N90774	Hs.132207	ESTs; Moderately similar to !!!! ALU SUBFAMIL.	2.9
55	121713	AA419198	Hs.105577	ESTs	2.9
	129080 129404	H19307 AA172056	Hs.108507 Hs.111128	ESTs ESTs	2.9 2.9
	129457	X55330	Hs.207776	aspartylglucosaminidase .	2.9
60	130352	D87450	Hs.154978	KIAA0261 protein	2.9
60	133415	X69699 AA287115	Hs.73149 Hs.99697	paired box gene 8 ESTs	2.9 2.9
•	120649 131257	AA256042	Hs.24908	ESTS	2.9
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	2.9
65	116734	F13789	Hs.93796	DKFZP586D2223 protein	2.9 2.9
65	105028 114986	AA126719 AA251010	Hs.25282 Hs.87807	ESTs ESTs	2.9
	105651	AA282481	Hs.18439	ESTs	29
	101714	M68874*	11 405544	Human phosphatidylcholine 2-acythydrolase (cP	2.9 2.9
70	123398 106007	AA521265 AA411462	Hs.105514 Hs.11042	ESTs ESTs; Weakly similar to vell 1 [H.saplens]	29
70	109450	AA232183	Hs.173042	ESTs; Weakly similar to IIII ALU SUBFAMILY J	2.9
	104685	AA010530	Hs.9599	Human BAC clone GS025M02 from 7q21-q22	29
	108677 116028	AA115629 AA452112	Hs.118531 Hs.42644	ESTs thloredoxin-like	2.9 2.9
75	105404	AA243303	Hs.21187	ESTs	2.9
. •	132365	AA598694	Hs.46541	Homo sapiens PAC clone DJ0894A10 from 7q32-q3	2.9
	119638	W52480	Hs.56148	ESTs; Moderately similar to NY-REN-58 antigen	2.9 2.9
	124637 130588	N80716 AA287735	Hs.75798 Hs.16411	Human DNA sequence from clone 1183121 on chro Human DNA sequence from clone 1189824 on chro	2.9
80	105640	AA281623	Hs.7525	ESTs; Weakly similar to KIAA0742 protein [H.s	2.9
	131818	Z39297	Hs.3281	neuronal pentrado ()	2.9
	119298 128742	T23820 D00763	Hs.155478 Hs.251531	cyclin T2 proteasome (prosome; macropaln) subunit; alph	2.9 2.9
	115089	AA255876	Hs.86919	. ESTs; Weakly similar to Illi ALU SUBFAMILY J	2.9

	100468	D89289	Hs.118722	fucosyltransferase 8 (alpha (1;6) fucosyltran	2.8
	132920	106133	Hs.606	ATPase: Cu++ transporting; alpha polypeptide	2.8
	113490	T88700	Hs.173374		2.8 2.8
5	133451 128770	Y00764 H98645	Hs.73818 Hs.143460		2.8
,	129122	N62515	Hs.108790	ESTs	2.8
	104827	AA035630	Hs.8551	i ve netitive spinored incer-	2.8
	111348 130987	N90041 R45698	Hs.9585 Hs.21893		2.8 2.8
10	102139	U15932	Hs.2128	dual specificity phosphatase 5	2.8
	114902	AA236359	Hs.39504	ESTs	2.8
	106094	AA419461	Hs.18127		2.8 2.8
	126438 107129	N93125 AA620553	Hs.137300 Hs.4756		2.8
15	104491	N71513	Hs.39328	ESTs	2.8
	105043	AA132239	Hs.11810	2010 11000) 011111 0 10 11 (01111)	2.8 2.8 ·
	106855 109695	AA486182 F09530	Hs.17975 Hs.180591		2.8
	120455	AA251083	Hs.104347		2.8
20	130861	N23393	Hs.20509	ESTs	2.8
	131649	AA481254	Hs.30120		2.8 2.8
	128517 100486	AA280617 HG1112-HT11	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien Ras-Like Protein Tc4	2.8
	116729	F13700	Hs.115823	ribonuclease P; 40kD subunit	2.8
25	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor 2)	2.8
	115465	AA286941	Hs.43691 Hs.15071	ESTs chaperonin containing TCP1; subunit 8 (theta)	2.8 2.8
	100137 125837	D13627 H05323	Hs.146401	endolhelial monocyte-activating polypeptide	2.8
	131562	U90551	Hs.28777	H2A histone family; member L	2.8
30	129445	AA306121	Hs.111515	ESTs; Weakly similar to predicted using Genef	2.8 2.8
	129239 106507	D31544 AA452584	Hs.109701 Hs.91585	ESTs; Moderately similar to weak similarity (protein phosphatase 1; regulatory (Inhibitor)	2.8
	101664	M60752	Hs.121017	H2A histone family; member A	2.8
	129426	AA412087	Hs.168272	EST; Highly similar to protein inhibitor of a	2.8
35	103437	X98260	Hs.82254	M-phase phosphoprotein 11	2.8 2.8
	129821 130160	F11019 Z39228	Hs.12696 Hs.151344	cortactin SH3 domain-binding protein UDP-Gal:betaGicNAc beta 1;3-galactosyitransie	2.8
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-associated	2.8
40	116204	AA465701	Hs.108646	ESTs Color Color Color Color Color	2.8 2.8
40	125914	AA262925	Hs.180034 Hs.27842	cleavage stimutation factor; 3' pre-RNA; subu ESTs; Wealdy simitar to simitar to 1-acyl-gly	2.8
	131510 106291	AA207114 AA435551	Hs.30824	ESTs	2.8
	122761	AA459298	Hs.105039	ESTs; Weakly similar to IIII ALU SUBFAMILY J	2.8
45	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f Homo saplens clone 24881 mRNA sequence	2.8 2.8
43	108535 116226	AA084505 AA478729	Hs.226440 Hs.76450	EST8	2.8
	120268	AA173939	Hs.193902	ESTs; Weakly similar to inner centromere prot	2.8
	128654	H20689	Hs.103180	acth-like 6	2.8 2.7
50	116726 132640	F13681 U33821	Hs.42309	ESTs Tax1 (human T-cell leukemla virus type I) bin	2.7
50	133273	AA147725	Hs.69469	dendritic cell protein	2.7
	108846	AA132983	Hs.44155	DKFZP586G1517 protein	2.7
	105621	AA280865	Hs.6375	Homo sepiens mRNA; cDNA DKFZp564K0222 (from c	2.7 2.7
55	129164 133618	AA282183 U78524	Hs.109045 Hs.75251	ESTs DEAD/H (Asp-Giu-Ala-Asp/His) box binding prot	2.7
55	120521	AA258785	Hs.107476	ATP synthase; H+ transporting; mitochondrial	2.7
	116429	AA609710	Hs.82837	Human chromosome 3p21.1 gene sequence	2.7 2.7
	110984 100372	N52008 D79997	Hs.80120 Hs.184339	UDP-N-acetyl-alpha-D-galactosamine:polypeptid KIAA0175 gene product	2.7
60	125134	W19228	Hs.100748	ESTs	2.7
	129254	AA453624	Hs.1098	deoxynucleotidyltransferase; terminal	2.7 2.7
	102339	U37022 AA456646	Hs.95577 Hs.28661	cyclin-dependent kinase 4 ESTs	2.7
	106589 119118	R44122	Hs.42743	ESTs; Weakly similar to predicted using Genef	2.7
65	105973	AA406320	Hs.21201	DKFZP566B0846 protein	2.7
	106317	AA436568	Hs.172140	ESTS	2.7 2.7
	115551 103789	AA365527 AA096178	Hs.177861 Hs.70337	ESTs; Highty similar to CGI-110 protein (H.sa immunoclobulin superfamily; member 4	27
	105079	AA143190	Hs.12677	ESTs; Highly similar to CGI-147 protein [H.sa	2.7
70	109299	AA205649	Hs.86371	zinc finger protein 254	27
	122089	AA432136	Hs.98682	ESTs serine/threonine kinase 2	2.7 2.7
	129108 129385	L20321 D82675	Hs.1087 Hs.110950	Homo sapiens clone 25007 mRNA sequence	2.7
	131412	U34044	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium d	2.7
75	104052	AA393164	Hs.97644	mammaglobin 2	2.7 2.7
	116254	AA481146	Hs.41086 Hs.12314	ESTs; Weakly similar to OXYSTEROL-BINDING PRO Homo sapiens mRNA; cDNA DKFZp586C1019 (from c	2.7
	106878 114652	AA488872 AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED SPLICE	2.7
	106831	AA482014	Hs.29463	centrin; EF-hand protein; 3 (CDC31 yeast homo	2.7
80	101445	M21259	Hs.1066	smail nuclear ribonucleoprotein polypeptide E ribosomai protein L17	2.7 2.7
	124428 114471	N36881 AA028074	Hs.82202 Hs.103387	ESTs	2.7
	102051	U07550	Hs.1197	heat shock 10kD protein 1 (chaperonin 10)	2.7
	106916		Hs.24170	ESTs; Wealdy similar to ribosomal S1 protein	2.7

	116142	AÅ460649	Un 20457	ESTs	2.7
	109912	H05509	Hs.39457 Hs.24639	EST8	2.7
	103193	X70476	Hs.75724	coatomer protein complex; subunit beta 2 (bet	2.7
5	102046 104567	U07151 R64534	Hs.182215 Hs.101469	ADP-ribosylation factor-like 3 ESTs	2.7 2.7
•	112996	T23539	Hs.7165	zinc finger protein 259	2,7
	118138	N57773	Hs.93560	ESTs; Weakly similar to trg [R.norvegicus]	27 27
	123095 124315	AA485724 H94892	Hs.192119 Hs.6908	ESTs v-ral simian leukemia viral oncogene homolog	2.7
10	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (from cl	2.7
	132834	H77546	Hs.57898 Hs.5092	ESTs; Highly similar to NY-REN-49 antigen [H. nucleolar protein (KKE/D repeat)	· 2.7 2.7
	107529 130648	Y12065 AA075427	Hs.17296	ESTs: Weakly similar to /prediction	2.7
1.5	106685	AA461551	Hs.16251	ESTs; Highly similar to 73 kDA subunit of cle	2.6
15	133848 134880	AA093287 AA092376	Hs.76728 Hs.90608	ESTs · 15 kDa selenoprotein	2.6 2.6
	128871	AA400271	Hs.106778	Homo saplens mRNA for putative Ca2+-transport	2.6
	106846	AA485223	Hs.34892	ESTs	2.6
20	119892 132309	W84548 AA460917	Hs.94896 Hs.2780	ESTs jun D proto-oncogene	2.6 2.6
20	132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	2.6
	114365	Z41688	Hs.18653	ESTs	2.6 2.6
	114162 133370	Z38909 AA156897	Hs.22265 Hs.72157	ESTs DKFZP564I1922 protein	2.6
25	106818	AA480890	Hs.3542	ESTs 🗸	2.6
	133501	W16684	Hs.74284	ESTs; Moderately similar to Similar to S.cere	2.6 2.6
	100530 130553	HG1869-HT1 AA430032	Hs.252587	Male Enhanced Antigen pituitary tumor-transforming 1	2.6
20	108917	AA137078	Hs.173648	ESTs	2.6
30	122249	AA436679	Hs.258543	ESTs; Highly similar to CGI-07 protein (H.sap	2.6 2.6
	119598 119902	W45531 W84865	Hs.94642 Hs.40094	ESTs Human DNA sequence from clone 167A19 on chrom	2.6
	133272	AA465016	Hs.69423	kaflikrein 10	2.6
35	132575	AA045365	Hs.5188	ESTs; Wealdy similar to 60S RIBOSOMAL PROTEIN	2.6 2.6
33	130459 133083	AA460264 N70633	Hs.155983 Hs.6456	KIAA0677 gene product chaperonin containing TCP1; subunit 2 (beta)	2.6
	131130	T19399	Hs.23255	nucleoporin 155kD	2.6
	112043 116146	R43317 AA460701	Hs.26312 Hs.193200	glioma amplified on chromosome 1 protein (leu ESTs	2.6 2.6
40	122378	AA446100	Hs.103617	ESTs	2.6
	103134	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	133395 115652	AA491296 AA405098	Hs.72805 Hs.38178	ESTs ESTs	2.6 2.6
	104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2.6
45	134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	2.6
	112869 100092	T03313 AF000231	Hs.4747 Hs.75818	dyskeratosis congenita 1; dyskerin RAB11A; member RAS oncogene family	2.6 2.6
	102635	U66838	Hs.79378	cyclin A1	2.6
50	104490	N71503	Hs.43087	ESTs; Weakly similar to dysferlin (H.sapiens)	2.6
50	106813 106872	AA479922 AA487907	Hs.181022 Hs.18282	ESTs ESTs; Highly similar to unknown [H.saplens]	2.6 2.6
	107022	AA599041	Hs.28866	programmed cell death 10	2.6
	107113	AA610073	Hs.23900	ESTs; Wealdy similar to digophrenin-1 like p	2.6 2.6
55	113281 115586	T66300 AA399218	Hs.112356 Hs.92423	Homo saplens mRNA for lipoyltransferase; comp ESTs	2.6
•••	115779	AA424183	Hs.70945	ESTs	2.6
	122895	AA469946	Hs.105325 Hs.104576	ESTs carbohydrate (keratan sulfate Gal-6) sulfotra	26 26
	124726 129775	R15740 R94659	Hs.12420	EST8	2.6
60	131991	AA251909	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	2.6
	132518	D57975	Hs,5064	ESTs ESTs: Highly similar to ubiquitin C-terminal	2.6 2.6
	134612 130313	AA451712 AA620323	Hs.171581 Hs.154320	ubiquitin-activating enzyme E1C (homologous t	2.6
	131971	R70167	Hs.3611	ESTs	2.6
65	133175	AA134767 U10323	Hs.66666 Hs.75117	ESTs Interleukin enhancer binding factor 2; 45kD	2.6 2.6
	102083 125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen; integrin-as	2.6
	121822	AA425107	Hs.97016	ESTs; Moderately similar to SH3 domain-bindin	2.6
70	106719 130029	AA465171 AA236412	Hs.236844 Hs.236510	ESTs ESTs; Moderately similar to PFT27 [M.musculus	2.6 2.6
70	124328	H97781	Hs.14415	ESTs; Highly similar to CGI-108 protein [H.sa	2.6
	105387	AA236951	Hs.108636	chromosome 1 open reading frame 9	2.6 2.6
	103073 116294	X59417 AA489000	Hs.74077 Hs.93748	proteasome (prosome; macropain) subunit; alph ESTs; Moderately similar to TRANSCRIPTION FAC	26
75	135339	D59269	Hs.127842	Homo saplens mRNA full length Insert cDNA do	2.6
	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	2.6
	102504 131076	U52077 H44386	Hs.247948 Hs.22666	Human mariner1 transposase gene; complete con ESTs	2.6 2.6
	114096	Z38342	Hs.27007	chromosome condensation 1-like	2.6
80	120402	AA234339	Hs.50282	GTP-binding protein ragB	2.6 2.6
	102125 134653	U14550 AA452818	Hs.107573 Hs.87385	sialytransferase ESTs	2.6
•	101959	\$80343	Hs.180832	arginyl-iRNA synthetase	2.6
	116766	H13260	Hs.95097	. ESTs	2.6
				15/	

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	104954	AA074514	Hs.26213	ESTs; Wealty similar to protein [H.saplens]	2.5
	108771	AA127924	Hs.71034	ESTs	2.5
	116439	AA610068	Hs.43913	PIBF1 gene product	2.5
_	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	2.5
5	132792	AA401903	Hs.242985	hemoglobin; gamma G	2.5 2.5
	129620 120296	AA010686 AA191353	Hs.239720 Hs.22385	ESTs; Wealdy similar to KIAA0691 protein (H.s ESTs; Wealdy similar to KIAA0970 protein (H.s	25
	115615	AA401186	Hs.48617	ESTs	2.5
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A) expre	2.5
10	106288	AA435536	Hs.24336	ESTs	2.5
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	2.5 2.5
	104525 128917	R16007 AA204876	Hs.75355 Hs.206097	ubiquitin-conjugating enzyme E2N (homologous oncogene TC21	2.5
	102299	U32907	Hs.155545	37 kDa teucine-rich repeat (LRR) protein	2.5
15	115363	AA282071	Hs.152759	activator of S phase kinase	2.5
	130399	AA449417	Hs.155358	Homo saptens mRNA for putative glucosyltransf	2.5
	130752	D50927 ·	Hs.18895	tousled-like kinase 1 geranylgeranyl diphosphate synthase 1	2.5 2.5
	132724 106743	AA417962 AA476352	Hs.55498 Hs.21938	ESTs; Weakly similar to KIAA0704 protein (H.s	2.5
20	128949	AA190993	Hs.8850	a disintegrin and metalloproteinase domain 12	2.5
	125685	AI040346	Hs.4943	hepatocellular carcinoma associated protein;	2.5
	105826	AA398243	Hs.21806	ESTs; Moderately similar to similar to NEDD-4	2.5
	110841	N31610	Hs.18645	ESTs; Wealdy similar to partial COS [C.elegan	2.5 2.5
25	111987 132669	R42036 AA188378	Hs.6763 Hs.54602	KIAA0942 protein ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.5
	100398	D84557	Hs.155462	minichromosome maintenance deficient (mis5; S	. 2.5
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subunit [2.5
	114481	AA033562	Hs.151572	ESTS	2.5 2.5
30	113404 100260	T82323 D38491	Hs.70337 Hs.174135	immunoglobulin superfamily; member 4 KIAA0117 protein	2.5
50	103563	Z22534	Hs. 150402	activin A receptor; type I	2.5
	104573	R68952	Hs.29780	ESTs	2.5
	105025	AA126336	Hs.22744	ESTs; Weakly similar to ZINC FINGER PROTEIN 1	2.5
35	105524 106157	AA258158 AA425367	Hs.22153 Hs.32094	ESTs; Wealtly similar to KIAA0352 [H.saplens] ESTs	2.5 2.5
33	107243	D59489	Hs.34727	ESTs	2.5
	109920	H05733	Hs.30558	ESTs	2.5
	109981	H09552	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	. 2.5
40	114518	AA046407	Hs.106469	suppressor of var1 (S.cerevislae) 3-like 1	2.5 2.5
40	114768 118906	AA149007 N91000	Hs.182339 Hs.94433	Ets homologous factor ESTs	2.5
	119025	N98926	Hs.55209	ESTs; Weakly similar to DMR-N9 PROTEIN (H.sap	2.5
	131712	N29502	Hs.30991	KIAA0957 protein	2.5
15	132233	X04708	Hs.93574	homeo box D3	2.5
45	132740	AA227751	Hs.55896 Hs.73291	ESTs ESTs; Weakly similar to similar to the beta t	2.5 2.5
	115239 128820	AA278550 F10338	Hs.106309	Friend of GATA2	2.5
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	2.5
50	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypeptide F	2.5
50	121361	AA405494	Hs.183052	ESTS	2.5 2.5
	134133 102502	X93920 U51678	Hs.180383 Hs.78050	dual specificity phosphatase 6 small acidic protein	2.5
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity to Ye	2.5
	132874	AA425776	Hs.58609	ESTs	2.5
55	109646	F04543	Hs.5028	DKFZP564O0423 protein	2.5
	111197	N68093	Hs.22909 Hs.154672	ESTs methylene tetrahydrofolate dehydrogenase (NAD	2.5 2.5
	102968 124911	X16398 R88992	Hs.123645	ESTs .	2.5
	106628	AA459657	Hs.12311	Homo saplens clone 23570 mRNA sequence	2.5
60	116988	H82527		ys69e12.s1 Soares relina N2b4HR Homo saplens	2.5
	131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (2.5 2.5
	133578 100420	X78627 D86983	Hs.75066 Hs.118893	translin p53-responsive gene 2	2.5
	130743	W87710	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from d	2.5
65	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sap	25
	115117	AA256492	Hs.49007	poly(A) polymerase	2.5
	124582	N68477 AA025911	Hs.108408 Hs.24994	ESTs; Highly similar to CGI-78 protein (H.sap ESTs; Highly similar to CGI-53 protein (H.sap	2.5 2.5
	104771 108059	AA043944	Hs.62663	ESTs	2.5
70	105628	AA281251	Hs.35696	ESTs; Weakly similar to putative zinc finger	2.5
-	109261	AA195255	Hs.61779	ESTs	2.5
	119789	W73140	Hs.50915	kallikrein 5	2.5 2.5
	130512 134402	AA045304 U25165	Hs.181271 Hs.82712	ESTs; Highly similar to CGI-120 protein (H.sa fragile X mental retardation; autosomal homol	2.5 2.5
75	104769	AA025887	Hs.114774	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.5
	125787	. AA744748	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	2.5
	131775	AA459555	Hs.31921	KIAA0648 protein	25

TABLE 78:
Pkey: Unique Eos probeset Identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
	101335	46413_1	L49054 N87447 AA248791 AA452193 AI015525 AI762070 AA781526 AW183498 AA625682 AI268713 AA400391 AI193725 AW590304
_			W56350 AA936057 AI990398 AA406183 AA628888 AA844206 AA621117 AI141092 AI608150 BE379750 AI351482 AA693527 AA405119 AA400562 AW368723 AA463811 AW242927 R50034 W56334 F21257 AA164314 BE074125 AA470924 AI307439 W16738 AA026647
5	100906	4242 4	T35999 T19178 AA164313 A1744010 A015468 A1014921 AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 A1795876 AA644165 T36030 AW392852
	100900	4312_1	AA446421 AW881866 AI469428 BE548103 T96204 R94457 N78225 AI564549 AW004984 AW780423 AW675448 AW087890 AA971454
			AA305698 AA879433 AA535069 A3394371 AA928053 A378367 N59764 A3364000 A431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 A1202011 R00723 A1753769 A1460161 AW079585 AW275744 A1873729 D25791 BE537646 T81139
10			R00722
	102221	3861_1	NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836 AW162352 AW162351 AW162752 AI962216 AI537346 AA853902 H17667 BE045346 BE559802 BE255391 AA985217 AA235051
			Al129757 AW366451 T34489 D56106 D56351 Al936579 AW023219 AW889335 AW889120 AW889232 AW889175 BE093702 AW889349
15			AA147546 A1952998 AA912579 A1143356 AW902211 R64717 AW157236 A1815242 D45274 AW263991 AA442920 AA129965 AL035713 A1923255 A1949082 A1142826 A1684160 A1701987 A1678954 A1827349 BE463635 AW628092 AW302281 AA493203 BE348856 BE536419
13			AW193969 AW673561 AW592609 AI224044 H43943 AA091912 R49532 R48353 AI568409 R48256 AI198046 H27986 H43899 AI678759
			A1680310 A1624220 H17052 AA156410 N56062 A1699430 AA684529 T09406 T10459 AA627506 A1379584 N83831 N88633 AW022651 AA971281 AA248036 A1039197 A1914689 AA973825 AL047305 AA129966 A1798369 AW264348 A1445879 A1658759 N67924 A1933507
00			Al216121 Al333174 T10972 Al375028 Al186756 Al273778 AA610487 Al797946 AA853903 AA903939 Al338587 Al278494 AW627595
20	101714	30725_1	AA904019 M58874 AL022147 M72393 AL049797 BE439441 T27650 Al766240 AW150345 AW778943 Al827464 BE439479 AA587049 Al277900
			A1984983 A1630935
	116803 116988	55078_4 185904_1	H47357 W33034 H55976 H55975 R67830 AA527091 F24482 AW841585 R66514 AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
25	132640	179_1	AW162087 AA224538 AA471218 AA088655 AA375275 BE440052 AF090891 AA324435 AF063549 AI110675 AA322223 AW953306
			AA233590 AW949864 AW949859 AA383721 AA081878 U33821 NM_006024 AA350900 AA081588 A1148087 AF268075 AA088185 A1142478 AA081824 A1887930 AA070570 BE185248 A1459825 BE257794 AA420459 AA420859 AA777997 AA081219 AW815721
	•		AW854758 AA157932 BE018208 AW378974 AL041212 Al247564 AW581897 Al002897 BE543242 Al811690 AW852076 AW852270
30			AA360969 AA094943 AA090680 AW601554 AA099673 AA662226 AA356814 AA330174 AA187544 C02751 AA315460 BE168358 AW080447 AIB13764 AI624222 AW156901 AI954032 AW473780 AI861975 AA173643 AW511541 AI951492 BE301686 AA669760
			BE182212 AA081009 T69431 AI186207 AA604124 AA707346 AA173953 Al016700 AI125916 AA358962 Al673719 T90593 T90497 T10776
			AW513002 AW304292 AA724885 AW474759 AI811621 AW058925 AA666305 AI580161 AI128023 AW471151 AA534849 AA666358 AI078833 AI139223 AI244874 AI381658 AW263441 AI432440 AW802882 N66401 AA224251 AI167469 AI141060 AA099214 AI537130
35			AL120428 AA948655 D53110 AA076099 AA938617 AA826543 Al357914 AA565098 AA807994 Al288812 AA632832 AA157933 AA639802
33			AA634268 AA282337 AA551431 AA557374 AA256923 AA872943 AA009665 H89626 AA810386 T92925 T36145 AA632190 AA130436 AJ686635 AA130437 AW392904 AW392839 AW392848 AW392836 AA729737 AA070450 AW392890 W04825 AA771848 AA084634
			AA481985 AI263840 AI801006 AA235380 AI954229 AI559330 AI208724 AA887638 T25894 AA041269 W44443 AI581770 W46171
			AAB78485 W46535 AA197336 AA894945 AA394224 A1766834 A1582590 A1033007 AA481889 AW190598 AW392855 R27279 AA398137 A1248407 A1241386 A1991753 A1826585 AA865699 A1096806 A1833030 AA041279 AW888745 A1703279 N70572 A1912553 BE549931
40			A1240422 AW376187 AW591692 AA975905 AW614967 AA009666 W44332 AA664659 T06561 8E468150 A1650695 AA587920 A1473310
			AI032991 AA256499 AW104241 BE163782 AI984973 BE163613 AI263906 AA628191 AA282072 BE163769 BE163775 AI492939 AI473315 D56907 AA587930 H89480 AI362373 AA598483 D56595 AI167590 C16223 AI935415 D62555 D62884 D63130 AI760286 AI650286
			AW173598 AI499145 AI122566 AW903408 AI810569 AA854936 BE049510 D62065 D61900 D62101 R27475 AI469835 AI669086 N80399
45	103427	43892_1	N48922 N48746 AA481381 R22858 H13912 AC004549 AW602500 AW768788 BE514383 AA071273 AW247987 AW673286 BE312102 AW749824 BE071985 AW577383 BE071945 BE072005 AW577355 BE071965
	402024	450 04	AW239231 BE072000 BE071960 AW577360 AW749830 AW373020 X97303 AW999522 BE000192 BE562219 BE266655 BE264970 R64730 AF214731 T19173 BE258318 AF161446 BE542228 BE363856 BE206748 BE543260 AA640735 AA788907 BE251313 BE221852
	103631	152_34	AW855357 AA224407 AW855346 BE150454 AW070651 BE326867 AW051698 AI829278 AI470927 AW855345 AI804942 AI971004
50			BE046620 AI863664 AA808492 AI915971 BE046949 AW590711 AI468066 BE409685 AA332653 BE385394 AA852623 BE255591 BE254968 AA211871 BE255493 BE257727 BE255389 BE257491 BE262528 BE261296 BE313277 BE261714 BE314316 Z28434 AA315545
30			BE008562 BE012093 BE161393 T31969 AA305848 AW955238 BE619156 Al191748 AA323396 AW361760 AA216118 BE264939 AA325954
			AW580281 AA302597 AW888908 AW88893 BE312970 AA134402 H52679 AA478191 T34090 AW961505 Z24771 AA179552 R57244 BE315207 AW583121 AI372747 T33143 AW377460 T33141 R14922 AW352414 H93249 AW405576 T33102 R89545 N46625 H08434
~ ~			BE165062 AW367891 H93121 H47325 T30931 AW402852 H47410 Z20368 T18928 T30758 H93254 AW389725 R96628 AJ372407 R88995
55			A1815980 AW157278 AW607664 AW163288 AA133492 AA099328 AA157348 A1816063 AW449556 AA157252 AW608980 H66576 AW821127 T32030 AW856058 AA032188 Z42120 R18582 AW402392 BE408021 AA280989 AA039427 AA035354 AW328008 T94186
			R97481 AA181444 AA774697 BE613141 AW630221 H13066 Al124578 AW754481 BE262112 AW839942 H60108 AW364002 AW363800
			BE547161 BE082634 AA642471 BE619719 BE082719 W28879 AW794944 C01685 Al291127 AW166099 Al936102 Al478929 R70284 AA872914 W31065 N54216 Al568741 H56262 NM_017425 Z48570 Al831777 T75007 AA354867 AA427988 Al922844 AA733170
60			AW821145 BE081547 AW881571 AW881573 AW055249 AA204724 AI417415 AI127303 AI355013 AI039527 AW593259 AA576745
	•		A457317 AW593236 H93126 BE396072 AL134941 AW629175 AI424011 AA115732 AA179986 AI334944 AW367922 AW152304 AA806752 AI312418 AW935023 BE301136 AA032258 AI829922 AI372406 BE177074 AW513743 AI151526 AA975643 AA478034 AI814920 AW080063
			AI032624 BE177107 AA319768 AW935098 AI017620 AA974477 D51441 C14225 AL043583 D80145 AI690771 AW009711 AW881570
65			AIZ20431 N51090 AI143003 AA961480 AA039351 AI094885 AI096520 AA179553 AA593974 AI373929 AA677252 AA687374 AA886867 AA312863 AI150654 AI138450 AA133209 H99388 AI565632 AW070496 AI539748 H59455 AI811537 H52680 T74907 AI499657 R96870
00			AA854796 AA427863 AA224345 AA889899 Al347782 AA931056 Al076059 Al360841 Al797975 Al362268 Al200968 BE350785 R97433
			N98499 AA134403 AA035355 AW263162 Al369607 D80144 Al376627 Al520801 AA365942 Al707705 Al123495 T33101 H08716 AA804238 AA922201 AA723522 AW183592 Al445884 F34614 AW022342 AA363998 AA568793 AA152475 D31233 AA852622 AA099862 Al129147
70			AA922699 AA782664 T33142 T30009 T32913 AI676138 AI914657 N34899 AI372746 AI265911 AI352444 AA443158 AA910603 AI420273
70			AA868050 AL277700 C14224 AW082087 R41447 Z38385 AL911845 AL961888 R91976 F04560 AA661955 AL857675 AA369666 AA424207 N79953 AA382958 AA894626 AL884964 AA846989 AA215454 AL742580 AL339437 AL806879 AL091373 AA782558 AL026868 AW590904
			AW204599 BE348235 AI819318 AA122324 AA939221 AW139711 AA131608 AW613548 AA122286 AI309179 AA437247 AW339322
	129097	25953_1	AIG71306 AW439848 AA131701 AI078075 N64624 AA812881 AI140547 BE243933 AA355449 T29766 F08396 N83324 NM_006953 S50223 AI207648 AA258092 AA113952 AI311718 AI128612 AW607449 M77172
75			AJ951311 X52346 AA903307 AJ569810 N55421 W77876 R37223 R83788 AA031666 H47092 AA133451 AA311095 AA906963 H87667
			N5605B AA393593 W24864 H10710 F06925 F07239 AW386140 AA32501B AA235950 AW373176 N57158 AA258093 N39467 R21609 BE089979 R34173 AW889005 AA745644 A1693852 AA424914 AA744771 W72632 A1291213 AA524318 A1472134 A1911230 AA528418
			AA115745 AA775720 Al671134 AA975044 AW298117 AA321015 N26288 AW952194 AI743379 AI204233 AI801026 AA830690 AI146980
80			AW104611 Al338576 R21507 Al367623 BE244484 Al269308 AA031667 Al884346 AA731989 AA988943 AA235951 AA807887 AA642645 Al246489 N29739 Al216718 Al383349 Al038618 Al351476 AA806031 Al914178 H10711 Al095573 H89220 AW470854 AA729015 R83353
			AA782239 R34295 H87165 AW419059 Al653689 Z40349 H89114 AW074506 AA397785 AA888377 Al911228 F03193 Al468783 AA702615
	120695	9683_3	AIB30829 AA748323 R37224 AA424915 AA731647 H47183 AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201
			AI633384 AA425910 AI017004 AI241295 AA402816 AA291468
			167

	100352	37786_1	AL133887 D64159 AF112218 AI766633 AL039303 AL133888 BE620604 AW976259 AW262792 AW591383 AI365413 N36652 AA807027 AI472041 BE620065
	101084	13883_1	AW409934 AW245855 AU077157 AW163245 AW161434 AW250083 AA316055 BE621134 AA171883 BE272494 L05425 BE250310 NM_013285 BE311494 AA858436 AA308223 AW362598 AA373618 BE394454 AA126101 AA581348 AA303227 AA058438 AA126544
5			AL 135350 AW996947 AA405201 AA46682 W79685 AW246249 AW577763 AW002316 AA320025 AW753913 AT79554 AW070550 BE250413 AW250835 BE076336 AI925558 AI907634 AW804193 AW804270 AA902387 AW804232 AW804255 AW607751 AI909114
	•		AW157242 AA934590 AI628921 AJ470650 AW409935 AW172793 AA401208 AW162279 AA888018 BE206452 AI826742 AA857353 AA483614 AA126418 AA722289 AA780182 AW768894 AW1683614 AW156969 AI244063 AA863491 AJ376281 AA582490 AA846248
10			A1474094 AW246802 AA446557 AA128000 A1699045 A1702310 A1253092 AA171554 AA831455 AW118384 A1954511 A1760439 A1867001 AA493881 W81287 AA515590 AA659237 AA635139 AA659293 AA766044 AA196109 N32569 A1907635
	100502	26409_1	U15979 X17544 W52755 NM 003836 Z12172 AW370136 BE262564 T49116 A333753 BE262238 BE313737 H38153 AW583056 R28890 BE259532 D16897 AA885610 AA911293 AA319627 R94472 R29022 AA443405 R96397 W04904 W01746 W01204 N74203 N56621
1.5			AA701996 AW418723 N53220 AA602813 AA576129 AA593786 AA911577 AA575957 A1149135 AW573058 AA772985 A1188918 A1372065 AA575838 W60010 Al004576 A1131265 AA319845 T50070 Al335742 AA235245 W32706 AA447372 R96355 N59573 AA904616 Al291224
15			BE467454 T49117 Al268620 AA928248 AA449494 AA318817 T49929 R94473 H38154 Al076649 AW935307 AW605112 AW935433 AW935342 AW935310 AW935345 Al298308 AW935395 AW935384 Al184857 AA319871 T29465 C21134 Z19785 AA329107 T52079
	102398	entrez_U42359	AW935346 C06234 AI951555 T49928 AA371745 AA369296 AA346673 R82547 T50006 L42359
20			

20

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Table 8A lists about 54 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip erray such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 3rd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 4th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 8A: ABOUT 54 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Tide: UniGene Title

30

ratio: ration turnor vs. normal tissues

	Pkey	Ex. Accn	UG ID	Title	ratio
35	130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	12.1
	101249	L33881	Hs.1904	protein kinase C; lota	11.8
	132528	AA283006	Hs.50758	chromosome-associated polypeptide C	11.5
	102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.0
	115536	AA347193	Hs.62180	ESTs	10.0
40	129571	X51630	Hs.1145	Wilms tumor 1	9.3
	105298	AA233459	Hs.26369	ESTs	7.8
	121779	AA422038	Hs.98367	ESTs	7.3
	104301	D45332	Hs.6783	ESTs	6.9
	132191	AA449431	Hs.158688	KIAA0741 gene product	6.7
45	102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.6
	101804	M86699	Hs.169840	TTK protein kinase	6.5
	132572	AA448297	Hs.237825	signal recognition particle 72kD	5.9
	106738	AA470145	Hs.25130	ESTs	5.8
	108857	AA133250	Hs.62180	ESTs	5.8
50	115291	AA279943	Hs.122579	ESTs	5.8
-	132632	N59764	Hs.5398	guanine-monophosphale synthetase	5.8
	116401	AA599963	Hs.59698	ESTs	5.7
	132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7 (35kD	5.7
	129097	\$50223	110.101101	HKR-T1=Kruppel-like zinc finger protein [huma	5.6
55	134520	N21407	Hs.257325	ESTs	5.5
	108778	AA128548	Hs.90847	general transcription factor IIIC; polypeptid	5.4
	131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (barnacan)	5.2
	116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.2
	108055	AA043562	Hs.62637	ESTs	5.1
60	132939	U76189	Hs.61152	exostoses (multiple)-like 2	5.1
••	115909	AA436666	Hs.59761	ESTs . ·	5.0
	120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.0
	123494	AA599786	Hs.112110	ESTs	5.0
	109648	F04600	Hs.7154	ESTs	4.9
65	132624	AA164819	Hs.53631	ESTs	4.9
••	111234	N69287	Hs.21943	ESTs; Wealty similar to ORF YGL221c [S.cerevi	4.9
	135242	M74093	Hs.9700	cyclin E1	4.9
	123005	AA479726	Hs.105577	ESTs	4.8
	116296	AA489033	Hs.62601	Homo sepiens mRNA; cDNA DKFZp588K1318 (from c	4.7
70	100661	HG2874-HT		Ribosomal Protein L39 Homolog	4.6
	111345	N89820	Hs.14559	ESTs	4.6
	102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	4.5
	106459	AA449741	Hs.4029	glioma-amplified sequence-41	4.5
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	4.5
75	129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	4.5
. •	130376	R40873	Hs.155174	KIAA0432 gene product	4.4
	120619	AA284372	Hs.111471	ESTs	4.4
	122802	AA460530	Hs.256579	ESTs	4.4
	116416	AA609219	Hs.39982	ESTs	4.3
80	115094	AA255921	Hs.88095	ESTs	4.2
	126802	AA947601	Hs.97056	ESTs	4.2
	126892	A1160190	Hs.76127	hect (homologous to the E6-AP (UBE3A) carboxy	4.2
	105516	AA257971	Hs.21214	ESTs	4.1
	131985	AA434329	Hs.36563	. ESTs	4.1

	114965 120821 134621 134161	AA347419 (L02547 (Hs.72472 Hs.96870 Hs.172865 Hs.79440	ESTs Homo septens mRNA full length insert cDNA do cleavage stimulation factor, 3" pro-RNA; subu IGF-II mRNA-binding protein 3	4.0 4.0 4.0 4.0	÷
5	TABLE 88 Pkey: Uni CAT numb	: que Eos probeset er: Gene cluster (identifier num number	•		
10	Accession	Genbank access	ion numbers			
••	Pkey 101249	CAT Number 2520_1	AW087514	A_002740 L33881 AA095249 BE080871 AW605320 N 4 A1480090 A1873147 T57875 A1217404 AA827196 A1 4 A1032193 A1953696 A1630583 AA062633 BE541355	279471 AA969093 AA815168 AA98889	
15	100661 116401	23182_1 95855_1	BE623001 AW89394	* ALOSO96 AA383604 AW966416 N53295 AA460213 A\ D AW978851 AA034240 A1686323 A1767653 AA82951 A835700 AA599963 T20152 AA533167	N571519 AA603655	1869 AA835698 AA447216 Al623248
	116416	373989_1	AW75367	5 R11789 AW001886 AA609219 AW780420 AI86055 42970 R63752	Al280331 Al334300 Al288870 AA6693	43 N29918 BE537790 AA934687
20	132191	54683_4	AA507576 AI189144 AI743979 AI380330	. A1610269 A1380079 R40309 A1203932 A1342128 A13 A1016691 W45515 AA551452 AA449431 T10046 AA4 A1283341 AW340338 AA774643 AW104778 A107802 A1247787 AA770467 A1200154 A1089863 A1089890 A A A8907692 N21250 AW904736 A190337 A4987722	124059 N62822 AW197701 AA465242 A 0 N21487 H97562 AA970063 BE327945 1695738 W88524 A1471010 AA700191 A	U418989 Al942433 Al891115 BE302316 5 F03880 F03885 AA970699 Al298468 AA778937 BE440182 R79225 AA338236
25			AA465598	AA321185 AW130492 AI824479 AI682992		
	130941	2774_1 47548_1	AW24890	59 D49394 BEŹ52349 AWZ49320 AWZ49140 AWZ50 3 AA731733 AA804189 AA703169 Al435492 Al07628 7 AAA53863 AA442475 AF086541 AA365801 Al6925	8 AA912176 AW248713 AA743457 R08	3170 C06167 R02351
30		_		7 AA365503 Al632902 AA659686 AA665087 C00396 3 NM_012086 AA128292 S81493 AL137453 BE61405		R5542 RE085598 AT 120654 R13165
	108778	18565_1	AA429300 AI126654 AW29514 AA42823	5 R13465 R55236 AW994182 W00838 AW994417 AV AA626457 AA291327 H67983 H66271 H67976 AW2: 3 Al433661 AW608381 AA873402 Al217453 Al95335 3 Al001932 A7735550 Al951370 AA766807 S81492 A	V994404 AW994426 AW994321 AA5161 70955 AA758221 AI023487 AI921811 AI 8 AA262143 AA928495 AI475268 AI167 A918976 AI040967 R70939 AA469065 T	147 AA345603 AW953009 BE315104 1953370 AF085850 R70992 N25129 7211 AW385961 AA259045 A1762630 170340 AA477615 AA478070 A1017743
35			Al206773	A1635824 A1186039 AA741312 A1040184 H67656 AA A1879827 R64193		
	102136	17647_1	AA300570	S U15552 NM_014597 AA223318 AA171806 BE2694 2 AW117711 AW356303 AW366302 AW366308 AW3 6 BE064947 BE064722 T10372 AW838681 AI811119	66304 AW366300 AI908432 AW591937	Al358420 AW272622 C75067 Al926471
40			A1953413	Al064798 Al420425 AA191324 BE503222 Al632721	AA180035 AA558329 W44843 T10610 \	W38442 BE542869 AI125024 BE279566
45	108857	61_1	AK00146 Al215522 Al475165	6 Al589491 AA559096 Al090265 AA548959 AA22322 8 AA190315 AA374880 AW961179 AA307782 AA315 Al216389 N87835 R12261 R57094 Al660045 AA347 AA300756 R40626 Al122827 AA133250 Al952488 A AB72789 Al919056 Al611216 AK001472 BE568761	295 AA347194 AW953073 AW368190 A 193 R16712 AW119006 N55905 N8776 A970372 AA889845 AW069517 Al5243	.W368192 AA280772 AA251247 N85676 8 AW900167 AI341261 AI818674 D20285
43	102305	18424_1	AL04320 AA20720 AW90233	2 U33286 NM_001316 AF053641 AL048759 N99830 / 7 AA315560 AA113938 AW386317 AW386316 L4454 14 AW993922 BE003403 AA251521 AA382754 AA38	AA263091 AW408174 N90467 R84306 / 16 AW386335 AA243317 AA713588 AA1 1152 AA382619 H58600 H67810 T70379	92541 AA649035 BE300737 AW752491 9 T82109 D81644 D60375 H59003
50			AA36586 AA83731 AA23699 AJ754062	2 AA471242 H17790 F11801 T84903 R78076 BE614 6 AW954410 Al539769 T39128 AL121103 AA192466 1 AA075484 AA075621 AA778294 AA587266 F69722 7 AA459274 Al150191 AA165156 Al19839 AA7892£ 1 Al753243 AA934719 AW439362 H02008 C17463 A 18C934097 Al826398 H58956 T17222 AW139044 Al7	AA213367 AI963800 BE090601 Z20096 2 AA446118 X85624 AI334209 AI587101 88 AI139373 AA236574 AI127770 AA676 400951 AA227639 N66040 R89384 AA8	6 Bes66508 A1969470 Be044090 T65536 1 A1281280 AA568602 AA946837 C75603 8954 A1140786 AA113939 A1187231 172668 A1344110 W95420 AA164700
55			A1868711 A1278406 BE39797 AA45950	AA582354 AA524392 R01549 R01641 Z21083 AA57 3 AW609291 AA137249 AA142866 AA639188 AW609 1 AW609285 T65602 T99684 T97378 AW609365 T8 3 N95643 AW821210 AW813461 AW582064 AW669 56 AW592070 AW609276 AW609280 AW669290 AW	28463 T39127 AA989472 F09450 AA084 271 AW149760 A1026112 AA236620 AA 84 AB72223 T99083 AA19983 AW30 293 AW609320 AW609270 AW582085 A 85 AB7101 AW882107 AW609273 AW6093	4485 BE004378 AW974353 AA137250 937248 U90736 AW005487 AW674427 03874 T35523 AA586445 Z39669 AW582071 AW609318 AW813451 117 AW609256 AW609305 AW582063
60	•		F06655 / AA91262 AW0233	\W605343 AA446426 BE090595 AW969578 T79852. \4 D60376 T10180 AA705847 A1018123 AA493197 T6 53 H77483 H68082 R42337 H58601 T97267	A1082505 N63239 A1973168 A1086182 A 37083 R77739 AA953087 R00885 A1370	VA846711 AI874213 AA730605 AI927257
	109648 132528	708849_1 11027_8	T78736	A1362549 A1671064 T23526 F03426 F04694 F04600 / AA284422 AA283006		
65	101804	26687_1	M86699	NM_003318 AL133475 AA122377 Z21415 R57092 A	A806569 AA811904 BE538323 R41558	AA421620 Al337292 AA470077
	132572	31281_1	A(92965)	71 ĀA543024 A1677941 A1472200 A1215042 AA73231 8 AA227827 AF069765 AW408768 NM_006947 AF07 81 AA355433 AA481126 AW403053 BE542282 A1929 90 W93905 W96519 A1863832 AA443177 AA730942	7019 AA220974 H07969 C14621 D5229 818 AL120605 AW753079 AW391834 B	94 BE512960 BE614138 BE258539 BE018603 BE395282 W21406 AW663259
70			AW0818 AI92140 N74716 T90801	19 AA714970 A122630 W04887 AW662427 AA6026 4 AA143770 AA587675 BE302192 AA813080 A14933 AW366249 AA68581 AA516399 A1274726 A1131244 A1383246 A1740957 T86758 A1471248 A1864233 AA9 6 T99348 A1924643 AW103910 A1802993 A10803991	80 W93645 AA582946 AW008812 AA31 86 AW327435 AW340871 A1143616 AAI I AL572604 A1929236 AW327971 R6563 10590 A1079094 AW805781 AA709025 /	1187 AA463631 AI421918 AI400518 687231 AA218961 AI362249 AI378345 7 N90309 H07877 W96488 AI358806 AW196707 AW327436 AI903790
75			AW7692 AF08613 R35393 AJ13147 AA3083	95 W32639 AA363094 N89012 W39751 A1291329 A1 31 AA373679 AA165043 AA355705 A1243507 A10277 AA448435 AA334659 AW879356 AA436527 AW9720 2 N50381 AA736938 A1089112 AA863053 A1359793 45 AA347241 AA355159 T85701 BE162893 T89703	291371 AA829411 A1985219 A1422775 / 98 AA573461 AA757260 A1370979 AA5 144 W25165 AA521219 A1094141 A13021 AA962268 T27353 D82590 AA448297 A	AA918940 AA363108 AA192633 74149 AA558276 N70650 Al478948 098 AW578551 AW578534 AW390535 1277168 Al368457 AA872737 AA330346
80	131985	113870_1	AA5030 AA4343	80 A082341 A0535159 165701 BE18235 19570 20 A1858190 A1686571 AW615203 AW073888 AW17: 29 AA171844 A1684143 AA953518 AW470108 A1870' AA404225 AA075632 AA172293 H51911	2459 A1828762 AW150534 A1859795 AA 100 AA706376 A1539668 A1683712 AAO	.411046 A1539195 AA404609 A1638559 75579 A1682137 AA291512 AA554431
	132624	42095_1	AA3261	08 W74020 AW612698 AI750909 AA487800 AI27069 AA525338 AA526640 HB4308 AA278942 AA164818	15 AA044941 H20708 AA296750 AA018 AA847110 T82335 N25519 AA021474 N	401 AA378581 AW964159 AA018887 I31381 N38297 AA838191 AA318932

			AA961206 N41430 N41439 AW630477 W37595 BE394538 AA365256 N47771 N34873 AA988105 AI242138 AW148523 AI978761 N50882 AA527448 AW086200 AI750910 N50868 AA709437 N51946 AI222179 AA732883 H95742 AW615360 N53720 W37490 R87362 AA613273 H98999 A468022 AI368442 AI460122 N20486 N24087 AA164819 N24878 AW471270 AW590458 R68240 AA594434 N20460 AI419626 AW500664 AI033658 AA593215 AA907408 AA713508 AI422627 H85551 AA923571 D62680 AW627456 H96206 AA016289 AA485896 N25691
5	132632	4312_1	AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 A1795876 AA644165 T36030 AW392852 AA446421 AW881888 A1459428 BE548103 T96204 R94451 N78225 A1564549 AW004984 AW780423 AW675448 AW007890 AA971454 AA305698 AA879433 AA535069 A1394371 AA928053 A1378367 N59764 A1364000 A4431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 A1202011 R00723 A1753763 A1460161 AW079595 AW275744 A1873729 D25791 BE537646 T81139 R00722
10	102610	9336_1	U65011 NM_006115 AW182053 BE383930 BE407839 BE409930 BE408826 AW370292 AA312859 AA136204 AW365852 AW365735 BE622732 AW339295 AA781195 AI017284 AW375329 AW376366 AW178384 AW178333 AW178424 AW365726 AF025440 AW172852 AI570998 AW117792 AI885499 BE465516 BE207427 AW130942 AW313316 AW1770892 BE207426 AW173563 AW168292 AW173565 AI810101 AI744983 AI861974 BE207404 AI744982 AI613210 AW591505 AW169285 AI521444 AI745044 AI627904 AI690634 AI289305 AA861253 AI6132799 BE207425 A1146594 AA902662 AI082468 AI014752 AA613844 AA725693 AA136089 AI290092 AA565489 AI689083 AI859014 AW051225 AA665758 AA466991 AA564738 T19428 AI567170 AW166726 AW084200 AW188723 AA617626 AI918664 AW381473
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20			A1275409 A139121 A1927568 A1927562 A139471 AA160473 N78795 A1719983 A1718928 AA723097 A1335776 N39140 N59184 A1587600 A1864812 AA732097 N74667 AA832398 H89600 D18825 A1554833
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25			W73953 AA244153 W86034 AI948872 AI952678 AW087811 AI333591 AI869883 AI926911 W48865 ALQ48024 AA214485 AI972622 A1151368 W48738 AA214487 AA334640 A1678170 AA927525 AA581588 W96338 AA265470 AI471919 AW611488 AA211834 AI365198 A1698365 AW002238 AA507624 W96150 AA446490 ALD48025 AA852400 AA362221 AI338376 R35083 AA290812 R10397 AA975988 AW236462 Z43032 H16669 F13487 F196759 AE457277 BF067642 AA344398 AW949533 AA279472 AW902406 AW070440 BE395195 H00835 AA300750
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40			A1266084 N49879 AW024457 A1246246 A1934031 A1369270 A1003836 AAD10063 AA494361 A1284151 A1919536 N34884 N69287 AW510465 A1388609 AW081421 AA706205 A1085317 A1140633 A1347104 AA602547 A1686707 AA872686 AA694028 A1094546 Z40832 A1382838 AA610132 AA501433 H84120 A1140722 AW674839 BE503822 AW663895 BE327472 AW393494 A1340087 W04189 AW393499 H56506 BE089878 BE301950 A1025475 AA724446 BE275324 H15210 AW957667 AA634543 A1682259 AF117108 BE396917 NM_006547 U97188 U76705 BE560799 BE396918 BE269531 BE560268 BE560346 AA836048
45	134161	16074_1	AL023775 BE545535 AA427803 C18804 D58801 AA303353 U46218 BE539704 AA187966 AA252545 AA261821 D63197 AI824109 AI088047 AI424833 AI807368 AI250857 AA741476 AI146832 AA169615 AI809821 AI274288 AW136704 AI206172 AA917039 AA243584 AI808611 AW674709 AA935733 AW450092 AA905172 AA471196 AA302256 AW673348 AI352044 AW511295 AA247134 W81035 AA722962 AW662471 R64432 AW044616 AI086619 AW628546 AW043682 AA425750 AI743038 AI368723 AA187143 AI376987 AI803976 AI275537 AW471358 AW104877 AA195464 W81072 AW197351 AA932674 AI393420 AI434998 R63822 AW085083 AI240272 W87006 AA011347 H58428 AI497895 R73273
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70	135242	5782_1	AW380506 BE150744 AW380468 AW380546 BE150713 D60029 H88099 BE546301 BE150731 AW368467 BE091348 AJ583187 M73812 AW339829 M74093 BE252510 BE252518 BE536901 U40788 W95578 BE018493 BE544205 N83637 AI671049 AW439693 AW300786 AW374970 AA592950 AV215885 AV215884 BE302101 AV168210 AW771831 T54213 AW452924 AA834019 W95471 AA628312 AW304866 AA5707076 AJ556973 T54121
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80	126802	116467_4	Al341077 Al825719 BE552285 AA738076 AW085903 R28242 AW805510 AW805503 AW805500 AW805819 AW517040 AW473670 AW516701 T30141 AA894497 BE349504 Al272007 Al985274 BE501962
	126892	38252_1	AW102975 AI801727 AW197918 T24046 AA947601 AW900958 AF121856 BE242657 U83194 AA226732 AI160190 AA948725 AI079958 AW513369 W39443 AW408479 W06854 AA094683 AI985095 AA316847 H95313 N78438 R81582 H95034 R79674 AA488552 W25292 W31697 W19918 T30640 R08688 H78637 AA165100 Z41909

5		•	AA165080 R34212 AA150886 T82168 N77082 W56864 R19848 AA888217 AA314539 AW750293 N62714 R58039 AA845453 N63268 W03474 M41923 AIZ64123 AIR08533 AA824288 AW198143 N99916 AA902465 AA775397 AA772387 AI567675 AA227473 AI082614 R58334 N788878 R34329 AW438902 AA164685 AA558790 AI590102 AA863422 BE002626 AA9334039 AI289102 W15351 H38397 AA725325 GE180993 W05350 AI510771 W06341 AA488414 R79863 N91264 R78884 AA312948 T71267 AW959659 AI086695 N90421 AI278098 AA164538 AI300271 AA854381 R81331 AA700449 H06174 AW518427 AA876534 AA160778 N32393 H78685 T85364 BE002808 AW95189 N90337 BE252097
	105298	8689_1	T71401 H06438 N40268 N31015 R77046 T99588 T85462 W25298 T59815 H09416 T85403 W32150 N79109 R76812 BE387790 BE276849 BE246825 BE246900 AA380487 AA332996 AW408727 AK000294 Al636887 AW197272 AW590657 AW594006 Al768979 Al751632 AA580098 AA313261 AA300475 AA133237 AA233499 BE242126 BE242259 BE242254 AA314374 AW951210 AW939345 AA173535
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15	120438	166102_1	AW293675 AI675617 AW009004 H23498 AW015242 AA831493 AI292346 AI076966 AI191561 AA243441 AI183309 AA252613 AI038422 AI306531 AW051480 AI348605 AA195119 AI817119 AI091896 AA738440 AA195013 AA976687 AA459659 AI246250 BE219252 AI703457 AA243291 AA243401 AA989100 AA931640 AA459782
20	105516	9334_1	AK001289 AL354813 AA147472 AA490803 BE207628 AW816113 AA085574 AW503392 AA299910 AW750305 BE079539 BE079484 BE512838 AK001593 AW968772 AW967440 AW206280 AA251270 Al627886 AA303599 AA147473 BE206616 AA490611 AA715039 AW590866 AW590447 Al864512 AA204731 AA894490 BE001138 AA612785 AA237035 AA149960 Z44257 R12986 AA44846 Al734041 AA422167 BE220551 R66041 R32927 R32942 AA256773 AW386142 R53730 N54624 AW880298 AA253485 AW594441 H98989 AW614348 AI654838 AA779793 AW237213 N66035 A186812 AA947479 BE158011 Al859480 AW860579 N52010 AA806305 Al628445 AW270990 AA778165 AA149949 AI650728 AA749108 AA687257 Al261661 AA74742 AA481351 AA206339 AA903407 AW473306 AI688930 AA262281
25			AA448310 AA748820 Al347430 BE465692 R32839 AW510564 AA436408 AA257971 AA253362 AA938330 AA513150 AA976840 AA687117 Al281547 AA046243 R32825 Al631554 AW139818 Al244536 R52946 AW235443 R40183 AA299909 AA811958 Al302918 Z40213 BE158047 BE158060 AA767245 AW748159 AW500735 AA094074
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55	115094 129571	190995_1 1726_1	AA633165 AA449741 AA831821 AA903673 AA682588 AW673075 AA255920 Alb17197 AA255921 Alb12925 AW874669 AA493440 X51630 M80232 X81631 S75264 AA172249 AA134066 AA130278 AA130187 AA130291 AA031554 Al246677 Z21455 AI745434 AW273544 AW088613 AW471307 AI745483 Al399854 Alb83952 AA031555 AA298075 AI935945 T29809 AA172099 AA356120
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	115291	22325_1	BE545072 AI540751 AA301103 AI916675 N85422 BE563965 AA327978 AI816094 AK001515 BE501319 AA279943 BE138895 AA343765 AW963051 AW082308 AI823992 AI653752 AI589007 AI816135 AI566535 BE501307 AW272765 AW242239 AA766315 AI014927 AA578848 AI354483 AI476548 AI038579 AA973322 AA992180 AW472921 BE504789 AI392988 AA506076 AA769228 AI370562 AL137710 BE005655 AW965920
70	130376 115536	248274 61_1	AV95032073 RA0973 AK001468 AA190315 AA374980 AW961179 AA307782 AA315295 AA347194 AW953073 AW368190 AW368192 AA280772 AA251247 N85676 AI215522 AI218389 N87835 R12261 R57094 AI660045 AA347193 R16712 AW118008 N55905 N87768 AW900167 AI341261 AI818674 D20285 AI475165 AA300756 R40626 A1122827 AA133250 AI952488 AA970372 AA889845 AW069517 AI524385 AA190314 AI673359 AA971105 AI351088 AI872789 AI919056 AI611216 AX001472 BE568761 AA581004
75	114965 131228	153955_1 8262_1	AT33881 AA165164 AB26437 AI972791 AA165165 BE219575 AT32586 AB21571 AA250737 AW136875 AI984273 AI249271 AW207469 AL078814 AA354351 AF020043 AW281396 BE550484 NM_005445 BE046917 AW934249 AI651654 AI631615 AW771344 AI969758 AI699982 AA247175 AI244676 D44780 AW593978 AI638479 AI373676 AW089547 AL121432 AA554698 AI016991 AI087260 AW49939 AF087163 W40482 AW316558 AI537184 AW381979 W40150 AI810562 AA573151 AI630288 AI675561 AI674420 AW840733
80			AW022653 AA114219 AJ005015 AL046587 AAB78141 AW271896 AW085287 AA150465 BE536295 AA463412 BE093222 AA213739 AA485586 AI825913 AA706307 AJ337348 R31995 AI819641 R32095 AW976653 AA742375 AA142957 AI808214 AW468303 AJ205987 AJ206347 AJ769095 BE501840 AA113866 AJ093931 AJ752855 AA612743 AA463411 AA279157 AJ123791 AA213570 AJ207305 AW627814 R31945 R32040
	116238	10772_1	AV560717 NM_015437 AL050285 R95774 AI867094 AA443833 AI367670 AA609046 AI440298 AI613139 AI291826 AW028954 AI123242 AI824715 AW079750 AA479362 AW150151 AI952267 AA814094 AI168431 AI566595 AI521422 AI920793 AW051241 N70051 AI689429

			AI783813 AI769315 AI743691 AI915645 AA479473 C21435 N50944 N50902 AW978102 H23837 BE087538 AA316516
	122802	287993_1	AI687303 AW571681 AI554465 AI684252 AI581056 AA604098 AI628160 AI859843 AA424021 AA460530 BE042778 AW273200 AW273223
			AW167288 AW083347 AI654306 AW517496 AW104706 AW273214 BE139512 AW189487 AW130822 AW167419 AI289485 AW150010
5			H88004 AI743745 AW088710
J	123494	21202_1	AW179019 AW179011 AF135160 NM_014050 AF078860 BE018005 AK000285 AF151038 BE245156 AW179007 AA345114 BE619758
			BE619209 W25509 AA314339 AA336674 AA337956 AW954843 AW390412 N46786 AA316235 AA314286 R15686 BE535633 N57134 N46483
			AW368462 AA923517 AA665223 AI418513 AA837523 AI359320 AI309273 AI522278 N40939 AA904977 AA938272 N30240 AA887965
			A1671972 A1028109 AA094652 AA883262 AA887781 A1744447 AW592944 A1077790 AW860883 AW148667 N89861 AA557195 A1191824
10			AI433166 AI719760 AA453089 AA630656 AA300976 AA639620 AW675033 AA284393 AW886987 AI476335 AI332939 BE301513 AA452920
10			AW674302 AI925483 AW170412 AI698717 AI375985 BE220535 AI688151 AW514809 AW062346 AA599786 BE350848 AI560848 AI023075
			AA864875 AA166871 AI807947 AW514579 AI978602 AI860340 AA830886 AI374788 AI283592 AA683152 AA743159 AI379932 AI432056
	440000	44000 0	A1128904 AW150433 N38909
	116296	11967_2	AW149502 Z43342 AW002826 AL049382 AA442545 AW971471 BE220243 AW968952 AA043607 AW299245 AA659892 Al038768 H26330
15			BE463534 AI628252 AA836139 AI277291 AA489033 AA741239 AI209064 AI300253 AI275761 Z39417 C01835
13			

Table 9A lists about 382 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the railo of "average" ovarian cancer to "average" normal adult ovaries was greater than or equal to 10. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult ovaries level was set to the arithmetic mean amongst various non-malignant ovaries. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues (see Table 7A) was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 382 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY Pkey: Primekey
Ex. Acon: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title

20

25

ratio: ratio tumor vs. normal tissues

30	Pkey	Ex. Acon	UGID	Title	ratio
50	134454	L33930	Hs.173996	CD24 antigen (small cell lung carcinoma clust	86.2
	102927	X12876	Hs.65114	keratin 18	84.7
	115909	AA436666		ESTs	72.3
			Hs.59761		66.8
35	123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [65.4
22	115674	AA406542	Hs.71520	ESTs	
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin; bone	63.1
	101839	M93036	Hs.692	membrane component; chromosomal 4; surface ma	56.8
	115221	AA262942	Hs.79741	ESTs	56.1
40	108059	AA043944	Hs.62663	ESTs	52.3
40	121853	AA425887	Hs.98502	ESTs	47.8
	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	47.0
	103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	46.5
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-lik	45.5
45	102979	X17042	Hs.1908	proteoglycan 1; secretory granule	44.6
45	130967	AA134138	Hs.182579	Horno sapiens leucine aminopeptidase mRNA; com	44.5
	102009	U02680	Hs.82643	protein tyrosine kinase 9	40.4
	126960	AA317900	Hs.161756	ESTs	39.6
	103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	39.1
	133829	AA453783	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	39.0
50	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapiens]	38.9
	102803	U89916	Hs.26126	claudin 10	38.8
	104943	AA065217	Hs.169674	ESTs	38.7
	106605	AA457718	Hs.21103	Homo saplens mRNA; cDNA DKFZp564B076 (from cl	38.4
	120655	AA287347	Hs.238205	ESTs	38.1
55	102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	36.3
	104052	AA393164	Hs.97644	mammaglobin 2	36.0
	109166	AA179845	Hs.73625	RAB8 Interacting; kinesin-like (rabkinesin6)	35.9
	101332	L47276		Horno saplens (cell line HL-6) alpha topolsome	35.0
	106167	AA425906	Hs.7956	ESTs .	34.5
60	101042	J05428	Hs.10319	UDP glycosyltransferase 2 family; polypeptide	34.3
	125852	H09290	Hs.76550	Homo saplens mRNA; cONA DKFZp564B1264 (from c	33.7
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin; uteri	32.3
	126410	R51912	Hs.12409	somatostatin	32,1
	134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	32.0
65	125739	AA428557	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	31.6
	132254	L20826	Hs.430	plastin 1 (1 isoform)	31.4
	112610	R79392	Hs.23643	ESTs .	30.9
	101441	M21005	Hs.100000	S100 calcium-binding protein A8 (calgranulin	30.6
	116345	AA496981	Hs.199067	HER3 receptor tyrosine kinase (c-erbB3; ERBB3	30.1
70	108860	AA133334	Hs.129911	ESTs	29.8
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	29.2
	107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	28.9
	106210	AA428239	Hs.10338	ESTs	28.9
	134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chronic g	28.0
75	125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	27.5
. •	107222		Hs.82689	tumor rejection antigen (gp95) 1	27.4
	102260		Hs.159557	karyopherin alpha 2 (RAG cohort 1; importin a	26.9
	134691		Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	26.8
	105588		Hs.10867	ESTs	26.3
80	130718		Hs.18376	ESTs	26.3
	111185		Hs.12844	EGF-like-domzin; multiple 6	25.6
	131965		Hs.35962	ESTs	25.6
	132903	AA235404	Hs.5985	Homo saplens done 25186 mRNA sequence	25.6
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride chann	25.5
	114000	E41303	1101100	COINTINGATION ANIMAL MILL ANIMAL ANGUM	20.0

	101185	L19872	Hs.170087	aryl hydrocarbon receptor	25.2
	128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	25.1
	116724	F13665	Hs.65641	ESTs	24.9
_	111929	R40057	Hs.112360	promintn (mouse)-like 1	24.9
5	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	24.8
	131210	AA430047	Hs.24248	EST8	24.7
	101714	M68874		Human phosphatidyicholine 2-acylhydrolase (cP	24.6
	100154	D14657	Hs.81892		24.6
				KIAA0101 gene product	
10	134656	X14787	Hs.87409	thrombospondin 1	24.3
10	100294	D49396	Hs.75454	antioxidant protein 1	23.9
	104080	AA402971	Hs.57771	kallikrein 11	23.7
	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	23.7
					23.7
	115697	AA411502	Hs.63325	ESTs; Weakly similar to alrway trypsin-like p	
	130350	U02020	Hs.239138	pre-B-cell colony-enhancing factor	23.7
15	105870	AA399623	Hs.23505	ESTs	23,6
	118528	N67889	Hs.49397	ESTs	23.4
	105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST yk386g7.5 co	23.2
					23.2
	109680	F09255	Hs.4993	EST8	
	131501	'AA121127	Hs.181307	H3 histone; family 3A	23.2
20	100824	HG4058-HT4	328	Oncogene Amt1-Evi-1, Fusion Activated	23.1
	111890	R38678	Hs.12365	ESTs	23.0
					22.8
	101543	M31166	Hs.2050	pentaxin-related gene; rapidly induced by IL-	
	102095	U11313	Hs.75760	sterol carrier protein 2	22.8
	114988	AA251089	Hs.94578	ESTs; Weakly similar to phosducin; retinal [H	22.8
25	120695	AA291468	-	ESTs	22.8
	130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	22,8
					22.7
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphosenne aminotr	
	109141	AA176428	Hs.193380	ESTs	22.6
	102345	U37283	Hs.58882	Microfibril-associated glycoprotein-2	22.6
30	115652	AA405098	Hs.38178	ESTs	22.4
50	100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	22.3
	105463	AA253370	Hs.32646	ESTs	22.2
	132624	AA164819	Hs.53631	ESTs	22.2
	119743	W70242	Hs.58086	ESTs	22.0
35	132528	AA283006	Hs.50758	chromosoma-associated polypeptide C	22.0
55					21.8
	107174	AA621714	Hs.25338	ESTs	
	134495	D63477	Hs.84087	KIAA0143 protein	21.8
	131985	AA434329	Hs.36563	ESTs	21.5
	105832	AA398346	Hs.21898	ESTs	21.2
40	126160	N90960	Hs.247277	ESTs; Wealdy similar to transformation-relate	21.2
				ESTs	20.9
	114846	AA234929	Hs.44343		
	109703	F09584	Hs.24792	ESTs; Wealdy similar to ORF YOR283w (S.cerevi	20.9
	135154	AA126433	Hs.173242	sorting nextn 4	20.8
	131185	M25753	Hs.23960	cyclin 81	20.7
45	105616	AA280670	Hs.24968	ESTs	20.5
73					20.2
	131148	C00038	Hs.23579	ESTs	
	129337	R63542	Hs.110488	KIAA0990 protein	20.2
	133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	20.1
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	19.9
50	133711	J04130	Hs.75703	small inducible cytokine A4 (homologous to mo	19.8
50					19.7
	131818	Z39297	Hs.3281	neuronal pentraxin II	
	125303	Z39821	Hs.107295	ESTs	19.6
	109112	AA169379	Hs.72865	ESTs	19.5
	105376	AA236559	Hs.8768	ESTs; Wealty similar to till ALU SUBFAMILY SQ	19.2
55	103505	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	19.1
55					19.1
	100661	HG2874-HT3		Ribosomal Protein L39 Homolog	
	129571	X51630	Hs.1145	Wilms tumor 1	19.0
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the beta t	18.9
	131562	U90551	Hs.28777	H2A histone family; member L	18.9
60	131272	AA423884	Hs.139033	paternally expressed gene 3	18.9
00				ECTs: Monda classes gold o	18.8
	130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROTEIN (
	103245	X76648	Hs.28988	glutaredoxin (thlottransferase)	18.7
	101809	M86849		Homo sapiens connexin 26 (GJB2) mRNA, complet	· 18.6
	105344		Hs.8645	ESTs	18.4
65	135225		Hs.9667	butyrobetaine (gamma); 2-oxoglutarate dioxyge	18.4
05					
	116786		Hs.83429	tumor necrosis factor (ligand) superfamily; m	18.3
	131510		Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	18.2
	124059	F13673	Hs.99769	ESTs	18.0
	103352		Hs.78853	uracil-DNA glycosylase	17.9
70			Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	17.9
7 0	132742				
	135242		Hs.9700	cyclin E1	17.9
	123494	AA599786	Hs.112110	EST8	17.8
	129168	T90621	Hs.109052	chromosome 14 open reading frame 2	17.7
	128517		Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien	17.6
75				UDP-Gat:betaGlcNAc beta 1;3-galactosyltransfe	17.6
13	130160		Hs.151344		
	103448		Hs.204238	lipocalin 2 (oncogene 24p3)	17.5
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	17.5
	122946		Hs.105341	ESTs	17.5
	125819		Hs.251871	CTP synthase	17.5
QΛ					
80	131689		Hs.30696	transcription factor-like 5 (basic helix-loop	17.5
	115061	AA253217	Hs.41271	ESTs	17.3
	113702	T97307	Hs.161720	ESTs; Moderately similar to IIII ALU SUBFAMIL	17.3
	115291		Hs.122579	ESTs	17.3
	102567		Hs.146847	TRAF family member-associated NFKB activator	17.2
	105301		, 10071		1

	129229 129351	AA211941 AA167268	Hs.109643 Hs.62349	polyadenylate binding protein-interacting pro Human ras inhibitor mRNA; 3' end	17.2 17.2
	110769 113182	N22222 T55234	Hs.9676	yw34b06.s1 Morton Fetal Cochlea Homo saplens Human DNA sequence from clone 30M3 on chromos	17.1 17.0
5	115892	AA435946	Hs.50831	ESTs	17.0
•	123114	AA486407	Hs.105235	ESTs; Moderately similar to KIAA0454 protein	17.0
	123442	AA598803	Hs.111496	ESTs	17.0
	123339	AA504253	Hs.101515	ESTs	16.9
10	123689	AA609556	Hs.256562	ESTs	16.9
10	131941	D62657	Hs.35086	ubiquitin-specific protease 1	16.8
	120649	AA287115	Hs.99697	ESTs	16.8
	102139	U15932	Hs.2128	dual specificity phosphatase 5	16.8 16.7
	115522	AA331393 AA215333	Hs.47378 Hs.97101	ESTs putative G protein-coupled receptor	16.7
15	135243 131257	AA215333 AA256042	Hs.24908	ESTs	16.5
15	109508	AA233892	Hs.55902	ESTs; Weakly similar to IIII ALU SUBFAMILY SX	16.3
	132701	AA279359	Hs.55220	BCL2-associated athanogene 2	16.3
	134449	L34155	Hs.83450	taminin; alpha 3 (niceln (150kD); katinin (16	16.3
	126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske Iron	16.3
20	106124	AA423987	Hs.7567	ESTs	16.2
	115363	AA282071	Hs.152759	activator of S phase kinase	16.2
	117588	N34895	Hs.44648	ESTs	16.1
	131245	AA620599	Hs.24766	DKFZP564E1962 protein	16.1
25	101674	M61916	Hs.82124	laminin; beta 1	16.0 16.0
25	126819 134039	AA305536 S78569	Hs.161489 Hs.78672	ESTs laminin; alpha 4	16.0
	130648	AA075427	Hs.17296	ESTs; Weakly similar to Iprediction	15.9
	102823	U90914	Hs.5057	carboxypeplidase D	15.8
	128470	AA447504	Hs.100261	Homo sapiens mRNA; cDNA DKFZp5648222 (from cl	15.8
30	115844	AA430124	Hs.234607	ESTs	15.7
	132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	15.7
	130155	L33404	Hs.151254	kallikreln 7 (chymotryplic; stratum comeum)	15.7
	101008	J04162	Hs.763	Fc fragment of IgG; low affinity Illa; recept	15.7
25	120472	AA251875	Hs.104472	ESTs; Wealthy similar to Gag-Pol polyprotein [15.6
35	116844	H64938	Hs.38331	ESTs .	15.6
	106753	AA476944	Hs.7331	ESTs	15.6
	114767	AA148885	Hs.154443	minichromosome maintenance deficient (S. cere	15.5 15.5
	114768	AA149007	Hs.182339 Hs.70337	Ets homologous factor immunoglobulin superfamily; member 4	15.5
40	127370 101507	A1024352 M27492	Hs.82112	interleukin 1 receptor; type i	15.4
40	102519	U52969	Hs.80296	Purkinje cell protein 4	15.4
	102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	15.4
	111244	N69556	Hs.24724	MFH-amplified sequences with leucine-rich tan	15.4
	120404	AA234921	Hs.96427	KIAA1013 protein	15.3
45	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltran	15.2
	129519	AA298786	Hs.112242	ESTs .	15.1
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA blading motif pro	15.0
	109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycoprotein	14.9
50	115967	AA446887	Hs.42911	ESTs	14.9 14.9
30	104636	AA004415 X93920	Hs.106106	ESTs	14.9
	134133 134444	X93920 X04470	Hs.180383 Hs.251754	dual specificity phosphatase 6 secretory leukocyte protease inhibitor (antil	14.8
	132998	Y00062	Hs.170121	protein tyrosine phosphalase; receptor type;	14.8
	131997	D82399	Hs.136644	Homo saciens clone 23714 mRNA sequence	14.6
55	134056	R27358	Hş.7886	ESTs; Weakly similar to Pelie associated prot "	14.6
	101249	L33881	Hs.1904	protein kinase C; lota	14.5
	105298	AA233459	Hs.26369	EST8	14.5
	107119	AA620307	Hs.27379	ESTs	14.5
C O	115839	AA429038	Hs.40541	ESTs	14.5
60	122802	AA460530	Hs.256579	ESTs	14.5
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosyltransf	14.3
	130269	AA284694	Hs.168352	nucleoporin-like protein 1	14.3
	134374 106370		Hs.8236	ESTs sprouty (Drosophila) homolog 2	14.3 14.2
65		AA443841 AA291710	Hs.18676	collagen; type IV; alpha 3 (Goodpasture antig	14.1
05	130919 132923		Hs.21276 Hs.60679	TATA box binding protein (TBP)-associated fac	14.1
	107968		Hs.61539	ESTs	14.1
	125390		Hs.75187	translocase of outer milochondrial membrane 2	14.1
	107148		Hs.5889	ESTs: Weakly similar to W01A11.2 gene product	14.1
70	110788		Hs.15420	ESTs	14.0
	109481		Hs.90680	ESTs; Wealty similar to WD40 protein Clao 1 (13.9
	105646	AA282147	Hs.5888	ESTs	13.9
	106030		Hs.12802	development and differentiation enhancing fac	13.8
75	132618		Hs.5344	adaptor-related protein complex 1; gamma 1 su	13.7
75	133230		Hs.6838	ras homolog gene family; member E	13.7
	124803		Hs.164866	cyclin K	13.6
	121381		Hs.97865	ESTs; Weakly similar to WASP-family protein [13.6 13.5
	105200		Hs.24641 Hs.23317	ESTs ESTs	13.5
80	105627 114986		Hs.87807	EST8	13.5
00	118036		Hs.196008	ESTS	13.5
	134672		Hs.87627	ESTs; Weakly similar to cDNA EST EMBL:T00542	13.5
	110915		Hs.29724	ESTs	13.3
	117984		Hs.47368	ESTs	13.3

	132550	AA029597	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	13.3
	124315	H94892	Hs.6906	v-rai simian laukemia virai oncogene homolog	13.2
	102547 125134	U57911 W19228	Hs.46638 Hs.100748	chromosome 11 open reading frame 8 ESTs	13.2 13.2
5	111806	R33468	Hs.24651	ESTS	13.1
-	106983	AA521195	Hs.10887	similar to lysosome-associated membrane glyco	13.0
	106498	AA452141	Hs.7171	ESTS	13.0 13.0
	110787 122860	N24716 AA464414	Hs.12244 Hs.112159	ESTs; Wealdy similar to C4489.1 (C.elegans) ESTs	13.0
10	131535	AA504642	Hs.28436	ESTs; Wealdy similar to coded for by C. elega	13.0
	116188	AA464728	Hs.184598	ESTs	13.0
	107243 129300	D59489 C20976	Hs.34727 Hs.110165	ESTs ESTs; Highly similar to ribosomal protein L26	12.9 12.9
	134487	R38185	Hs.83954	Homo sapiens unknown mRNA	12.8
15	102348	U37519	Hs.87539	aldehyde dehydrogenase 8	12.8
	131839	H80622 W47620	Hs.33010 Hs.56009	KIAA0633 protein 2-5'oligoadenylate synthetase 3	12.8 12.8
	119620 120802	AA343533	Hs.128777	ESTs; Weakly similar to predicted using Genef	12.7
00	102250	U28014	Hs.74122	caspase 4; apoptosis-related cysteine proteas	12.7
20	105539	AA258873	Hs.25242	ESTs	12.7 12.7
	114965 118001	AA250737 N52151	Hs.72472 Hs.47447	ESTs ESTs	12.7
	100448	D87469	Hs.57652	EGF-tike-domain; multiple 2	12.6
25	130920	D50975	Hs.75525	calreticulin	12.6
25	131075	Y00757 AA256323	Hs.2265 Hs.25264	secretory granule; nauroendocrine protein 1 (DKFZP434N126 protein	12.6 12.5
	105496 109235	AA193592	Hs.42300	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ	12.5
	118215	N62195	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthas	12.5
30	134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	12.5 12.4
30	106897 133050	AA489790 S67325	Hs.167496 Hs.63788	RAN binding protein 6 propionyl Coenzyma A carboxylase; bela polype	12.4
	109683	F09308	Hs.27607	ESTs	12.3
	121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [H.s	12.3
35	102876 101804	X03663 M86699	Hs.174142 Hs.169840	colony stimulating factor 1 receptor; former TTK protein kinase	12.2 12.2
33	129017	H13108	Hs.107968	ESTs	12.1
	105812	AA394126	Hs.20814	ESTs; Highly similar to CGI-27 protein (H.sap	12.1
	106459	AA449741	Ks.4029	glioma-amplified sequence-41	12.0 12.0
40	107059 107080	AA608545 AA609210	Hs.23044 Hs.19221	RAD51 (S. cerevisiae) homolog (E coll RecA ho ESTs	12.0
	110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	12.0
	112253	R51818	Hs.104222	Homo saplens mRNA; cDNA DKFZp566L034 (from cl	12.0
	116760 120314	H11054 AA194166	Hs.155342 Hs.221040	protein kinase C; delta KIAA1038 protein	12.0 12.0
45	123005	AA479726	Hs.105577	ESTs	12.0
	132572	AA448297	Hs.237825	signal recognition particle 72kD	12.0
	110561	H59617 S75256	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING	12.0 11.9
	101923 134992	H05625	Hs.92414	HNL=neutrophil lipocalin (human, ovarian canc ESTs	11.8
50	105516	AA257971	Hs.21214	ESTs	11.8
	105248	AA226968	Hs.22826	ESTS	11.7 11.7
	109130 115955	AA172040 AA446121	Hs.20161 Hs.44198	ESTs; Weakly similar to IgE receptor beta sub Homo saptens BAC clone RG054D04 from 7q31	11.7
	116135	AA460314	Hs.94179	ESTs	11.7
55	116284	AA487252	Hs.237809	ESTs; Weakly similar to hypothetical protein	11.7
	132384 134753	AA479933 Y09216	Hs.46967 Hs.173135	Human DNA sequence from clone 167A19 on chrom dual-specificity tyrosine-(Y)-phosphorytation	11.7 11.7
	125136	W31479	Hs.129051	ESTs	11.7
60	133928	N34096	Hs.7768	ubiquitin-conjugating enzyme E2E 1 (homologou	11.6
60	117395	N26330	Hs.93701	ESTs EST11857 Uterus tumor i Homo saplens cDNA 5'	11.5 11.5
	127007 130567	AA299360 L07493	Hs.1608	replication protein A3 (14kD)	11.5
	135073	AA452000	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1824 (from c	11.5
65	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	11.4 11.4
05	115536 133240	AA347193 D31161	Hs.62180 Hs.68613	ESTs ESTs	11.3
	106521	AA453431	Hs.14732	malic enzyme 1; NADP(+)-dependent; cytosolic	11.3
	107674	AA011027	Hs.41143	KIAA0581 protein	11.3
70	114149 132478	Z38814 H20906	Hs.27196 Hs.49500	ESTs . KIAA0746 protein	11.3 11.2
,,	104252	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	11.2
	102438		Hs.790	microsomal glutathione S-transferase 1	11.2
	106726		Hs.7141 Hs.77443	ESTs actin; gamma 2; smooth muscle; enteric	11.2 11.2
75	100116 110970		Hs.77443 Hs.96870	Homo sapiens mRNA full length insert cDNA clo	11.2
	130417		Hs.155485	huntingtin-interacting protein 2	11.2
	132906	AA142857	Hs.234896	ESTs; Highly similar to germinin (H.saptens)	11.2
	107853 103467		Hs.59461 Hs.78712	DKFZP434C245 protein aminolevulinate; delta-; synthase 1	11.2 11.1
80	100438		Hs.91417	topolsomerase (DNA) II binding protein	11.1
	102654	U68494	Hs.24385	Human hbc647 mRNA sequence	11.1
	103172 106856		Hs.116774 Hs.15839	integrin; alpha 1 ESTs; Wealdy similar to similar to oxysterol-	11.1 11.1
	108255		Hs.172608	ESTs	11.1

	404000	1100000		the section with miss migra-coals 40 ferms of	44.4
	124308 129057	H93575 X62466	Hs.227145 Hs.214742	Homo saplans mRNA; cDNA DKFZp564J142 (from cl CDW52 antigen (CAMPATH-1 antigen)	11.1 11.1
	128845	AA455658	Hs.10649	basement membrane-induced gene	11.1
_	129025	AA420992	Hs.103441	ESTs; Wealty similar to testicular tektin B1-	11.0
5	107638	AA009528	Hs.42743	ESTs; Wealty similar to predicted using Genef	11.0
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	11.0
	115262 102580	AA279112 U60808	Hs.88594 Hs.152981	COR diametrican customs (absorbalidate or	11.0 10.9
	105614	AA458934	Hs.179912	CDP-diacylglycerol synthase (phosphatidate cy ESTs	10.9
10	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [H.sa	10.9
	115764	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) homolog	10.9
	121770	AA421714	Hs.11469	KIAA0896 protein	10.9
	132191	AA449431 Y10659	Hs.158688 Hs.250911	KIAA0741 gene product	10.9 10.9
15	133214 133914	N32811	Hs.77542	interleukin 13 receptor; alpha 1 ESTs	10.8
	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	10.8
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.8
	104147	AA451992	Hs.226799	ESTs; Highly similar to HSPC039 protein [H.sa	10.8
20	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	10.8 10.8
20	115881 129950	AA435577 M31516	Hs.184942 Hs.1369	G protein-coupled receptor 64 decay accelerating factor for complement (CD5	10.8
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypepilde	10.8
	133784	AA214305	Hs.76173	ESTs	10.8
0.5	134248	AA292677	Hs.80624	ESTS	10.8
25	105565	AA278302	Hs.18349	ESTs; Wealdy similar to partial CDS [C.elegan	10.8
	127999	AA837495	Hs.69851 Hs.48644	ESTs; Wealdy similar to Wiskolt-Aldrich syndr	10.8 10.7
	108040 130367	AA041551 Z38501	Hs.8768	ESTs ESTs; Wealty similar to !!!! ALU SUBFAMILY SQ	10.7
	108539	AA084677	Hs.54558	ESTs; Weakly similar to protein B [H.saplens]	10.7
30	111345	N89820	Hs.14559	ESTs	10.7
	115583	AA398913	Hs.45231	LDOC1 protein	10.7
	128965	T17440	Hs.107418	ESTs	10.7
	101396	M15796	Hs.78996 Hs.41270	proliferating cell nuclear antigen procollagen-lysine; 2-oxoglutarate 5-dioxygen	10.6 10.6
35	132164 101275	U84573 L37936	Hs.3273	Ts translation elongation factor; milochondri	10.6
55	104660	AA007160	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from cl	10.6
	108609	AA100694	Hs.69499	Human DNA sequence from BAC 15E1 on chromosom	10.6
	112041	R43300	Hs.22929	ESTs	10.6
40	114208	Z39301	Hs.7859	ESTS	10.6 10.6
40	118537 106919	N67974 AA490885	Hs.75431 Hs.21766	fibrinogen; gamma polypeptide ESTs	10.6
	115984	AA447687	Hs.91109	ESTs	10.6
	105538	AA258860	Hs.32597	ring finger protein (C3H2C3 type) 6	10.6
4.5	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	10.5
45	116710	F10577	Hs.70312	ESTs	10.5
	119780 112996	W72967 T23539	Hs.191381 Hs.7165	ESTs; Weakly similar to hypothetical protein zinc finger protein 259	10.5 10.5
	103029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating ac	10.5
	101255		Hs.149894	mitochondrial translational initiation factor	10.4
50	107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subun	10.4
	125617		Hs.164950	ESTs	10.4
	131475	Z39053	Hs.27263	ESTs .	10.4 10.4
	132073 101469		Hs.38516 Hs.169248	ESTs Human somatic cytochroms c (HCS) gene; comple	10.4
55	102437		Hs.221986	aquaporin S	10.3
	104301	D45332	Hs.6783	ESTS	10.3
	127236	AJ341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	10.3
	101465	M22612	Hs.241395	protease; serine; 1 (trypsin 1)	10.3
60	113805	W42957	Hs.250617 Hs.177486	ESTs amyfold beta (A4) precursor protein (protease	10.2 10.2
00	133536 169799	Y00264 F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	10.2
	113523		Hs.16686	ESTs	10.2
	116195		Hs.72402	ESTs	10.2
ce	134542		Hs.85112	insulin-like growth factor 1 (somatomedin C)	10.2
65	125298		Hs.235350	YDD19 protein	10.2 10.2
	119367 134470		Hs.90905 Hs.83758	ESTs CDC28 protein kinase 2	10.2
	134288		Hs.8117	ESTs	10.1
	105127		Hs.11817	ESTs; Weakly similar to contains similarity t	10.1
70	110627	H70485	Hs.35225	ESTs; Weakly similar to MBNL protein [H.saple	10.1
	115188		Hs.88367	ESTs	10.1
	132632		Hs.5398	guanine-monophosphate synthetase	10.1 10.1
	124049 100079		Hs.74519 Hs.23311	primase; polypeptide 2A (58kD) KIAA0367 protein	10.1
75	113987		Hs.9841	ESTs: Moderately similar to COMPLEMENT C1Q SU	10.0
-	117280		Hs.172241	ESTs	10.0

TABLE 9B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers 80

CAT Number 23182_1 Accession BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655 Pkey 100661

	101332	25130_1	J04088 NM_001087 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813
			BE081283 ÃA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044
			A1765634 A1948838 AW235336 AW172827 AA095289 BE046383 A1734240 W16699 A1660329 A1289433 AA933778 AW469242 AA468838 AA806983 AA625873 W78031 BE206307 AA550803 A1743147 A1990075 AA948274 AA129533 Al635399 AA605313 A1624669 AW594319
5			AI221834 AI337434 AA307706 BE550282 AI760467 AI630636 AI221521 AW674314 AW078889 AI933732 AI686969 AI186928 AW074595
		•	A1127488 AL079844 A1910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427
			AW383395 H09977 AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AI375913 BE384156 W24652
			AM402701 AW403113 K94438 M73128 M3328 M390828 AA090828 AA090801 129028 AW85107 F L47277 L47278 AIS15913 BES04150 W24552 AA746288 AA568223 BE090591 H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594
10			AASB34B3 AWB73194 AW575166 A1128799 AIB03319 AL042776 AW074313 A1887722 A1032284 AA447521 A1123885 N23334 A1354911
			AW090687 AA236763 AA435535 AA236910 AA047124 AA236734 AW514610 H93467 AA962007 AI446783 AA127259 AI613495
			A1686720 A1587374 AA336731 AA702453 A1859757 AA216786 A1251819 A1469227 AA806022 A1092324 N71868 AA968782 AA236919
			AA809450 AA227220 AA765284 A1192007 AA768810 AA805794 AA729280 AA806238 AW768817 N71879 A1050686 AA505822 AA668974 A1688160 BE045915 AW466315 AA731314 AA649568 AA834316 AW591901 AW063876 AW294770 A1300266 A1336094
15			ALGEG380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01676 Al457474 AW466316 AA550969 AA630788
	100824	5_36	AI393237 AI521317 AI751348 AF025841 D43968 AW994987 L34598 AF025841 D89789 D89788 D89790 AW998932 AI971742 AI310238
			X90976 AW139668 AW574Z80 Al365552 AA877452 AV657554 C75229 AA376077 Al798056 AW609213 W25586 H30149 BE075089
			BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127 AW467960 BE158135 BE158126 BE158145 N92860 AA847246 AI961688 AI361423 AA878154 AA043767 AI863712 AI559226 AW339007 AI371266 AI368901 AA046624 AA134739
20			N92000 MACH 240 M30 1000 M30 1423 MAD 18134 MACHATA MOOJ 12 M333220 M4539007 M37 1200 M300301 MACHAOLA M754739 AW449154 AA130232 Al458720 AA962511 AI700627 R70437 AW004008 AA045229 Al671572 H99599 AA043768 Al685454 Al871685
			N29937 X90977 AA524240 AI142114 AI825750 AI567805 AI631365 AI347893 AA134740 F20669 AA046707 AW793216 AW963298
			AW959380 AA363265 Al784593 Al268201 R69451 AV657618 Al695588
	101714	30725_1	M68874 AL022147 M72393 AL049797 BE439441 T27650 AI766240 AW150345 AW778943 AI627464 BE439479 AA587049 AI277900
25	101809	32963 1	A1984983 A1630935 M86849 AA315280 NM 004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563
23	101003	02300_1	AW384544 AW384566 AW376307 AW376323 AW839085 AA257102 AW376317 AW276060 AW271245 AW376298 AW384497 AI598114
			AW264544 Al018138 AW021810 AA961504 AW086214 AW771489 AW192483 Al290266 AW192488 AW384490 AW007451 AW890895
			AA554460 AA613715 AW020066 AJ783695 AJ589498 AJ917637 AW264471 AW384491 AJ816732 AW368530 AW368521 AW368463
30			AA461087 Al341438 Al970613 Al040737 Al418400 AA947181 AA962716 Al280695 AW769275 AW023591 Al160977 AA055400 NT1882 AA490466 AW243772 AW318636 Al076554 AW511702 N69323 H88912 AA257017 Al952506 H88913 Al912481 AA600714 BE465701
50			N64149 C00523 N64240 A4677120
	101923	30543_1	X99133 XB3006 W38398 AA401137 AA298242 AA366738 AA308126 AW583781 AA298668 AW845024 BE140204 AW845005 U47734
			AA837575 NM_005564 AA329732 AA421943 BE171567 S75256 A1750047 A1762213 AA100735 AW612993 A1474120 AW062884
35			AI940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 AI939989 AA076188 BE182636 AA169569 AA167439 AI283967 AA167783 AA076140 AI749649 AA166792 AI708618 AA400973 AA514773 AA514789 AA164458 AA167440 AA074845
33			AA221944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459 AW176400 AW475086 AA857522 AA148193
			AA838234 AA593897 Al284506 AW153324 AA148194 AW583341 Al669077 AW264913 AA074902 Al680515 AA169874 AA169614
			AA079651 AW591737 AW190644 AA076565 AA662747 AA075898 AA535642 N27757 Al306666 AA074727 N79823 AA524360 Al826800
40			AA173827 BE140374 BE004062 AW265060 BE184103 A1199258 AA857853 AA299459 AA837890 A1626104 AA503624 BE183618
40			BE183717 AA573267 Al833071 AW270590 AA506601 BE004010 AA837854 Al675895 Al810491 Al184883 AW664712 AA076046 AA515574 AW352267 A1797418 AA172395 Al749194 Al559933 AA502597 AA321220 Al866124 Al695633 AA494293 AW085635
			AA165649 AA165663
	127007	19921_1	AB037771 BE005079 AA394189 AW959650 AA299360 AA398081 W37627 AW750817 AW630138 AI522058 BE326323 AA374890
45			AW418534 AW997510 AW995214 AW959649 AA504426 D79223 D79621 AI276062 AI973155 AA653470 AA337687 AI382521 AW084427
45	440700		D57078 W37628 Al610506 Z30230 Al567034 AA766091 H25097 H25078 AW991507 AA319736
	110769	229824_1	BE000831 AA541787 AW173038 AA327931 AW117510 AW664665 Al066624 Al478955 Al863075 Al073744 AA490170 R46651 Al075653 F02865 N22222 AW972956
	120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210
60			AA970201 A1633384 AA425910 A1017004 A1241295 AA402816 AA291468
50			

Table 10A lists about 733 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymatrix/Eos-Hu03
GeneChip array such that the ratio of average ovarian cancer to average normal adult tissues was greater than or equal to 3.0. The average ovarian cancer level was set to the about the 80th percentile amongst various ovarian cancers. The average normal adult tissues level was set to the 90th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 10A: ABOUT 733 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

60 Pkey: Primekey
Ex. Acon: Exemplar Accession
UG ID: UnlGene ID
Title: UniGene title

ratio: ratio tumor vs normal fissues

65	Pkey	Ex. Accn	UGID	Title	ratio
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	66.1
	418179	X51630	Hs.1145	Wilms turnor 1	33.5
	400292	AA250737	Hs.72472 ·	BMPR-lb; bone morphogenetic protein receptor	30.0
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
70	415511	AI732617	Hs.182362	ESTs .	28.1
. •	422956	BE545072	Hs.122579	ESTs	28.1
	410929	H47233	Hs.30643	ESTs	27.4
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	25.2
	449034	AI624049	Hs.277523	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo saplens cDNA	23.7
75	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	22.7
, ,	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1	21.9
	448243	AW369771	Hs.77496	ESTs	21.3
	430691	C14187	Hs.103538	ESTs	21.2
0Λ	444783	AK001468	Hs.62180	ESTs	20.8
80	407638	AJ404672	Hs.288693	EST	20.1
	423739	AA398155	Hs.97600	ESTs	19.7
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0
	451110	A1955040	Hs.301584	EST8	18.8
	426427	M86699	Hs.169840	. TTK protein kinase	18.7

	428227	AA321649	11- 00/0	INTERESPOND CAMILLA INDUCCE	10.2
	419854		Hs.2248 Hs.87836	INTERFERON-GAMMA INDUCED Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3 18.3
	439706		Hs.59761	ESTs	18.3
_	428579		Hs.184942	G protein-coupled receptor 64	17.4
5	410247		Hs.61345	RU2S	17.0
	428153		Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
	415076		Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
10	424905 423685	NM_002497 BE350494	Hs.153704 Hs.49753	NIMA (never in mitosis gene a)-related kinase	16.2 15.9
10	428187		Hs.285529	Homo saplens mRNA for KIAA1561 protein, parti ESTs	15.9
	438817		Hs.163242	ESTs	15.9
	424906		Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	15.9
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation	15.7
15	412723		Hs.179912	ESTs	15.3
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	15.2
	443646	A1085198	Hs.298699	ESTS	15.1
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ 10518 fis, clone NT2RP20	14.8 14.6
20	428976 418738	AL037824 AW388633	Hs.194695 Hs.6682	ras homolog gene family, member I solute carrier family 7, member 11	14.3
20	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	14.2
	438209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	14.1
	427356	AW023482	Hs.97849	ESTS	.13.9
~~	418601	AA279490	Hs.86368	calmegin *	13.8
25	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7
	428532	AF157326	Hs.184786	TBP-interacting protein	13.6
	402408	A1275570	Un 479094	U ECTo: NED4 to och D41	13.6 13.4
	447350 451807	Al375572 W52854	Hs.172634 Hs.27099	ESTs; HER4 (c-erb-B4) DKFZP564J0863 protein	13.4
30	423575	C18863	Hs.163443	ESTs	13.2
50	443211	AI128388	Hs.143655	ESTs	13.2
	437872	AK002015	Hs.5887	RNA binding motif protein 7	13.0
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
0.5	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from c	12.7
35	442655	AW027457	Hs.30323	ESTs	12.5
	452096	BE394901	Hs.226785	ESTS	12.4 12.3
	414972	BE263782	Hs.77695 Hs.130526	KIAA0008 gene product ESTs	12.3
	435039 447033	AW043921 AI357412	Hs.157601	EST - not in UniGene	12.3
40	433764	AW753676	Hs.39982	ESTs	12.2
	442611	BE077155	Hs.177537	ESTs	12.0
	408562	A1436323	Hs.31141	Homo saplens mRNA for KIAA1568 protein, parti	11.9
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.8
45	421478	A1683243	Hs.97258	ESTs	11.8
45	426635	BE395109	Hs.129327	ESTs	11.8
	415989	A1267700	Hs.111128	ESTS	11.7 11.5
	433159 452249	AB035898 BE394412	Hs.150587 Hs.61252	kinesin-like protein 2 ESTs	11.4
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	11.3
50	442353	BE379594	Hs.49136	ESTs	11.3
	447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	450480	X82125	Hs.25040	zinc finger protein 239	11.3
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
55	435496	AW840171	Hs.265398	ESTs, Wealdy similar to transformation-relate	11.2
55	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1 11.1
	445258 432677	A1635931	Hs.147613 Hs.278611	ESTs UDP-N-acetyl-alpha-D-galactosamine:polypeplid	11.0
	429782	NM_004482 NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-blnd	10.9
	404567	1111/2000104	INCESTOR	0	10.8
60	423811	AW299598	Hs.50895	homeo box C4	10.7
	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	10.6
	441627	AA947552	Hs.58086	ESTs	10.3
	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOS	10.3
65	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkinesin6)	10.2 10.1
05	427469 415227	AA403084 AW821113	Hs.269347 Hs.72402	ESTs ESTs	10.1
	445413	AA151342	Hs.12677	CGI-147 protein	10.0
	425734	AF056209	Hs.159396	peptidylgtycine alpha-amidating monooxygenase	10.0
	421451	AA291377	Hs.50831	ESTs	10.0
70	410044	BE566742	Hs.58169	highly expressed in cancer, rich in laucine h	9.8
	427878	C05766	Hs.181022	CGI-07 protein	9.7
	408460	AA054726	Hs.285574	ESTS	9.7
	422972	N59319 AJ583187	Hs.145404	ESTs	9.7 9.7
75	443715 440901	AA909358	Hs.9700 Hs.128612	cyclin E1 ESTs	9.6
15	453160	A1263307	Hs.146228	ESTs	9.6
	415211	R64730.comp		ESTs; Highly similar to SPERM SURFACE PROTEIN	9.5
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	9.5
	400250			0	9.5
80	410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	9.3
	442957	A1949952	Hs.49397	ESTS	9.3
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas Putative prostate cancer tumor suppressor	9.3 9.2
	434401 453628	Al864131 AW243307	Hs.71119 Hs.170187	ESTs	9.1
	*********	7311433VI	113,110101	, 2010	

	452055	AJ377431	11- 000770	ESTs	
	424086	AJ351010	Hs.293772 Hs.102267	lysyl coldase	9.1 9.1
	442875	BE623003	Hs.23625	Homo sapians clone TCCCTA00142 mRNA sequence	9.1
_	416208	AW291168	Hs.41295	ESTs	9.0
5	407168	R45175	Hs.117183	gb:yg40f01.s1 Soares infant brain 1NIB Homo s	9.0
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	8.9
	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fls, clone OVARC10	8.9
	433527	AW235613	Hs.133020	ESTs	8.9
10	409928 423020	AL137163 AA383092	Hs.57549 Hs.1608	hypothetical protein dJ47384	8.8 8.7
10	425665	AK001050	Hs.159066	replication protein A3 (14kD) ESTs	8.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	8.6
	449433	AI672096	Hs.9012	ESTs	8.6
1.5	453878	AW964440	Hs.19025	ESTs	8.6
15	450505	NM_004572	Hs.25051	plakophilin 2	8.6
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	8.5
	414315 425492	Z24878 AL021918	Hs.158174	gb:HSB65D052 STRATAGENE Human skeletal muscle	8.5
	435181	AA669339	Hs.28838	zinc finger protein 184 (Kruppel-like) KIAA1571 protein	8.5 8.5
20	436396	AI683487	Hs.299112	Homo saplens cDNA FLJ11441 fis, clone HEMBA10	8.5
	418384	AW149266	Hs.25130	ESTs	8.4
	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation initi	8.4
	409041	AB033025	Hs.50081	KIAA1199 protein	8.4
25	447078	AW885727	Hs.301570	ESTs '	8.4
25	448674	W31178	Hs.154140	EST8	8.3
	433393	AF038564	Hs.98074 Hs.49765	atrophin-1 interacting protein 4	8.3
	433496 421155	AF064254 H87879	Hs.102267	VERY-LONG-CHAIN ACYL-COA SYNTHETASE lysyl oxidase	8.3 8.2
	438394	BE379623	Hs.27693	CGI-124 protein	8.2
30	400298	AA032279	Hs.61635	STEAP1	8.1
	409092	AI735283	Hs.172608	ESTs	8.1
	440250	AA876179	Hs.134650	ESTs	8.1
	409143	AW025980	Hs.138965	ESTs	8.1
25	407771	AL138272	Hs.62713	ESTs	8.1
35	419088	AI538323	Hs.77496	ESTs	8.1
	431725 431750	X65724 AA514988	Hs.2839 Hs.283705	Norrie disease (pseudoglioma) ESTs	7.9 7.9
	435635	AF220050	Hs.181385	uncharacterized hematopoletic stem/progenitor	7.9
	441826	AW503603	Hs.129915	phosphothesterase related	7.9
40	417728	AW138437	Hs.24790	KIAA1573 protein	7.8
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	7.8
	421039	NM_003478	Hs.101299	cullin 5	7.8
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	7.8
45	429609	AF002246	Hs.210863	cell adhesion molecute with homology to L1CAM	7.8
43	415139	AW975942	Hs.48524	ESTS	7.7
	450192 423992	AA263143 AW898292	Hs.24596 Hs.137206	RAD51-interacting protein Homo sapiens mRNA; cDNA DKFZp564H1663 (from c	7.7 7.7
	436211	AK001581	Hs.80961	polymerasa (DNA directed), gamma	7.7
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	7.5
50	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA, subu	7.5
	433330	AW207084	Hs.132816	ESTs	7.5
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	7.5
	427660	A1741320	Hs.114121	Homo saplens cDNA: FLJ23228 fis, clone CAE066	7.5
55	422095 436476	A1868872 AA326108	Hs.288966 Hs.53631	ceruloplasmin (ferroxidase) ESTs	7.5 7.5
55	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.4
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein 3	7.4
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.4
	439262	AA832333	Hs.124399	ESTs	7.4
60	435420	Al928513	Hs.59203	ESTs	7.3
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	7.3
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	7.3
	411571 409916	AA122393	Hs.70811 Hs.57435	hypothetical protein FLJ20516	7.2 7.2
65	418007	8E313625 M13509	Hs.83169	solute carrier family 11 (proton-coupled diva Matrix metalloprotease 1 (interstitial collag	7.2
05	420900	AL045633	Hs.44269	EST8	7.2
	424001	W67883	Hs.137476	KIAA1051 protein	7.2
	400301	X03635	Hs.1657	Estrogen receptor 1	7.1
70	400238			0	7.1
70	413573	A1733B59	Hs.149089	ESTs	7.1
	428071	AF212848	Hs.182339	transcription factor ESE-38	7.1
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	7.1
	453062 456965	AW207538 AW131888	Hs.61603 Hs.172792	ESTs ESTs, Weakly similar to hypothetical protein	7.1
75	430303	A1819068	Hs.209122	ESTs, weakly strillar to hypothetical protein	7.1
	446142	AI754693	Hs.145968	ESTs	7.0
	417791	AW965339	Hs.111471	ESTs	7.0
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	7.0
00	451797	AW663858	Hs.56120	ESTs	7.0
80	452909	NM_015368	Hs.30985	pannexin 1	7.0
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	7.0 7.0
	436281 449897	AW411194 AW819642	Hs.120051 Hs.24135	ESTs transmembrane protein vezatin; hypothetical p	7.0 6.9
	414142	AW368397	Hs.150042	ESTs	6.9
				• -	•

	440000				
	448776 419423	BE302464 D26488	Hs.30057 Hs.90315	transporter similar to yeast MRS2	6.9 6.9
	420908	AL049974	Hs.100261	KIAA0007 protein Homo sapiens mRNA; cDNA DKFZp5648222 (from cl	6.8
	452971	A1873878	Hs.91789	ESTs	6.8
5	413597	AW302885	Hs.117183	ESTs .	6.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP12	6.8
	437478	AL390172	Hs.118811	ESTs	6.7
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	6.7
10	421184	NM_003616	Hs.102456	survival of motor neuron protein interacting	6.7
10	410227 446608	AB009284 N75217	Hs.61152 Hs.257846	exostoses (multiple)-like 2 ESTs	6.6 6.6
	438167	R28363	Hs.24286	ESTs	6.6
	445459	AJ478629	Hs.158465	ESTs	6.6
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	6.6
15	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	8.6
	410292	AA843087	Hs.124194	ESTs	6.5
	415716	N59294	Hs.301141	Homo saptens cDNA FLJ11689 fis, clone HEMBA10	6.5
	424770 438122	AA425562 Al620270	Hs.129837	gb:zw46e05_r1 Scares_total_fetus_Nb2HF8_9w Ho ESTs	6.5 6.5
20	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	6.5
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked molety X	6.5
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.5
	418203	X54942	Hs.83758	CDC28 protein kmase 2	6.5
25	439901	N73885	Hs.124169	ESTs	6.5
23	428758	AA433988	Hs.98502	Homo saplens cDNA FLJ14303 fis, clone PLACE20	6.4
	404552 404599	•		0	6.4 6.4
	419503	AA243642	Hs.137422	ESTs	6.4
	420149	AA255920	Hs.88095	ESTs	6.4
30	440411	N30256	Hs.156971	ESTs, Weakly similar to Weak similarity with	6.4
	449108	Al140683	Hs.98328	ESTs	6.4
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metallopr	6.4
	453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromos	6.4
35	410273	BE326877	Hs.281523	ESTs	6.3
55	434486 454036	AA678816 AA374756	Hs.117142 Hs.93560	ESTs ESTs, Weakly similar to unnamed protein produ	6.3 6.3
	403381	M314130	115.55500	0	6.2
	421308	AA687322	Hs.192843	ESTs	6.2
	419346	A1830417		gb:wh94d12x1 NCI_CGAP_CLL1 Homo sapiens cDNA	6.2
40	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP038	6.2
	453047	AW023798	Hs.286025	EST ₈	6.2
	442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic,	6.1
	410102	AW248508	Hs.279727	ESTs;	6.1 6.1
45	410004 413335	A1298027 A1613318	Hs.299115 Hs.48442	ESTs ESTs	6.1
45	424945	Al221919	Hs.173438	hypothetical protein FLJ10582	6.1
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	6.1
	451229	AW967707	Hs.48473	ESTs	6.1
60	452641	AW952893	Hs.237825	signal recognition particle 72kD	6.1
50	433172	AB037841	Hs.102652	hypothetical protein ASH1	6.1
	425465	L18964	Hs.1904	protein kinase C; iota	6.1
	437117 423440	AL049256 R25234	Hs.122593 Hs.143434	ESTs contactin 1	6.0 6.0
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.0
55	433252	AB040957	Hs.151343	KIAA1524 protein	6.0
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	6.0
	436954	AA740151	Hs.130425	ESTs	5.9
	436032	AA150797	Hs.109276	latexin protein	5.9
60	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	5.9
UU	444078 418379	BE246919 AA218940	Hs.10290 Hs.137516	U5 snRNP-specific 40 kDa protein (hPrp8-bindi fidgetin-like 1	5.9 5.9
	438081	H49548	Hs.298964	ESTs	5.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	5.8
	450459	Al697193	Hs.299254	ESTs	5.8
65	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3) mRNA	5.8
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced ge	5.8
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.7
	429181	AW979104	Hs.294009	ESTS	5.7
70	454933 456553	BE141714 AA721325	Hs.189058	gb:QV0-HT0101-061099-032-c04 HT0101 Homo sapi ESTs, Weakly similar to cAMP-regulated guanin	5.7 5.7
	430371	D87466	Hs.240112	KIAA0276 protein	5.7
	425371	D49441	Hs.155981	mesothelin	5.7
	424513	BE385864	Hs.149894	mitochondriat transtational initiation factor	5.6
75	432015	AL157504	Hs.159115	ESTs	5.6
75	438109	A1076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN ALU SU	5.6
	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic teukemia viral	5.6
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypeptide	5.6 5.8
	416565 417830	AW000960 AW504786	Hs.44970 Hs.132808	ESTs epithelial cell transforming sequence 2 oncog	5.8 5.5
80	417830	AA249573	Hs.152618	ESTs	5.5
-0	422093	AF151852	Hs.111449	CGI-94 protein	5.5
	424583	AF017445	Hs.150926	fucose-1-phosphate guanylythransferase	5.5
	430388	AA356923	Hs.240770	nuclear cap blinding protein subunit 2, 20kD	5.5
	452534	AW083022	Hs.149425	Homo septens cONA FLJ11980 fis, clone HEMBB10	5.5

	452270	A14/002040	11- 50000	TOT-	
	453279 424188	AW893940 AW954552	Hs.59698 Hs.142634	ESTs	5.5 5.5
	453884	AA355925	Hs.36232	KIAA0185 gene product	5.5
_	424641	AB001106	Hs.151413	glia maturation factor, beta	5.5
5	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.5
	427975	AI536065	Hs.122460	ESTs	5.5
	424620	AA101043	Hs.151254	kalikrein 7 (chymotryptic; stratum comeum)	5.5
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y79AA10	5.5
10	417995 418946	AW974175 AI798841	Hs.188751 Hs.132103	ESTs ESTs	5.4 5.4
10	419963	AA743276	Hs.301052	ESTs	5.4
	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.4
	422670	AA371612	Hs.115351	ESTs	5.4
	432837	AA310693	Hs.279512	HSPC072 protein	5.4
15	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.4
	458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) fus	5.4
	425217 422938	AU076696 NM_001809	Hs.155174 Hs.1594	CDC5 (cell division cycle 5, S. pombe, homolo centromere protein A (17kD)	5.4 5.4
	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial COS [C.elegan	5.4
20	438279	AA805166	Hs.165165	ESTs, Moderately similar to ALUS_HUMAN ALU SU	5.4
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.3
	420328	Y19062	Hs.96870	staufan (Drosophila, RNA-binding protein) hom	5.3
	436586	A1308862	Hs.167028	ESTs	5.3
25	435793	AB037734	Hs.4993	ESTs .	5.3
23	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	5.3
	425154 453293	NM_001851 AA382267	Hs.154850 Hs.10653	collagen, type IX, alpha 1 ESTs	5.2 5.2
	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.2
	434891	AA814309	Hs.123583	ESTs	5.2
30	415263	AA948033	Hs.130853	ESTs	5.2
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	5.2
	412848	AA121514	Hs.70832	ESTs	5.2
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pro	5.2
35	431548 412719	AI834273 AW016610	Hs.9711 Hs.129911	Homo saplens cDNA FLJ13018 fis, clone NT2RP30 ESTs	5.2 5.2
33	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	5.1
	424078	AB006625	Hs.139033	paternally expressed gene 3	5.1
	433558	AA833757	Hs.201769	ESTs	5.1
40	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone LNG070	5.1
40	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	5.1
	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic protein receptor	5.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	5.1 5.0
	432358 409731	Al093491 AA125985	Hs.72830 Hs.56145	ESTs thymosin, beta, identified in neuroblastoma c	5.0 5.0
45	419699	AA248998	Hs.31246	ESTs	5.0
.,0	420313	AB023230	Hs.96427	KIAA1013 protein	5.0
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell deat	5.0
	425733	F13287	Hs.159388	Homo saptens clone 23578 mRNA sequence	5.0
50	434160	BE551196	Hs.114275	ESTs	5.0
50	435094	Al560129	Hs.277523	EST	5.0 5.0
	436812 432415	AW298067 T16971	Hs.289014	gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Ho ESTs	4.9
	406117	1103/1	113.203014	0	4.9
	438018	AK001160	Hs.5999	hypothetical protein FLJ 10298	4.9
55	447505	AL049268	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	4.9
	448621	A1097144	Hs.5250	ESTs, Weakly similar to BACR37P7.g (D.melanog	4.9
	453001	AW131636	Hs.191260	ESTs	4.9
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	4.9
60	418811 436754	AK001407 Al061288	Hs.88663 Hs.133437	hypothetical protein FLJ10545 ESTs, Moderately similar to gonadotropin indu	4.9 4.8
00	437212	A1765021	Hs.210775	ESTs	4.8
	447312	AJ434345	Hs.36908	activating transcription factor 1	4.8
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
c=	434690	A1867679	Hs.148410	ESTs	4.8
65	444172	BE147740	Hs.104558	ESTs	4.8
	424539	L02911	Hs.150402	activin A receptor, type I	4.8
	418677 406076	S83308 AL390179	Hs.87224 Hs.137011	SRY (sex determining region Y)-box 5 Homo saplens mRNA; cDNA DKFZp547P134 (from cl	4.8 4.8
	420179	N74530	Hs.21168	ESTs	4.7
70	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.7
	420850	BE139590	Hs.122406	ESTs	4.7
	425420	BE536911	Hs.234545	ESTs	4.7
75	428664	AK001656	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.7
13	419131 422278	AA406293 AF072873	Hs.301622 Hs.114218	ESTs ESTs	4.7 4.7
	422278 451684	AF216751	Hs.26813	CDA14	4.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR/MRP)	4.6
	408425	AW058674	Hs.44787	Homo saplens mRNA; cDNA DKFZp43400227 (from c	4.6
80	417168	AL133117	Hs.81376	Homo saptens mRNA; cDNA DKFZp586L1121 (from c	4.6
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	4.6
	442917	AA314907	Hs.85950	ESTs	4.6
	443268 452795	AJ800271 AW392555	Hs.129445 Hs.18878	hypothetical protein FLJ12496 hypothetical protein FLJ21620	4.6 4.6
	732133	A11032000	110,10070	, in production provides a services	7.0

	457300 459551	AW297436 AI472808	Hs.158849	Homo saptens cDNA: FLJ21663 fs, clone COL088 gb:t[70e07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom	4.6 4.6
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.6
5	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	4.6
5	449722 431689	BE280074	Hs.23960	cyclin B1	4.6 4.5
	425178	AA305688 H16097	Hs.267695 Hs.161027	UDP-Gal:betaGicNAc beta 1,3-galactosyltransfe ESTs	4.5
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	4.5
	436556	Al364997	Hs.7572	EST8	4.5
10	400534			0	4.5
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.5
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium d	4.5
	448305	AA625207	Hs.264915	Homo saplens cDNA FLJ12908 fis, done NT2RP20	4.5
	441006	AW605267	Hs.7627	OGI-60 protein	4.5
15	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	4.5
	447924	AI817226	Hs.170337	ESTs	4.5
	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (JEM-1)	4.5
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	. 4.4
20	432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.4
20	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	4.4
	414699	AIB15523	Hs.76930	synuclein, alpha (non A4 component of amyloid	4.4
	412733	AA984472	Hs.74554	KIAA0080 protein	4.4 4.4
	419790 433377	U79250 AI752713	Hs.93201 Hs.43845	glycerol-3-phosphate dehydrogenase 2 (mitocho ESTs	4.4
25	449535	W15267	Hs.23672	low density lipoprotein receptor-related prot	4.4
23	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAM	4.4
	443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	4.4
	423025	AA831267	Hs.12244	Homo saplens cDNA: FLJ23581 fis, clone LNG136	4.4
	408621	Al970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	4.3
30	416241	N52639	Hs.32683	ESTs	4.3
•	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYME	4.3
	435532	AW291488	Hs.117305	ESTs	4.3
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.3
	454193	8E141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo sapl	4.3
35	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	4.3
	406069			0	4.3
	419465	AW500239	Hs.21187	Homo saplens cDNA: FL123068 fis, clone LNG055	4.3
	418413	R95735	Hs.117753	ESTs, Weakly similar to antigen of the monod	4.3
40	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	4.3
40	418693	AI750878	Hs.87409	thrombospondin 1	4.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.2
	409763	AL043212	11a 04C	gb:DKFZp434H0623_r1 434 (synonym: htes3) Homo	4.2
	455601	Al368680	Hs.816	SRY (sex determining region Y)-box 2, partial	4.2
45	408908	BE296227	Hs.48915	serine/threonine kinase 15	4.2 4.2
72	413582 423248	AW295647 AA380177	Hs.71331 Hs.125845	Homo sapiens cDNA: FLJ21971 fis, clone HEP057 ribulose-5-phosphale-3-epimerase	4.2
	425024	R39235	Hs.12407	ESTs	4.2
	447153	AA805202	Hs.173912	eukeryotic translation initiation factor 4A,	4.2
	447406	BE618060	Hs.282882	ESTs	4.2
50	449347	AV649748	Hs.295901	ESTs	4.2
•	414279	AW021691	Hs.3804	DKFZP564C1940 protein	4.2
	428856	AA436735	Hs.183171	Homo saptens cDNA: FLJ22002 fis, clone HEP066	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	4.2
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	4.2
55	436406	AW105723	Hs.125346	ESTs	4.2
	438209	AL120659	Hs.6111	KIAA0307 gene product	4.2
	443653	AA137043	Hs.9663	programmed cell death 6-interacting protein	4.1
	454556	AW807073		gb:MR4-ST0062-031199-018-d06 ST0062 Homo sapi	4.1
60	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	4.1 4.1
UU	412593	Y07558	Hs.74088	early growth response 3	
	416566 426342	NM_003914	Hs.79378 Hs.169378	cyclin A1 multiple PDZ domain protein	4.1 4.1
	428417	AF093419	Hs.184227	F-box only protein 21	4.1
	429317	AK001699 AA831552	Hs.268016	solute carrier family 5 (Inosito) transporter	4.1
65	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT2RM40	4.1
05	422988	AW873847	Hs.97321	ESTs	4.0
	434657	AA641876	Hs.191840	ESTs	4.0
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1, 64k	4.0
•	443271	BE568568	Hs.195704	ESTs	4.0
70	421437	AW821252	Hs.104336	ESTs	4.0
	401644			0	4.0
	405095			0	4.0
	418417	R77182		gb:yi65e02.r1 Soares placenta Nb2HP Homo sapi	4.0
7.	420807	AA280627	Hs.57846	ESTs	4.0
75	429529	AA454190	Hs.193811	ESTs, Moderately similar to reduced expressio	4.0
	457726	Al217477	Hs.194591	ESTs	4.0
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	4.0
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PLACE10	4.0
0Λ	442768	AL048534	Hs.48458	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.0
80	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT2RP30	4.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0 4.0
	425692	D90041 Al077715	Hs.155956 Hs.39384	NAT1; arylamine N-acetyltransferase putative secreted ligand homologous to fix1	4.0
	407792 408353	BE439838	Hs.44298	hypothetical protein	4.0
	10000			·	

	421175	Al879099	Hs.102397	GIOT-3 for gonadotroph inducible transcripti	3.9
	420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	3.9
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	3.9
_	458924	BE242158	Hs.24427	DKFZP56601646 protein	3.9
5	400195			0	3.9
	401480			0	3.9
	410360	AW663690		gb:hj21g03.x1 NCI_CGAP_Li8 Homo saplens cDNA	3.9
	410908	AA121688	Hs.10592	ESTs	3.9
	420159	Al572490	Hs.99785	ESTs	3.9
10	422805	AA436989	Hs.121017	H2A histone family; member A	3.9
•	424639	Al917494	Hs.131329	ESTs	3.9
					3.9
	428555	NM_002214	Hs.184908	Integrin, beta 8	
	431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis, clone NT2RP20	3.9
15	433703	AA210863	Hs.3532	nemo-like kinase	3.9
15	437144	AL049466	Hs.7859	ESTs	3.9
	452728	AI915676	Hs.239708	ESTs	3.9
	430447	W17064	Hs.241451	SWI/SNF related, matrix associated, actin dep	3.9
	440594	AW445167	Hs.126036	ESTs	3.9
	408938	AA059013	Hs.22607	ESTs	3.9
20	427051	BE178110	Hs.173374	ESTs	3.9
	447568	AF155655	Hs.18885	CGI-116 protein	3.9
	457211	AW972565	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP I	3.9
	443475	A1066470	Hs.134482	ESTs	3.9
					3.9
25	433447	U29195	Hs.3281	neuronal pentraxin il	
25	428093	AW594506	Hs.104830	ESTs	3.8
	437938	A1950087		ESTs; Weakly similar to Gag-Pol polyprotein [3.8
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	3.8
	429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
	441859	AW194364	Hs.128022	ESTs, Wealty similar to FIG1 MOUSE FIG-1 PROT	3.8
30	437700	AA766060	Hs.122848	ESTs	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.8
	429474	AA453441	Hs.31511	ESTs	3.8
	431965	8E175190	110.01011	gb:QV2-HT0577-010500-165-g04 HT0577 Homo sapl	3.8
35			U- 2410F2		
"	454018	AW016892	Hs.241652	EST8	3.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.8
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone HSI156	3.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisiae	3.8
40	446402	Al681145	Hs.160724	ESTs	3.8
40	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxi	3.8
	400268			0	3.8
	418217	Al910647	Hs.13442	ESTs	3.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	3.8
45					3.8
73	417300	Al765227	Hs.55610	solute carrier family 30 (zinc transporter),.	
	414136	AA812434	Hs.178227	ESTs	3.8
	453945	NM_005171	Hs.36908	activating transcription factor 1	3.7
	400240			0	3.7
	407877	AW016811	Hs.234478	Homo sepiens cDNA: FLJ22648 fis, clone HSI073	3.7
50	450581	AF081513	Hs.25195	endometrial bleeding associated factor (left-	3.7
	418223	NM_014733	Hs.83790	KIAA0305 gene product	3.7
	411704	Al499220	Hs.71573	hypothetical protein FLJ10074	3.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta-5-de	3.7
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.7
55	402820	74001073	IMITETOLO	0	3.7
55		00472004	Hs.292478	ESTs	3.7
	408090	BE173621			
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor 4E	3.7
	418282	AA215535	Hs.98133	ESTs	3.7
60	418454	AA315308		gb:EST187095 Colon carcinoma (HCC) cell line	3.7
60	418668	AW407987	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repeat-con	3.7
	422290	AA495854	Hs.48827	hypothetical protein FLJ12085	3.7
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	3.7
	439907	AA853978	Hs. 124577	ESTs	3.7
	447479	AB037834	Hs.18685	Homo saplens mRNA for KIAA1413 protein, parti	3.7
65	451073	AJ758905	Hs.206063	EST8	3.7
05		AB033091		ESTs	3.7
	450377		Hs.24936		3.7
	414343	AL036166	Hs.75914	coated vesicle membrane protein	
	448807	AI571940	Hs.7549	ESTs	3.7
70	442821	BE391929	Hs.8752	Putative type II membrane protein	3.7
70	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	3.7
	418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	3.7
	411263	BE297802	Hs.69360	kinesin-like 6 (mitatic centromere-associated	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, done PLACE10	3.7
75	411402	8E297855	Hs.69855	NRAS-related gene	. 3.7
, ,					3.6
	450447	AF212223	Hs.25010	hypothetical protein P15-2	
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.6
	434228	Z42047	Hs.283978	ESTs; KIAA0738 gene product	3.6
00	434164	AW207019	Hs.148135	ESTs	3.6
80	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase kinas	3.6
	402222			. 0	.3.6
	404915			Ö	3.6
	404996			Ö	3.6
	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo sapi	3.6
	71.500			, governous contract of the attention of the	

	419750				
	413130	AL079741	Lb. 403444	Homo saptens cDNA FLJ14236 fis, clone NT2RP40	3.6
	420040		Hs.183114		
	426010	AA136563	Hs.1975	Homo saptens cDNA: FLJ21007 fis, clone CAE038	3.6
	427038	NM_014633	Hs.173288	KIAA0155 gene product	3.6
	439255	BE164500		gb:RC4-HT0469-230300-014-e10 HT0469 Homo sapl	3.6
5	458242	BE299588	Hs.28465	Homo saplens cDNA: FLJ21869 fis, clone HEP024	3.6
-					
	415115	AA214228	Hs.127751	hypothetical protein	3.6
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.6
	441205	AW137827	Hs.176904	EST8	3.6
	452693	T79153	Hs.48589	zinc finger protein 228 .	3.6
10					
10	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2)	3.6
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	3.6
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.6
	440048	AA897451	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	3.5
1.5	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)-like	3.5
15	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from c	3.5
	400666			0	3.5
		1107002	Hs.151380	ESTs	
	422646	H87863			3.5
	407846	AA426202	Hs.40403	Cbp/p300-Interacting transactivator, with Glu	3.5
	408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.5
20	401517			0	3.5
		A14/400024	Hs.75528	7	3.5
	413775	AW409934		nucleolar GTPase	
	417177	NM_004458	Hs.81452	falty-acid-Coenzyme A ligase, long-chain 4	3.5
	427943	AW959075		gb:EST371145 MAGE resequences, MAGE Homo sapi	3.5
	439107	AL046134	Hs.27895	ESTs	3.5
25					
	447268	Al370413	Hs.36563	Homo sapians cDNA: FLJ22418 fis, clone HRC085	3.5
	412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.5
	427134	AA398409	Hs.173561	EST	3.5
	430273	AJ311127	Hs.125522	ESTs	3.5
20	436671	AW137159	Hs.146151	ESTa	3.5
30	433037	NM_014158	Hs.279938	HSPC067 protein	3.5
	453745	AA952989	Hs.63908	Homo saplens HSPC316 mRNA, partial cds	3.5
		AF151064			
	400531		Hs.36069	hypothetical protein	3.5
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	3.4
	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	3.4
35	407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen 1NFLS	3.4
50			11- 40000		
	453779	N35187	Hs.43388	ESTs	3.4
	444858	AJ199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	3.4
	447688	N87079	Hs.19236	NADH dehydrogenase (ublquinone) 1 beta subcom	3.4
	424856	AA347746	Hs.9521	ESTs, Weakly similar to KIAA1015 protein [H.s	3.4
40					
40	407854	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.4
	404108			0	3.4
	403729			0	3.4
	404232			Ŏ	3.4
				-	
40	423687	AA329633	Hs.133011	ESTs, Highly similar to Z117_HUMAN ZINC FINGE	3.4
45	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	3.4
	439741	BE379646	Hs.6904	Homo saplens mRNA full length insert cDNA clo	3.4
	700/71				0.4
	444447	4 4 00 4077			2.4
	441447	AA934077	Hs.126980	EST8	3.4
	441447 448358	AA934077 R44433	Hs.126980 Hs.106614	ESTs Human DNA sequence from clone RP4-534K7 on ch	3.4 3.4
	448358	R44433	Hs.106614	Human DNA sequence from clone RP4-534K7 on ch	3.4
50	448358 450926	R44433 AI744361	Hs.106614 Hs.205591	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P	3.4 3.4
50	448358 450926 458477	R44433 AI744361 NM_000314	Hs.106614 Hs.205591 Hs.10712	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu	3.4 3.4 3.4
50	448358 450926	R44433 AJ744361 NM_000314 Y15221	Hs.106614 Hs.205591 Hs.10712 Hs.103982	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C	3.4 3.4 3.4 3.4
50	448358 450926 458477	R44433 AI744361 NM_000314	Hs.106614 Hs.205591 Hs.10712	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu	3.4 3.4 3.4
50	448358 450926 458477 421379 452822	R44433 AJ744361 NM_000314 Y15221 X85689	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HS1056	3.4 3.4 3.4 3.4 3.4
50	448358 450926 458477 421379 452822 441111	R44433 AI744361 NM_000314 Y15221 X85689 AI806867	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HS1056 ESTs	3.4 3.4 3.4 3.4 3.4
	448358 450926 458477 421379 452822 441111 447519	R44433 AI744361 NM_000314 Y15221 X85689 AI806867 U46258	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensih homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HS1056 ESTs	3.4 3.4 3.4 3.4 3.4 3.4
50 55	448358 450926 458477 421379 452822 441111 447519 446913	R44433 AI744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.16529	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Oys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan	3.4 3.4 3.4 3.4 3.4 3.4 3.4
	448358 450926 458477 421379 452822 441111 447519	R44433 AI744361 NM_000314 Y15221 X85689 AI806867 U46258	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensih homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HS1056 ESTs	3.4 3.4 3.4 3.4 3.4 3.4
	448358 450926 458477 421379 452822 441111 447519 446913 449581	R44433 AI744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AI989517	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.16529 Hs.181605	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HS1056 ESTs ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4
	448358 450926 458477 421379 452822 441111 447519 446913 449581 456132	R44433 AI744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AI989517 BE219771	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.23448 Hs.16529 Hs.181605 Hs.237146	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ/2621 fis, clone HS1056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ/4234 fis, clone NT2RP40	3.4 3.4 3.4 3.4 3.4 . 3.4 3.4 3.4
	448358 450926 458477 421379 452822 441111 447519 446913 449581 456132 448186	R44433 AJ744361 NM_000314 Y15221 X85689 AJ806867 U46258 AA430650 AJ989517 BE219771 AA262105	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14208 fis, clone NT2RP30	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55	448358 450926 458477 421379 452822 441111 447519 446913 446913 456132 448186 422611	R44433 AJ744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AJ89517 BE219771 AA262105 AA158177	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (alpha 11,5) fucosyltran	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
	448358 450926 458477 421379 452822 441111 447519 446913 449581 456132 448186	R44433 AJ744361 NM_000314 Y15221 X85689 AJ806867 U46258 AA430650 AJ989517 BE219771 AA262105	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14208 fis, clone NT2RP30	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55	448358 450926 458477 421379 452822 441111 447519 446913 449581 456132 448186 422611 441433	R44433 AJ744361 NM_000314 Y15221 X85689 AJ806867 U46258 AA430650 AJ989517 BE219771 AA262105 AA158177 AA33809	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 tucosyltransferase 8 (atpha 1,6) fucosyltran ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55	448358 450926 458477 421379 452822 441111 447519 446913 449581 456132 448186 422611 441433 417837	R44433 AJ744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AJ989517 BE219771 AA262105 AA158177 AA333809 AL079905	Hs.106614 Hs.205591 Hs.10712 Hs.10382 Hs.288617 Hs.126594 Hs.23448 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1103	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphalase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 tucosyltransferase 8 (atpha (1,5) fucosyltran ESTs transforming growth factor, beta 1	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55	448358 450926 458477 421379 452822 441111 447519 449513 449581 456132 448186 422611 441433 417837 450516	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430550 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.4094 Hs.118722 Hs.42746 Hs.42746 Hs.421943	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Oys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (etpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55	448358 450926 458477 421379 452822 441111 447519 446913 449581 456132 448186 422611 441433 417837 450516 407795	R44433 AJ744361 NM_000314 Y15221 X85689 AJ806867 U46258 AA430650 AJ989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA902656 AA195509	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP40 Homo sapiens cDNA FLJ14208 fis, clone NT2RP30 (tucosyltransferase 8 (spha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 Interacting factor 3, S.pombe homo lymphocyte activation-associated protein	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55 60	448358 450926 458477 421379 452822 441111 447519 449513 449581 456132 448186 422611 441433 417837 450516	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430550 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.4094 Hs.118722 Hs.42746 Hs.42746 Hs.421943	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Oys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (etpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55 60	448358 450926 458472 421379 452822 441111 447513 449581 455132 448183 422611 441433 417837 450516 407795 419200	R44433 AJ744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AJ989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA90256 AA9125509 AV966405	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.418722 Hs.41103 Hs.21943 Hs.272239 Hs.288856	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HS1056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NTZRP40 Homo sapiens cDNA FLJ14234 fis, clone NTZRP30 fucosyltransferase 8 (atpha 1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pormbe homo lymphocyte activation-associated protein prefoldin 5	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55	448358 450926 458477 421379 452822 441111 445913 445913 445913 445913 445913 44513 44186 422611 44143 417837 450516 407793 419200 423161	R44433 A1744361 NM_000314 Y15221 X85689 AI866867 U46258 AA430650 AI989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AW966405 AL049227	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.21943 Hs.21943 Hs.21943 Hs.21943 Hs.21943 Hs.2283856	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (atpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NiF3 (Ngg1 interacting factor 3, S. pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55 60	448358 450926 421379 421379 452822 441111 447519 446913 449581 456132 441433 417837 450516 407795 419200 423161 445579	R44433 A1744361 NM_000314 Y15221 X85689 A1806667 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333009 AL079905 AA933809 AV966405 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.272239 Hs.272239 Hs.28856 Hs.124776 Hs.58800	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (atpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems mRNA; cDNA DKFZp564N1116 (from c Homo septems cDNA FLJ12488 fis, clone NT2RM20	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55 60	448358 450926 421379 421379 452822 441111 447519 449513 449513 449513 441433 417437 450516 407795 419200 423161 445679 435014	R44433 AJ744361 NM_000314 Y15221 X85689 AJ806867 U46258 AA430650 AJ99517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA195509 AW966405 AJ49227 AJ343868 BE560898	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.181605 Hs.237146 Hs.18722 Hs.42746 Hs.1103 Hs.21943 Hs.21943 Hs.21943 Hs.21943 Hs.218756 Hs.124776 Hs.124776	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (atpha 11,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 floosomal protein L17 Isolog	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
55 60	448358 450926 421379 421379 452822 441111 447519 446913 449581 456132 441433 417837 450516 407795 419200 423161 445579	R44433 A1744361 NM_000314 Y15221 X85689 A1806667 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333009 AL079905 AA933809 AV966405 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227 AL049227	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.272239 Hs.272239 Hs.28856 Hs.124776 Hs.58800	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (atpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems mRNA; cDNA DKFZp564N1116 (from c Homo septems cDNA FLJ12488 fis, clone NT2RM20	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4
556065	448358 450926 458477 421379 452822 441111 447519 446913 449513 449513 449186 422611 441433 417837 450516 407726 419200 423161 445579 435571 446619	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AW966405 AL049227 AI343888 BE560838 AL076643	Hs. 106614 Hs. 205591 Hs. 10712 Hs. 103982 Hs. 288617 Hs. 126594 Hs. 26594 Hs. 16529 Hs. 181605 Hs. 237146 Hs. 4094 Hs. 118722 Hs. 42746 Hs. 1103 Hs. 21943 Hs. 272239 Hs. 288856 Hs. 124776 Hs. 58800 Hs. 10026 Hs. 313	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 tucosyltransferase 8 (atpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pornbe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
556065	448358 450926 458477 421379 452822 441111 445581 456132 448186 422611 441433 417837 450516 407795 419200 423161 445579 435014 446619 43619 439170	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430550 A1989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AW966405 AL049227 AL04927	Hs.106614 Hs.205591 Hs.103982 Hs.126594 Hs.126594 Hs.16529 Hs.181605 Hs.4094 Hs.118722 Hs.42746 Hs.21943 Hs.21943 Hs.21943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.3165539	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Oys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetrespan ESTs Homo sepiens cDNA FLJ14234 fis, clone NT2RP40 Homo sepiens cDNA FLJ14238 fis, clone NT2RP40 Homo sepiens cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (etpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sepiens mRNA; cDNA DKFZp564N1116 (from c Homo sepiens cDNA FLJ12488 fis, clone NT2RM20 fibosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55 60	448358 4509277 421379 452822 441111 447519 446913 449581 456132 448185 422611 441433 417837 450516 407795 419200 423161 445679 435014 446619 439170 429830	R44433 AJ744361 NM_000314 Y15221 X85689 AI806667 U46258 AA430650 AI99517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA195509 AW966405 AL049227 AJ343868 BE560898 AU076643 AA332265 AL37278	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.272239 Hs.28856 Hs.124776 Hs.28856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.165539 Hs.165539 Hs.1655539	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase B (alpha (1,5) fucosyltran ESTs transforming growth factor, bela 1 NIF3 (Ngg1 Interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP343D193 protein	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
556065	448358 450926 458477 421379 452822 441117 447519 446913 445613 445613 448186 422611 441433 417837 450516 407795 418200 423161 445619 439170 429830 429830 429833	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA195509 AW866405 AL049227 AI343388 BE560898 AL076643 AA322365 AL976643 AA322365 AL976643 AA322365 AL976643 AA322365 AL976643 AA322365	Hs.106614 Hs.205591 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239 Hs.288366 Hs.58800 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.2753841 Hs.37636	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphalase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14236 fis, clone NT2RP30 tucosyltransferase 8 (alpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 Interacting factor 3, S. pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens cDNA FLJ12486 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s.	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
556065	448358 4509277 421379 452822 441111 447519 446913 449581 456132 448185 422611 441433 417837 450516 407795 419200 423161 445679 435014 446619 439170 429830	R44433 AJ744361 NM_000314 Y15221 X85689 AI806667 U46258 AA430650 AI99517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA195509 AW966405 AL049227 AJ343868 BE560898 AU076643 AA332265 AL37278	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.272239 Hs.28856 Hs.124776 Hs.28856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.165539 Hs.165539 Hs.1655539	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase B (alpha (1,5) fucosyltran ESTs transforming growth factor, bela 1 NIF3 (Ngg1 Interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP343D193 protein	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
556065	448358 450926 458477 421379 452822 441111 445581 455132 448186 422611 44183 47583 417837 450516 407793 417837 450516 445679 435014 446619 439170 42843 42843 428830 428830 428831 44817	R44433 A1744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AI989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AW966405 AL049227 AI343868 BE560898 AL076643 AA332365 AL537278 AW96643 AL076643 AA332365 AL076643 AM3086180 NM_003642	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1172239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.10026 Hs.10026 Hs.105339 Hs.25841 Hs.37636 Hs.37636 Hs.37636	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,6) fucosyltran ESTs transfaming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens mRNA; cDNA DKFZp564N1116 (from c Homo sapiens mRNA; cDNA DKFZp564N1116 (from c Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs Weakly similar to KIAA1392 protein [H.s histone acetyltransferase 1	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
556065	448358 450926 450926 421379 452822 441111 447519 446913 449581 456132 448186 422611 441433 417837 450516 407795 419200 423161 445579 435014 44667 435014 44687 436917 436943 446943 446943 446943 446943 446943 446943 446943	R44433 A1744361 NM_000314 Y15221 X85689 A186667 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA195509 AW966405 AL049227 AI343868 BE560898 ALW576643 AA332365 AI537278 AW085180 NM_003642 H69912	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.27146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.27538 Hs.27538 Hs.27538 Hs.37636 Hs.313340 Hs.37636 Hs.37636 Hs.37636 Hs.37636 Hs.37636 Hs.37636 Hs.37636 Hs.37636 Hs.37636 Hs.37636	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sepiens cDNA FLJ14234 fis, clone NT2RP40 Homo sepiens cDNA FLJ14238 fis, clone NT2RP40 Homo sepiens cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF5 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sepiens cDNA FLJ12488 fis, clone NT2RM20 floosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone soelyltransferase 1 vaccinia related kinase 1	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55606570	448358 450926 458477 421379 452822 441111 447519 449513 449581 456132 448186 422611 441433 417837 450516 407795 419200 423161 435619 435619 436170 42830 42830 42830 42830 42830 42830 42830 42830 44817 408805 441134	R44433 AJ744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AI989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AW966405 AL04227 AJ343868 BE560898 AL076643 AA32365 AL076643 AA32365 AL0766405 BE560898 AL076643 AL0	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.272239 Hs.28856 Hs.124776 Hs.28856 Hs.124776 Hs.313 Hs.165539 Hs.258841 Hs.37636 Hs.37636 Hs.3340 Hs.48269 Hs.48269 Hs.7678	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14236 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,5) fucosyltran ESTs transforming growth factor, bela 1 NIF3 (Ngg1 Interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAAA1392 protein [H.s histone acetyltransferase 1 vaocintia related kinase 1 cellutar retinole acid-binding protein 1	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
556065	448358 450926 450926 421379 452822 441111 447519 446913 449581 456132 448186 422611 441433 417837 450516 407795 419200 423161 445579 435014 44667 435014 44687 436917 436943 446943 446943 446943 446943 446943 446943 446943	R44433 A1744361 NM_000314 Y15221 X85689 A186667 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA195509 AW966405 AL049227 AI343868 BE560898 ALW576643 AA332365 AI537278 AW085180 NM_003642 H69912	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.41103 Hs.21943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.165539 Hs.25841 Hs.37636 Hs.13340 Hs.48269 Hs.13340 Hs.48269 Hs.7678 Hs.63176	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sepiens cDNA FLJ14234 fis, clone NT2RP40 Homo sepiens cDNA FLJ14238 fis, clone NT2RP40 Homo sepiens cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF5 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sepiens cDNA FLJ12488 fis, clone NT2RM20 floosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone soelyltransferase 1 vaccinia related kinase 1	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55606570	448358 450926 458477 421379 452822 441111 446913 445913 445913 445913 445913 445913 456132 42611 441433 417837 450516 407725 419200 423161 445679 435071 445679 435071 445679 435071 445679 435071 445679 435071 445679 435071 445679 445	R44433 A1744361 NM_000314 Y15221 X85689 AI806867 U46258 AA430650 AI99517 BE219771 AA262105 AA158177 AA933809 ALD79905 AA902656 AA195509 ALD49227 AI343868 BE560898 ALD76643 AA32265 AI557278 AV966405 ALD49227 AI343868 BE560898 ALD76643 AA32265 ALD49227 AI34386180 NM_003642 H69912 W29092 AI453137	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.41103 Hs.21943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.165539 Hs.25841 Hs.37636 Hs.13340 Hs.48269 Hs.13340 Hs.48269 Hs.7678 Hs.63176	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP40 Homo sapiens cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (atpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein perfoldin 5 Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acetylfransferase 1 vaocinia related kinase 1 celtuter retinoic acid-binding protein 1 ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55606570	448358 450926 458477 421379 452822 441111 445513 445518 425611 44143 450516 407793 417807 425161 445619 43517 43517 436517 436517 436517 408805 441134 408532 409517	R44433 A1744361 NM_000314 Y15221 X85689 AI866867 U46258 AA430650 AI989517 BE219771 AA262105 AA158177 AA93809 AL079905 AA902656 AA195509 AW966405 AL049227 AI343868 BE56089 AU976643 AA332365 AL537278 AW966180 NM_003642 H69912 W29092 AL453137 X90780	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.23448 Hs.16529 Hs.181605 Hs.24746 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.10026 Hs.313 Hs.255841 Hs.37636 Hs.37636 Hs.37636 Hs.37636 Hs.46269 Hs.46269 Hs.63176 Hs.63176 Hs.63176 Hs.63176 Hs.63176	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (etpha (1,6) fucosyltran ESTs Transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 flosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acetyltransferase 1 vaccinia related kinase 1 celtudar retincle acid-binding protein 1 ESTs troponin I, cardiac	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55606570	448358 450926 421379 421379 452822 441111 447519 446913 449581 456136 422611 441433 417837 450516 407795 419200 423161 445679 435014 446679 435014 446834 445879 435014 446834 445879 435014 446833 44683 44683 46	R44433 A1744361 NM_000314 Y15221 X85689 Al806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA02656 AA195509 AW966405 AL049227 AL343868 BE560898 ALW76643 AA342365 AL537278 AW085180 NM_003642 H59912 W29092 AL53137 X90780 AL621276	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.27146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239 Hs.28856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.255841 Hs.37636 Hs.165539 Hs.25841 Hs.37636 Hs.165539 Hs.26668 Hs.16767 Hs.56668 Hs.56668 Hs.56668 Hs.165998	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP40 Homo septems cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems mRNA; cDNA DKFZp564N1116 (from c Homo septems cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acelytiransferase 1 vaccinia related kinase 1 celtutar retinoic acid-binding protein 1 ESTs troporin I, cardiac DKFZP564M2423 protein	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55606570	448358 450926 458477 421379 452822 441111 447519 446913 445613 445613 448186 422611 441433 417837 450516 407756 418200 423161 446619 439170 428830 449817 408532 449817 408532 409517 41834 408532 409517 41834 408532 409517 41834 436427	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA902656 AA195509 AW866405 AL049227 AI343388 BE560898 AL076643 AA32265 AL056180 NM_003642 H69912 W29092 A453137 X90780 AI621276 AI344378	Hs. 106614 Hs. 205591 Hs. 103982 Hs. 288617 Hs. 126594 Hs. 16529 Hs. 181605 Hs. 237146 Hs. 4094 Hs. 118722 Hs. 427746 Hs. 1103 Hs. 21943 Hs. 272239 Hs. 288856 Hs. 124776 Hs. 58800 Hs. 10026 Hs. 313 Hs. 165539 Hs. 225841 Hs. 37636 Hs. 13340 Hs. 48269 Hs. 48269 Hs. 463176 Hs. 56668 Hs. 165998 Hs. 165999	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphalase and tensh homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 tucosyltransferase 8 (alpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S. pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens cDNA FLJ12486 fis, clone NT2RM20 rhosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [HLs histone acelytransferase 1 vaocinia related kinase 1 cellutar refincic acid-binding protein 1 ESTs tropontin 1, cardiac DKFZP564M2423 protein ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
5560657075	448358 450926 421379 421379 452822 441111 447519 446913 449581 456136 422611 441433 417837 450516 407795 419200 423161 445679 435014 446679 435014 446834 445879 435014 446834 445879 435014 446833 44683 44683 46	R44433 A1744361 NM_000314 Y15221 X85689 Al806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA02656 AA195509 AW966405 AL049227 AL343868 BE560898 ALW76643 AA342365 AL537278 AW085180 NM_003642 H59912 W29092 AL53137 X90780 AL621276	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.27146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239 Hs.28856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.255841 Hs.37636 Hs.165539 Hs.25841 Hs.37636 Hs.165539 Hs.26668 Hs.16767 Hs.56668 Hs.56668 Hs.56668 Hs.165998	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP40 Homo septems cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems mRNA; cDNA DKFZp564N1116 (from c Homo septems cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acelytiransferase 1 vaccinia related kinase 1 celtutar retinoic acid-binding protein 1 ESTs troporin I, cardiac DKFZP564M2423 protein	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
5560657075	448358 450926 458477 421379 452822 441111 445913 445913 445913 445913 445913 445913 445913 445913 445916 445919 435916 445619 435916 445619 435917 445619 435917 445805 441134 446619 445917 44	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AW966405 AL049227 A1343868 BE560898 AL076643 AA332365 AL537278 AW966405 AL049227 A1343868 BE560898 AL076643 AA332365 AL597278 AW966405 AL049227 A1343868 BE560898 AL076643 AA32137278 AW966405 AL049227 AI34337278 AW966405 AL049227 AI34337278 AW966405 AL049227 AI34337278 AW966405 AL049227 AI34337278 AW966405 AI34337278 AW966405 AI343378 AI343378 AI343378 AI343378 AI352393	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.16529 Hs.181605 Hs.4094 Hs.118722 Hs.42746 Hs.118722 Hs.42746 Hs.118723 Hs.21943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.10026 Hs.10026 Hs.13340 Hs.48269 Hs.7678 Hs.665398 Hs.63176 Hs.54668 Hs.165998 Hs.143399 Hs.143399 Hs.143399 Hs.143399 Hs.143399 Hs.126695	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (atpha (1,6) fucosyltran ESTs transfaming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S. pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sapiens mRNA; cDNA DKFZp564N1116 (from c Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [HLs histone acetyltransferase 1 vaocinia related kinase 1 cellular retinolc acid-binding protein 1 ESTs troporin I, cardiac DKFZP564M2423 protein ESTs ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55606570	448358 450926 421379 421379 452822 441111 446913 446913 446913 445581 456132 448186 422611 441433 417837 450516 407795 419200 423161 445619 435170 428430 42843 441134 40853 41134 4085517 41134 4085517 41134 4085517 41134 4085517 41134 4085662 41304 41304 41304 41304 41304 41304 41304 41304 41304 41304 41304 41304 41304 41304 41304 41304 41306	R44433 A1744361 NM_000314 Y15221 X85689 A1866867 U46258 AA430550 A1989517 BE219771 AA262105 AA158177 AA933809 ALD79905 AA902656 AA195509 AU966405 ALD49227 A1343868 BE560898 AU976643 AA332365 ALS37278 AW065180 NM_003642 H69912 W29092 A453137 X90780 AI621276 A1542333 BE159984	Hs. 106614 Hs. 205591 Hs. 103982 Hs. 288617 Hs. 126594 Hs. 16529 Hs. 181605 Hs. 237146 Hs. 4094 Hs. 118722 Hs. 427746 Hs. 1103 Hs. 21943 Hs. 272239 Hs. 288856 Hs. 124776 Hs. 58800 Hs. 10026 Hs. 313 Hs. 165539 Hs. 225841 Hs. 37636 Hs. 13340 Hs. 48269 Hs. 48269 Hs. 463176 Hs. 56668 Hs. 165998 Hs. 165999	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sepiens cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs transmembrane 4 superfamily member (tetraspan ESTs transmembrane cDNA FLJ14234 fis, clone NT2RP40 Homo sepiens cDNA FLJ14238 fis, clone NT2RP40 Homo sepiens cDNA FLJ14208 fis, clone NT2RP30 fucosyltransferase 8 (etpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo sepiens mRNA; cDNA DKFZp564N1116 (from c Homo sepiens cDNA FLJ12488 fis, clone NT2RM20 fibosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP340193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acelytiransferase 1 vaccinia related kinase 1 cellutar retinole acid-binding protein 1 ESTs troportin 1, cardiac DKFZP564M2423 protein ESTs ESTs ESTs ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
5560657075	448358 450926 421379 421379 452822 441111 447519 446913 449581 456136 441188 422611 441433 417837 450516 407795 419200 423161 445679 435014 446679 439170 429830 429843 44587 41134 408532 409517 41304 436624 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662 443662	R44433 A1744361 NM_000314 Y15221 X85689 Al806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA02656 AA195509 AW966405 AL049227 AL343868 BE560898 ALW76643 AA34378 AW905180 NM_003642 H59912 W29092 AL537278 AW905180 AL621276 AL6212	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.1816059 Hs.1816055 Hs.2371146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239 Hs.28856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.258856 Hs.1340 Hs.37636 Hs.13340 Hs.37636 Hs.13340 Hs.465699 Hs.56668 Hs.54668 Hs.54668 Hs.54668 Hs.54668 Hs.54668 Hs.5466998 Hs.165998 Hs.126695 Hs.125395	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems mRNA; cDNA DKFZp564N1116 (from c Homo septems cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acelytransferase 1 vaocintia related kinase 1 cellutar retinoic acid-binding protein 1 ESTs troporin I, cardiac DKFZP564M2423 protein ESTs ESTs ESTs ESTs ESTs gbtHSC3FE081 normalized infant brain cDNA Hom	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
5560657075	448358 459926 458477 421379 452822 441111 446913 445913 445913 445913 445913 445913 445913 445913 445916 441433 417837 450516 407725 419200 423161 445619 43571 446619 43571 446619 43571 446819 43571 446819 445817 446819	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430550 A1989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AL079905 AA902656 AA195509 AL049227 A1343868 BE560898 AL076643 AA32265 AL049227 A1343861 BUSE00898 AL076643 AA32265 AL076643 AL07	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.41943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.10026 Hs.10026 Hs.1031 Hs.165539 Hs.25841 Hs.37636 Hs.13340 Hs.48269 Hs.65176 Hs.54668 Hs.165998 Hs.126695 Hs.125395 Hs.125395	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (atpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pornbe homo lymphocyte activation-associated protein perfoldin 5 Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acetylfransferase 1 vaocinia related kinase 1 cellutar retinoic acid-binding protein 1 ESTs troporin I, cardiac DKFZP564M2423 protein ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55 60 65 70 75	448358 459926 458477 421379 452822 441111 445581 445581 455132 448186 422611 44183 47581 450516 407793 450516 445679 435014 446619 43517 435014 445619 43517 435014 445619 43517 435014 445619 43517 435014 445619 4	R44433 A1744361 NM_000314 Y15221 X85689 Al806867 U46258 AA430650 A1989517 BE219771 AA262105 AA158177 AA333809 AL079905 AA02656 AA195509 AW966405 AL049227 AL343868 BE560898 ALW76643 AA34378 AW905180 NM_003642 H59912 W29092 AL537278 AW905180 AL621276 AL6212	Hs.106614 Hs.205591 Hs.10712 Hs.103822 Hs.288617 Hs.126594 Hs.1816059 Hs.1816055 Hs.2371146 Hs.4094 Hs.118722 Hs.42746 Hs.1103 Hs.21943 Hs.272239 Hs.28856 Hs.124776 Hs.58800 Hs.10026 Hs.313 Hs.258856 Hs.1340 Hs.37636 Hs.13340 Hs.37636 Hs.13340 Hs.465699 Hs.56668 Hs.54668 Hs.54668 Hs.54668 Hs.54668 Hs.54668 Hs.5466998 Hs.165998 Hs.126695 Hs.125395	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily 8 (Cys-X-C Homo septems cDNA: FLJ22621 fis, clone HSI056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo septems cDNA FLJ14234 fis, clone NT2RP40 Homo septems cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (alpha (1,5) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo lymphocyte activation-associated protein prefoldin 5 Homo septems mRNA; cDNA DKFZp564N1116 (from c Homo septems cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acelytransferase 1 vaocintia related kinase 1 cellutar retinoic acid-binding protein 1 ESTs troporin I, cardiac DKFZP564M2423 protein ESTs ESTs ESTs ESTs ESTs gbtHSC3FE081 normalized infant brain cDNA Hom	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3
55 60 65 70 75	448358 459926 458477 421379 452822 441111 446913 445913 445913 445913 445913 445913 445913 445913 445916 441433 417837 450516 407725 419200 423161 445619 43571 446619 43571 446619 43571 446819 43571 446819 445817 446819	R44433 A1744361 NM_000314 Y15221 X85689 A1806867 U46258 AA430550 A1989517 BE219771 AA262105 AA158177 AA933809 AL079905 AA902656 AA195509 AL079905 AA902656 AA195509 AL049227 A1343868 BE560898 AL076643 AA32265 AL049227 A1343861 BUSE00898 AL076643 AA32265 AL076643 AL07	Hs.106614 Hs.205591 Hs.10712 Hs.103982 Hs.288617 Hs.126594 Hs.23448 Hs.16529 Hs.181605 Hs.237146 Hs.4094 Hs.118722 Hs.42746 Hs.41943 Hs.272239 Hs.288856 Hs.124776 Hs.58800 Hs.10026 Hs.10026 Hs.10026 Hs.1031 Hs.165539 Hs.25841 Hs.37636 Hs.13340 Hs.48269 Hs.65176 Hs.54668 Hs.165998 Hs.126695 Hs.125395 Hs.125395	Human DNA sequence from clone RP4-534K7 on ch ESTs, Weakly similar to zinc finger protein P phosphatase and tensin homolog (mutated in mu small inducible cytokine subfamily B (Cys-X-C Homo sapiens cDNA: FLJ22621 fis, clone HSi056 ESTs ESTs transmembrane 4 superfamily member (tetraspan ESTs Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14234 fis, clone NT2RP40 Homo sapiens cDNA FLJ14238 fis, clone NT2RP30 fucosyltransferase 8 (atpha (1,6) fucosyltran ESTs transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pornbe homo lymphocyte activation-associated protein perfoldin 5 Homo sapiens cDNA FLJ12488 fis, clone NT2RM20 ribosomal protein L17 isolog secreted phosphoprotein 1 (osteopontin, bone ESTs DKFZP434D193 protein ESTs, Weakly similar to KIAA1392 protein [H.s histone acetylfransferase 1 vaocinia related kinase 1 cellutar retinoic acid-binding protein 1 ESTs troporin I, cardiac DKFZP564M2423 protein ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.4 3.3 3.3

	421515 446351	Y11339 AW444551	Hs.105352 Hs.258532	GatNAc atpha-2, 6-statyttransferase I, long f ESTs	3.3 3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
5	418216 401508	AA662240	Hs.283099	AF15q14 protein O	3.3 3.3
,	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HS1009	3.3
	416530	U62801	Hs.79361	katlikrein 6 (neurosin, zyme)	3.3
	443171 458627	BE281128 AW088542	Hs.9030 Hs.97984	TONDU	3.3
0	412078	X69699	Hs.73149	ESTs; Weakly similar to WASP-family protein [paired box gene 8	3.3 3.3
_	414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	3.3
	401197	414470040	11- 440440	0	3.3
	422134 409044	AW179019 Al129586	Hs.112110 Hs.33033	ESTs ESTs	3.3 3.3
5	415198	H27332	Hs.99598	ESTs	3.2
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquilin-conjugat	3.2
	436525 409142	AA721428 AL136877	Hs.26145	Homo saplens cDNA FLJ14127 fis, clone MAMMA10 chromosome-associated polypeptide C	3.2 3.2
	428819	AL135623	Hs.50758 Hs.193914	KIAA0575 gene product	3.2
0	428728	NM_016625	Hs.191381	ESTs; Weakly similar to hypothetical protein	3.2
	421261	AA600853	Hs.98133	ESTs	3.2
	446219 457574	A1287344 H88717	Hs.149827	ESTS	3.2 3.2
	409172	Z99399	Hs.27774 Hs.118145	ESTs, Highly shrilar to AF161349 1 HSPC086 [H ESTs	3.2
5	419388	T67012	Hs.75323	prohibitin	3.2
	434187	AA627098	Hs.99103	ESTs, Weakly similar to 138428 T-complex prof	3.2
	445060 448254	AAB30811 Al829900	Hs.88808 Hs.22929	ESTs ESTs	3.2 3.2
_	452943	BE247449	Hs.31082	ESTs hypothetical protein FLJ10525	3.2 3.2
)	411393	AW797437	Hs.69771	B-factor, properdin	3.2
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.2
	408418	AW963897	Hs.44743	KIAA1435 protein	3.2
	442025 417006	AW887434 AW673606	Hs.11810 Hs.80758	ESTs, Wealdy similar to CD4.2 [C.elegans] aspartyl-IRNA synthelase	3.2 3.2
5	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransf	3.2
	444755	AA431791	Hs.183001	ESTs	3.2
	402829	AE464070	Lin nerne	OCC 131 ambia	3.2
	451593 419926	AF151879 AW900992	Hs.26706 Hs.93796	CGI-121 protein DKFZP586D2223 protein	3.2 3.2
)	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR	3.2
	445929	AI089660	Hs.7838	makorin, ring finger protein, 1	3.2
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	3.2
	418836 441020	A1655499 W79283	Hs.161712 Hs.35962	ESTs ESTs	3.2 3.1
5	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	3.1
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial	3.1
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.1
	410486 434540	AW235094 NM_016045	Hs.193424 Hs.5184	ESTs, Weakly similar to KIAA1064 protein [H.s TH1 drosophila homolog	3.1 3.1
)	409178	BE393948	Hs.50915	kalikrain 5	3.1
	439480	AL038511	Hs.125316	ESTs	3.1
	417848 446293	AA206581 AI420213	Hs.39457	ESTs	3.1
	408108	AJ420213 AJ580492	Hs.149722 Hs.42743	ESTs hypothetical protein	3.1 3.1
5	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	31
	410519	AW612264	Hs.131705	ESTs	3.1
	421987	Al133161	Hs.286131	CGI-101 protein	3.1
	440046 453931	AW402306 AL121278	Hs.6877 Hs.25144	hypothetical protein FLJ10483 ESTs	3.1 3.1
)	454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	3.1
	459089	F13036	Hs.27373	Homo saplens mRNA; cDNA DKFZp56401763 (from c	3.1
	418735	N48769	Hs.44609	ESTs .	3.1
	414245 410909	BE148072 AW898161	Hs.75850 Hs.53112	WAS protein family, member 1 ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAM	3.1 3.1
5	434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	3.1
	409239	AA740875	Hs.44307	ESTs	3.1
	429017	AA463605	Hs.238995	ESTs	3.1
	447072 426514	D61594 BE616633	Hs.17279 Hs.301122	tyrosylprotein sulfotransferase 1 bone morphogenetic protein 7 (osteogenic prot	3.1 3.1
0	448133	AA723157	Hs.73769	folate receptor 1 (adult)	3.1
	418792	AB037805	Hs.88442	KIAA1384 protein	3.1
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cere	3.1
	402077 440671	AW297920	Hs.130054	0 ESTs	3.1 3.1
5	419890	X17360	Hs.278255	homeo box D4	3.1
	406687	M31126	Hs.272620	pregnancy specific bata-1-glycoprotein 9	3.1
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. cerevi	3.1
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B; yeast)	31
0	443584 445525	A1807036 BE149866	Hs.101619 Hs.14831	ESTs ESTs	3.1 3.1
-	410441	BE298210		gb:601118016F1 NIH_MGC_17 Homo saplens cDNA c	3.1
	422634	NM_016010	Hs.118821	CGI-62 protein	3.0
	420022	AA256253	Hs.120817	ESTs MAA(379 amtein	3.0
	453912	AL121031	Hs.32556	KIAA0379 protein	3.0
				174	

	456844 414941	AI264155 C14865	Hs.152981 Hs.182159	COP-diacytghycerol synthase (phosphatidate cy ESTs	3.0 3.0
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on chrom	3.0
_	414725	AA769791	Hs.120355	Homo saptens cONA FLJ13148 fts, clone NT2RP30	3.0
5	444420	AJ148157	Hs.146766	ESTs	3.0
	431742 412519	NM_016652 AA196241	Hs.268281	CGI-201 protein troponin T1, skeletal, slow	3.0 3.0
	418348	AI537167	Hs.73980 Hs.96322	Homo sapiens cDNA: FLJ23560 fis, clone LNG098	3.0
	444261	AA298958	Hs.10724	MDS023 protein	3,0
10	457465	AW301344	Hs.195969	ESTs	3.0
	443933	AI091631	Hs.135501	Homo saplens two pore potassium channel KT3.3	3.0
	442150	AI368158	Hs.128864	ESTs	3.0
	414883	AA926960	Hs.77550	CDC28 protein kinase 1	3.0
15	442879	AF032922	Hs.8813	syntaxin binding protein 3	3.0
15	437949	U78519	Hs.41654	EST8	3.0 3.0
	403515 403864			0	3.0
	403664	AW207285	Hs.98279	ESTs	3.0
	426199	AA371865	Hs.97090	ESTs	3.0
20	426324	AW291787	Hs.200933	ESTs	3.0
	427738	NM_000318	Hs.180612	peroxisornal membrane protein 3 (35kD, Zellweg	3.0
	427837	U87309	Hs.180941	vacuolar protein sorting 41 (yeast homolog)	3.0
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.0
25	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicus]	3.0
23	446978	NM_001938	Hs.16697	down-regulator of transcription 1, TBP-bindin	3.0 3.0
	452431 452841	U88879 T17431	Hs.29499 Hs.65412	toll-like receptor 3 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	3.0
	432114	AL036021	Hs.225597	ESTs	3.0
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.saplens]	3.0
30	442607	AA507576	Hs.288361	KIAA0741 gene product	3.0
	453920	AI133148	Hs.36602	I factor (complement)	3.0
	430000	AW205931	Hs.99598	ESTs	3.0
	429164	AI688663	Hs.116586	ESTs	3.0
25	453331	Al240665	Hs.8895	ESTs	3.0
35	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar to syn	3.0
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	3.0
	401714			0	3.0 3.0
	400903 428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.0
40	443761	AJ525743	Hs.160603	ESTs	3.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chrom	3.0
	442580	AI733682	Hs.130239	ESTs	3.0
45	TABLE 10 Pkey: Uni CAT numb	B: ique Eos probes ber: Gene clusti	et Identifier num	iber	3.0
	TABLE 10 Pkey: Uni CAT numb Accession	B: ique Eos probes ber: Gene dush b: Genbank acc	et Identifier num er number ession numbers	tiber ,	3.0
	TABLE 10 Pkey: Uni CAT numb Accession Pkey	B: ique Eos probes er: Gene clusti : Genbank acc CAT Number	el Identifier num er number ession numbers Accessi	tiber ,	3.0
45 50	TABLE 10 Pkey: Uni CAT numb Accession	B: ique Eos probes ber: Gene dush b: Genbank acc	eel Identifier num er number ession numbers Accession R86913	nber v	
	TABLE 10 Pkey: Uni CAT numb Accession Pkey 407596 409763 410360	B: ique Eos probes per: Gene clust : Genbank acc CAT Number 1003489_1 115392_1 11972252	eel Identifier num er number ession numbers Accessi R86913 AL0432 AW6636	on R86901 H25352 R01.370 H43764 AW044451 W21298 12 AAD77675 AAD77655 R19502 BE545457 Al638421 R14093 190	•
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50	TABLE 10 Pkey: Unit CAT numb Accession Pkey 407596 409763 410360 410441	B: que Eos probes per: Gene dush c: Genbank acca CAT Number 1003489_1 11572252 120358_1	set Identifier num er number ession numbers Accessi R86913 AL0432 AW6638 BE2982 Al88508	on R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093 990 10 Al672315 AW086489 BE298417 AA455921 AA902537 BE3 95 Al476470 Al287650 Al885299 Al985381 AW592624 AW340	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658
	TABLE 10 Pkey: Uni CAT numb Accession Pkey 407596 409763 410360 410441 411560	B: ique Eos probes ser: Gene dust c Genbank acc CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1	tel Identifier num er number ession numbers Accessis R86913 AL0432 AW633 BE2982 AI88505 AW8511	on R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093 390 110 Al672315 AW086489 BE298417 AA455921 AA902537 BE3 35 Al476470 Al287650 Al885299 Al985381 AW592624 AW340 186 AW996967 BE143456	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658
50	TABLE 10 Pkey: Uni CAT numb Accession Pkey 407596 409763 410360 410441 411560 414315	8: ique Eos probes ser: Gene dust : Genbank acc CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1	tel Identifier num er number ession numbers Accessi R86913 AL0432 AW6636 BE2982 Al88505 AW8511 Z24878	on R86901 H25352 R01.370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093 930 110 Al572315 AW086489 BE298417 AA455921 AA902537 BE3 36 Al476470 Al287650 Al885299 Al985381 AW592624 AW340 186 AW998987 BE143456 AA494098 F13654 AA494040 AA143127	27124 R14963 AA086210 AW274273 Al333584 Al369742 Al039658 136 Al266558 AA456390 Al310815 AA484951
50	TABLE 10 Pkey: Unit CAT numb Accession Pkey 407596 409763 410360 410441 411560 414315 418417	B: que Eos probes per: Gene dust c Genbank acc CAT Number 103489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 1750818_1	tel Identifier num er number ession numbers Accessi R86913 AL0432 AW6533 BE2982 Al88503 AW851* Z24878 R77182	on R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077675 AA077655 R19502 BE545457 AI638421 R14093 690 110 AI672315 AW086489 BE298417 AA455921 AA902537 BE3 95 AI476470 AI287650 AI885299 AI985381 AW592624 AW340 186 AW9398967 BE143456 AA494088 F13654 AA494040 AA143127 R77197 R80484	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658
50 55	TABLE 10 Pkey: Unit CAT numb Accession Pkey 407596 409763 410360 410441 411560 414315 418454	B: ique Eos probes per: Gene dust c Genbank acc CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 1750818_1 175699_1	tel Identifier num er number ession numbers Accessis R86913 AL0432 AW6531 BE2982 AW8511 Z24878 R77182 AA3153	on R86901 H25352 R01.370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093 930 110 Al572315 AW086489 BE298417 AA455921 AA902537 BE3 36 Al476470 Al287650 Al885299 Al985381 AW592624 AW340 186 AW998987 BE143456 AA494098 F13654 AA494040 AA143127	27124 R14963 AA086210 AW274273 Al333584 Al369742 Al039658 136 Al266558 AA456390 Al310815 AA484951
50	TABLE 10 Pkey: Unit CAT numb Accession Pkey 407596 499763 410461 410441 411560 418417 418464 419346 424770	B: que Eos probes ber: Gene dust CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 1750818_1 175089_1 184129_1 243504_1	tel Identifier num er number ession numbers Accessi R86913 AL0432 AW6638 BE2982 Al88505 AW8517 Z24878 R77182 AA3163 Al83041 AA4255	on R85901 H25352 R01370 H43764 AW044451 W21298 12 AAU77575 AA077655 R19502 BE545457 AI638421 R14093 690 110 AI672315 AW086489 BE298417 AA455921 AA902537 BE3 65 AI476470 A1287650 AI885299 AI985381 AW592624 AW340 186 AW9995967 BE143456 AA494098 F13554 AA494040 AA143127 R77197 R80484 03 AA223392 BE538098 BE087173 17 AA236612 17 AA236612	27124 R14963 AA086210 AW274273 Al333584 Al369742 Al039658 136 Al266558 AA456390 Al310815 AA484951
50 55	TABLE 10 Pkey: Unit CAT numb Accession Pkey 407596 499763 410360 410441 411560 414315 418454 419346 424770 427943	B: ique Eos probes ber: Gene dust CAT Number 1003489_1 115392_1 11972252 120358_1 1249443_1 143512_1 1750818_1 175699_1 184129_1 243504_1 284802_1	tel Identifier num er number ession numbers R86913 AL0432 AW6635 BE2982 Al88503 AW851* Z24878 R77182 AA3153 AI83041 AA4255 AW959	on R86901 H25352 R01370 H43764 AW044451 W21298 R2 AAD77575 AA077655 R18502 BE545457 AI638421 R14093 690 110 AI672315 AW086489 BE298417 AA455921 AA902537 BE3 95 AI476470 AI287650 AI885299 AI985381 AW592624 AW340 R86 AW990967 BE143456 AA494098 F13654 AA494040 AA143127 R77197 R80484 108 AA223392 BE538098 BE087173 17 AA236612 662 AI880208 AA346646 N22655 AW811775 AW811786 075 W06838 AA417863	27124 R14963 AA086210 AW274273 Al333584 Al369742 Al039658 136 Al266558 AA456390 Al310815 AA484951
50 55	TABLE 10 Pkey: Unit CAT numb Accession Pkey 407596 409763 410360 410441 411560 414315 418454 418346 424710 427943 431965	B: ique Eos probes ber: Gene dust CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 175689_1 184129_1 243504_1 284802_1 33959_2	tel Identifier num er number ession numbers R66913 AL0432 AW6634 BE2982 AW8511 Z24878 R77182 AA3153 AB3044 AA4255 AW959 BE1751	on R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 AI638421 R14093 590 10 AI672315 AW086489 BE298417 AA455921 AA902537 BE3 95 AI476470 AI287650 AI885299 AI985381 AW592624 AW340 186 AW998967 BE143456 AA494098 F13654 AA494040 AA143127 R77197 R80464 108 AA223392 BE538098 BE087173 17 AA236612 6052 AI880208 AA346646 N22655 AW811775 AW811786 075 W06838 AA417863	27124 R14963 AA086210 AW274273 Al333584 Al369742 Al039658 136 Al266558 AA456390 Al310815 AA484951
50 55	TABLE 10 Pkey: Uni CAT numb Accession Pkey 407596 409763 410360 410441 411560 414315 418417 418444 419346 424770 427943 431965 436812	B: que Eos probes ber: Gene dush : Genbank acc CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 1750818_1 175699_1 184129_1 243504_1 284802_1 3959_2	Lel Identifier num er number ession numbers R86913 AL0432 AW6636 BE2982 Al88505 AW8517 Z24878 R77182 AA3153 Al83041 AA4255 AW959 BE1751 AW298	on R85901 H25352 R01370 H43764 AW044451 W21298 12 AAD77675 AA077655 R19502 BE545457 Al638421 R14093 390 110 Al672315 AW086489 BE298417 AA455921 AA902537 BE3 36 AL476470 A1287650 Al885299 Al985381 AW592624 AW340 186 AW995987 BE143456 AA494098 F13654 AA494040 AA143127 R77197 R80484 003 AA223392 BE538098 BE087173 17 AA236612 162 Al880208 AA346646 N22655 AW811775 AW811786 075 W06838 AA417863 190 BE003348	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658 136 Al266556 AA456390 Al310815 AA484951
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5055606570	TABLE 10 Pkey: Uni CAT numi Accession Pkey 407596 409763 410360 410441 411560 414315 418417 418454 419345 424770 427943 4319655 436812 437938	B: que Eos probes ber: Gene dush : Genbank acce CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 175699_1 184129_1 243504_1 284802_1 33959_2 427323_1 44573_2 470321_1 719912_1 1050256_1	Let Identifier numer number ession numbers ession numbers R86913 AL0432 AW6636 BE2982 AW8507 AW3517 AW3518 AW359 BE1757 AW359 AU557 AW359	on R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077675 AA077655 R18502 BE545457 Al638421 R14093 390 10 Al672315 AW086489 BE298417 AA455921 AA902537 BE3 36 Al476470 Al287650 Al885299 Al985381 AW592624 AW340 168 AW998967 BE143456 AA494098 F13654 AA494040 AA143127 1877197 R80484 168 AW23392 BE538098 BE087173 17 AA236612 169 AB20208 AA346646 N22655 AW811775 AW811786 1675 AW6838 AA417883 190 BE00338 AA417883 190 BE00338 AA417883 190 BE00338 AA417883 1910 BE00338 AA417883 1870208 R87040 N36809 AJ508119 AW967677 N35320 AJ25 187 1470208 R87040 N36809 AJ508119 AW967677 N35320 AJ25 187 1470208 R87040 N36809 AJ508119 AW967677 N35320 AJ25 187 14830484 188 148 148 148 148 148 148 148 148 148	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658 136 Al266556 AA456390 Al310815 AA484951 51473 H59397 AW971573 R97278 W01059 AW967671 AA908598 28571 T775102 R34725 AA884922 BE328517 Al219788 AA884444 33 AA663345 AW008282 AA488984 AA283144 Al890387 Al9503344 3386 AW150329 Al653832 Al762688 AA98877 AA488982 Al356394 629970 BE612881 AW276997 AW513601 AW512843 AA044209 819225 AW205862 Al683338 Al858509 AW276905 Al633006 AA972584 888 H84729 H60052 T92487 Al022058 AA780419 AA551005 W80701 8056 Al002839 R67840 AA300207 AW959581 T63226 F04005 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 BE140917 AW178135 AW178205 AW178209 AW17823 AW178200 AW845878 AW178131 AW178138 AW178105 AW845894 AW178109 AW845878 AW178121 AW178130 AW178134 AW178096 AW178198 AW178159 BE141189 AW178178 OAW345816 BE141580 AW178156
505560657075	TABLE 10 Pkey: Uni CAT numi Accession Pkey 407596 409763 410360 410441 411560 414315 418417 418454 424770 427943 431965 436812 437938	B: que Eos probes ber: Gene dush : Genbank acce CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 175699_1 184129_1 243504_1 284802_1 33959_2 427323_1 44573_2	Lel Identifier numer number ession numbers R86913 AL0432 AW6638 BE2982 AI88503 AW8517 Z24878 R77182 AA3153 AI83041 AA4255 AW959 BE1751 AW258 AI95000 AA2518 N92578 AI7413 AW103 AW856 AA9087 AW8478 AW178 AW178 AW178 AW178 AW178 AW178 BE1401 AW807 A	OR R85901 H25352 R01370 H43764 AW044451 W21298 R12 AA077675 AA077655 R19502 BE545457 AI638421 R14093 690 110 AI672315 AW086489 BE298417 AA455921 AA902537 BE3 65 AI76470 AI287650 AI885299 AI985381 AW592624 AW340 186 AW9986967 BE143456 AA494089 F13654 AA494040 AA143127 R77197 R80484 (03 AA223392 BE538098 BE087173 17 AA236612 AI680208 AA346646 N22655 AW811775 AW811786 O75 W06838 AA417863 90 BE003348 (05 AA223091 BE38098 BE087173 AW967677 N35320 AI28672 AV731645 AA810101 AW194180 AI690673 AW978773 BF N70208 R97040 N36809 AI308119 AW967677 N35320 AI2875 AI820501 AI820523 W87891 T85904 U71456 T82391 BE375 AI820501 AI820523 W87891 T85904 U71456 T82391 BE375 AI820501 AI820523 W87891 T85904 U71456 T82391 BE375 AI820501 AI820523 W7891 AW9874058 AL134043 AW25335 46 AI689062 AA282915 AW102898 AI872193 AI763273 AW1778131 AI539842 AA642789 AA856975 AW505512 AI981530 AW15338 AA180009 AA337499 AW981101 AA251669 AA251874 AI71 AW072629 AW513996 AA293273 AA859759 N7628 N223456 AI373032 AI564259 F00531 H83488 W37181 W78802 R61 AW178167 AW178167 AW178168 AW178168 AW1781169 AW178120 BE140918 L206 AW1781207 AW178162 AW178168 AW178169	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658 136 Al266556 AA456390 Al310815 AA484951 51473 H59397 AW971573 R97278 W01059 AW967671 AA908598 28571 T75102 R34725 AA884922 BE328517 Al219788 AA884444 33 AA663345 AW008282 AA488984 AA283144 Al890387 Al990344 33586 AW150329 Al653832 Al762688 AA988777 AA488892 Al356394 529370 BE612881 AW276997 AW513601 AW512843 AA044209 819225 AW205862 Al683338 Al858509 AW276935 Al633006 AA972584 888 H84729 H60052 T92487 Al022058 AA780419 AA551005 W80701 6056 Al002839 R67840 AA300207 AW959581 T63226 F04005 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 BE140917 AW178135 AW178205 AW178209 AW178230 AW178200 AW845878 AW178131 AW178130 AW178134 AW178096 AW178129 BE140915 AW178221 AW178130 AW178134 AW178096 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156 AW17819 BE141592 AW845901 BE141580 AW178155 BE141598
505560657075	TABLE 10 Pkey: Uni CAT numi Accession Pkey 407596 409763 410360 410441 411560 414315 418417 418454 424770 427943 431965 436812 437938	B: que Eos probes ber: Gene dush : Genbank acce CAT Number 1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 175699_1 184129_1 243504_1 284802_1 33959_2 427323_1 44573_2 470321_1 719912_1 1050256_1	Lel Identifier numer number ession numbers R86913 AL0432 AW6638 BE2982 AI88503 AW8517 Z24878 R77182 AA3153 AI83041 AA4255 AW959 BE1751 AW258 AI95000 AA2518 N92578 AI7413 AW103 AW856 AA9087 AW8478 AW178 AW178 AW178 AW178 AW178 AW178 BE1401 AW807 A	OR R85901 H25352 R01370 H43764 AW044451 W21298 12 AA077675 AA077655 R19502 BE545457 Al638421 R14093 390 110 Al672315 AW086489 BE298417 AA455921 AA902537 BE3 36 AL476470 A1287650 Al885299 Al985381 AW592624 AW340 186 AW995987 BE143456 AA494098 F13654 AA494040 AA143127 1877197 R80484 103 AA23392 BE5338098 BE087173 17 AA236612 162 Al880208 AA346646 N22655 AW811775 AW811786 075 W06838 AA417863 190 BE003348 067 AA731645 AA810101 AW194180 Al690673 AW976773 87 N70208 R97040 N36809 A1308119 AW967677 N35320 Al28 1975 Al820501 Al820632 W87811 R85904 U71456 T82391 AW2533 46 Al689062 AA282915 AW102898 Al872193 Al763273 AW17 813 Al539842 AA642789 AA656975 AW750512 Al981530 AW1 213 AL339842 AA642789 AA656975 AW50512 Al981530 AW1 214 AW072629 AW513996 AA293273 AA969759 N75628 N222 456 Al373032 AL564269 F00631 H83488 W37181 W78802 R6 500 AA832198 BE164502 1,13377223 T75099 183 AW178167 AW178162 AW178168 AW178160 AW17818 1810 AW845928 AW178216 AW178114 AW178212 BE140918 1810 AW845928 AW178216 AW178117 AW178158 1810 AW845928 AW178218 AW178171 AW178157 AW17818 1810 AW845928 AW178218 AW178171 AW178157 AW17818	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658 136 Al266556 AA456390 Al310815 AA484951 51473 H59397 AW971573 R97278 W01059 AW967671 AA908598 28571 T75102 R34725 AA884922 BE328517 Al219788 AA884444 33 AA663345 AW008282 AA488984 AA283144 Al890387 Al990344 33586 AW150329 Al653832 Al762688 AA988777 AA488892 Al356394 529370 BE612881 AW276997 AW513601 AW512843 AA044209 819225 AW205862 Al683338 Al858509 AW276935 Al633006 AA972584 888 H84729 H60052 T92487 Al022058 AA780419 AA551005 W80701 6056 Al002839 R67840 AA300207 AW959581 T63226 F04005 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 BE140917 AW178135 AW178205 AW178209 AW178230 AW178200 AW845878 AW178131 AW178130 AW178134 AW178096 AW178129 BE140915 AW178221 AW178130 AW178134 AW178096 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156 AW17819 BE141592 AW845901 BE141580 AW178155 BE141598

TABLE 10C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495
Strand: Indicates DNA strand from which exons were predicted
NL position: Indicates nucleotide positions of predicted exons

	PKBy	Ker	Strand	Nt_position
• •	400534	6981826	Minus	278637-279292
10	400666	8118496	Plus	17982-18115,20297-20456
	400903	2911732	Ptus	59112-59228
	401197	9719705	Ptus	176341-176452
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401508	7534110	Minus	110779-110983
15	401517	7677912	Plus	29278-29770
	401644	8576138	Plus	82655-83959
	401714	6715702	Plus	96484-96681
	402077	8117414	Ptus	65014-65195
~~	402222	9958106	Plus	3261-3834,3939-4269
20	402408	9796239	Minus	110326-110491
	402820	6456853	Minus	82274-82443
	402829	8918414	Plus	101532-101852,102006-102263
	403381	9438267	Minus	26009-26178
~ -	403515	7656757	Minus	173358-179553
25	403729	7543752	Minus	37662-37909-,
	403864	7709019	Minus	51753-51890,79290-79445
	404108	8247074	Minus	63603-64942
	404232	8218045	Minus	71800-71956
•	404552	7243881	Plus	19854-20010
30	404567	7249169	Minus	101320-101501
	404599	8705107	Plus	110443-110733
	404915	7341766	Minus	100915-101087
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405095	8072599	Plus	138877-139066
35	406069	9117732	Plus	68880-69374
	406117	9142932	Ptus	54304-54584 ·

Table 11A lists about 222 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted. 40

TABLE 11A: ABOUT 222 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primakey

Ex. Acon: Exemplar Accession

45

UG ID: UniGene ID

50

Title: UniGene title
PFAM domains: predicted protein structural domains
ratio: ratio turnor vs normal tissue

20						
	Picey	Ex. Acon	UGID	Title	PFAM domains	ratio
	400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenatic pro	pkinase, Activin_recp	30.0
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	25.2
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid m	C1g,Collagen	22.7
55	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular m	tsp_1	19.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	17.4
	443646	Al085198	Hs.298699	ESTs	TSPN,vwc,tsp_1,EGF	15.1
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unname	TM	14.1
	418601	AA279490	Hs.86368	calmegin	SS,calreticulin	13.8
60	428532	AF157326	Hs.184786	T8P-interacting protein	TM	13.6
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) rec	TM,neur_chan	11.8
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamin	TM, Glycos_transf_2,RI	11.0
	404567	NM_015902	Hs.278428	progestin induced protein (DD5)	TM,HECT,zf-UBR1	10.8
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,MAM,EGF	8.9
65	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	TM,MSP_domain	8.8
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, par	TSPN,vwc,tsp_1,EGF	8.5
	453370	A1470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran,ABC_membr	8.4
	400298	AA032279	Hs.61635	STEAP1	TM	B.1
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	7.9
70	429609	AF002246	Hs.210863	cell adhesion molecule with homolo	TM,fn3,lg	7.8
	412170	D16532 .	Hs.73729	very low density lipoprotein recepto	TM,tdl_recept_a,tdl_rec	7.4
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway	SS,IGFBP,Cys_knot,tsp	7.4
	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitia	SS,hemopexin,Peptidas	7.2
	424001	W67883	Hs.137476	KIAA1051 protein	Pep_M128_propep,Rep	7.2
75	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetica	TM	7.1
	446142	A1754693	Hs.145968	ESTs	Cadherin_C_term,cadhe	7.0
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP	Kunitz_BPTI,G-gamma	6.8
	438167	R28363	Hs.24286	ESTs	7tm_1	6.6
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and	Pep_M12B_propep,Rep	6.4
80	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose in	SS	5.8
	425371	D49441	Hs.155981	mesolhelin	SS	5.7
	407945	X69208	Hs.608	ATPase, Cu++ transporting, atpha p	TM,E1-E2_ATPasa,Hy	5.6
	424620	AA101043	Hs.151254	kalikrein 7 (chymotypila; stratum c	SS,trypsin	5.5
	420362	U79734	Hs.97206	. huntingtin interacting protein 1	TM,ENTH,I_LWEQ	. 5.4

	413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.3
	425154	NM_001851 AL033527	Hs.154850	collagen, type IX, elpha 1	Collagen, TSPN	5.2 5.1
	411945 415539	ALU33527 Al733881	Hs.92137 Hs.72472	v-myc avian myelocytomatosis viral BMPR-lb; bone morphogenetic pro	TGF-beta,TGFb_propep pkinase.Activin_recp	5.1
5	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.9
	424539	L02911	Hs.150402	activin A receptor, type I	Activin_recp.pkinase	4.8 4.7
	450375 451684	AA009647 AF216751	Hs.8850 Hs.26813	a disintegrin and metalloproteinase d CDA14	disintegrin,Reprolysin,P TM	4.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM_ABC_tran_ABC_m	4.6
10	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase d	IM	4.5
	400534 425506	AP000541 NM_003666	Hs.158205	predicted exons basic leucine zipper nuclear factor 1	TM,KRAB,zf-C2H2 TM,Folate_carrier	4.5 4.5
	413472	BE242870	Hs.75379	solute carrier family 1 (glist high aff	TM,SDF	4.4
1.5	449535	W15267	Hs.23672	low density tipoprotein receptor-rela	SS,ldl_recept_b,ldl_rece	4.4
15	452028	AK001859	Hs.27595	hypothetical protein FLJ 10997	Zn_carbOpept,Propep_M EGF,TSPN,tsp_1,tsp_3,	4.3 4.3
	418693 410361	AI750878 BE391804	Hs.87409 Hs.62661	thrombospondin 1 quanylate binding protein 1, interfer	TM,GBP	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	Frizzled,Fz,7tm_2	4.2
20	421502	AF111856	Hs.105039	solute carrier family 34 (sodium pho	TM, Na_PL_cotrans	4.2
20	412494 405095	AL133900 NM_014479	Hs.792 Hs.145296	ADP-ribosylation factor domain pro disintegrin protease	arf,zf-B_box,zf-C3HC4 Reprolysin,disintegrin	4.0 4.0
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pro	SS,wap	4.0
	407792	Al077715	Hs.39384	. putative secreted ligand homologous	SS	4.0
25	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-s	TM SS,TGF-beta,TGFb_pro	3.8 3.7
25	450581 432712	AF081513 AB016247	Hs.25195 Hs.288031	endometrial.bleeding associated fact sterol-C5-desaturase (fungal ERG3,	TM, Sterol_desat	3.7
	450447	AF212223	Hs.25010	hypothetical protein P15-2	TM_ANF_receptor,guan	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	TM	3.6
30	417389	BE260964	Hs.82045 Hs.2258	Midkine (neurite growth-promoting Matrix Metalloproteinase 10 (Strom	TM,PTN_MK SS,hemopexin,Peptidas	3.6 3.5
50	400666 406400	X07820 AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	SS,trypsin	3.4
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM,FHA,BRCT	3.4
	452822	X85689	Hs.288617	Homo saplens cDNA: FLJ22621 fis,	EGF,fn3,pktnase	3.4
35	446913 422611	AA430650 AA158177	Hs.16529 Hs.118722	transmembrane 4 superfamily memb fucosyltransferase 8 (alpha (1,5) fuc	TM,transmembrane4 SS	3.4 3.4
55	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZ	cadherin,Cadherin_C_te	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	TM,Sec7	3.3
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	SS,TM,trypstn ext.Ets	3.3 3.3
40	401197 436525	AA721428	Hs.26145	predicted exons Homo saptens cDNA FLJ14127 ffs,	TM	3.2
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	3.2
	411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fib	3.2
	407881 418836	AW072003 AI655499	Hs.40968 Hs.161712	heparan sulfate (glucosamine) 3-0-s ESTs	SS pkinase,Activin_recp	3.2 3.2
45	409178	BE393948	Hs.50915	kallikrein 5	SS, trypsin	3.1
	421987	A1133161	Hs.286131	CGI-101 protein	TM	3.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	SS TOTA amagelida T	3.1 3.1
	426514 448133	BE616633 AA723157	Hs.301122 Hs.73769	bone morphogenetic protein 7 (osteo folate receptor 1 (aduit)	SS,TGFb_propeptide,T TM	3.1
50	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10,hem	3.1
	456844	AJ264155	Hs.152981	CDP-diacylglycerol synthase (phosp	TM, Cytidylyltrans	3.0
	414725	AA769791	Hs.120355	Homo saptens cDNA FLJ13148 fis,	SPRY,7tm_1 Sema,ig	3.0 3.0
	407785 427738	AW207285 NM_000318	Hs.98279 Hs.180612	ESTs peroxisomal membrane protein 3 (35	TM,zl-C3HC4	3.0
55	452431	U88879	Hs.29499	toll-like receptor 3	TM,TIR,LRRCT	3.0
	453920	A1133148	Hs.36602	I factor (complement)	tdl_recept_a,trypsin,SRC	3.0 3.0
	453331 425776	AJ240665 U25128	Hs.8895 Hs.159499	ESTs parathyroid hormone receptor 2	disintegrin,Reprolysin,P TM,7tm_2	3.0
	42842B	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog	TM,pkinase	3.0
60	407910	AA650274	Hs.41296	fibronectin leucine rich transmembra	TM,LRRCT,LRRNT,LR	2.9
	408380	AF123050	Hs.44532	diubiquitin	TM,ubiquilin,7tm_3,AN	2.9 2.9
	407783 420757	AW996872 X78592	Hs.172028 Hs.99915	a disintegrin and metalloproteinase d androgen receptor (dihydrotestostero	disintegrin, Reprotysin TM, Androgen_recep, ho	2.9
	424406	D54120	Hs.146409	wingless-type MMTV integration sit	cadherin,Cadherin_C_te	2.9
65	428549	AA430064	Hs.220929	ESTs, Moderately similar to ARF-fa	arf	2.9
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkinase,ig TGFb_propeptide,TGF+	2.9 2.9
	452281 420440	T93500 NM_002407	Hs.28792 Hs.97644	ESTs mammaglobin 2	SS, Uteroglobin	29
	418848	AI820961	Hs.193465	ESTs	pkinase, Activin_recp	2.9
70	421991	NM_014918	Hs.110488	KIAA0990 protein	SS	2.9
	433190	M26901	Hs.3210	renin zinc finger protein 262	SS,asp TM	2.9 2.8
	424538 433002	NM_005095 AF048730	Hs.150390 Hs.279906	cyclin T1	SS	2.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated mem	TM,Lamp	2.8
75	430598	AK001764	Hs.247112	hypothetical protein FLJ 10902	TM	2.8
	428450	NM_014791	Hs.184339	KIAA0175 gene product hypothetical protein DKFZp434C03	TM,pkinase,KA1 TM	2.8 2.8
	450171 423554	AL133661 M90516	Hs.24583 Hs.1674	glutamine-fruciose-6-phosphate tran	TM,GATese_2,SIS	2.8
	430016	NM_004736		xenotropic and polytropic retrovirus	TM	2.8
80	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	Collagen, COLFI, TSPN	2.8
	424894	H83520	Hs.153678	reproduction 8	SS,UBX SS	2.8 2.7
	430651 414853	AA961694 U31116	Hs.105187 Hs.77501	kinesin protein 9 gene saroogiycan, beta (43kD dystrophin-	55 TM	2.7
	448595	AB014544	Hs.21572	. KIAA0644 gene product	TM,LRRCT,LRR .	2.7
					177	

	452835	AK001269	Hs.30738	ESTs .	TM	2.7
	403019	AAB34626	Hs.66718	RAD54 (S.cerevtslae)-like	SS,Anti_proliferet	2.7
	420281	AI523693	Hs.191533	ESTs	Cation_efflux	2.7
5	434815 432201	AF155582 AI538613	Hs.46744 Hs.135657	core1 UDP-galactose:N-acetylgalact TMPRSS3a mRNA for serine protea	SS trefoil,trypsin	26 26
•	430450	R23553	Hs.241489	hypothetical protein	SS	2.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras,arf	2.6
	421802	BE261458	Hs.108408	CGI-78 protein	TM	2.6
10	452355 417742	N54926 R64719	Hs.29202	G protein-coupled receptor 34 gb:EST22d11 WATM1 Homo saple	TM,7tm_1 ank_death,RHD,TIG	2.6 2.6
10	451346	NM_006338	Hs.26312	glioma amplified on chromosome 1	TM, ig, LRR, LRRNT, LR	2.6
	433147	AF091434	Hs.43080	platelet derived growth factor C	TM,PDGF,CUB	2.6
	420079	NM_014051	Hs.94896	PTD011 protein	SS,TM,	2.6
15	419918 432350	X80700 NM_005865	Hs.93728 Hs.274407	pre-B-cell leukemia transcription fac protease, serine, 16 (flymus)	homeobox,ig,Acyltransf SS	2.5 2.5
13	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	pkinase,Sema,Plexin_re	2.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR.ig	2.5
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM	2.5
20	433929	A1375499	Hs.27379	ESTS	EGF,ldT_recept_a,ld1_re TM_mito_carr	2.5 2.5
20	443562 414386	AF118838 X00442	Hs.9599 Hs.75990	solute carrier family 25, member 13 haptoglobin	sushi,trypsin	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltr	AIRS,formyLtransf,GA	2.5
	449207	AL044222	Hs.23255	nucleoporin 155kD	TM	2.5
25	416107	AA173846	Hs.79015	antigen identified by monoclonal ant	TM,ig	2.4 2.4
23	421750 414812	AK000768 X72755	Hs.107872 Hs.77367	hypothetical protein FLJ20761 monokine induced by gamma interfe	TM,PH SS,IL8	2.4
	406137	R42764	Hs.3248	mutS (E. coli) homolog 6	TM,Muts_C,Muts_N,P	2.4
	450710	AW953381	Hs.18627	ESTs, Weakly similar to G01447 GP	TM	2.4
30	430291	AV660345	Hs.238126	CGI-49 protein	TM	24
30	425184 451418	BE278288 BE387790	Hs.155048 Hs.26369	Lutheran blood group (Auberger b a ESTs	ig TM	2.4 2.4
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (TM,G-alpha	24
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A	SS,IL8	2.4
25	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM,RCT	23
35	416224	NM_002902	Hs.79088	reliculocalbin 2, EF-hand calcium bi	SS,efhand histone,Calc_CGRP_IA4	2.3 2.3
	452268 451668	NM_003512 Z43948	Hs.28777 Hs.26789	H2A histone family, member L ASPIC (acidic secreted protein in ca	SS,TM,	2.3
	400880	M84349	Hs.119663	CD59 antigen	SS,UPAR_LY6	2.3
40	421340	F07783	Hs.1369	decay accelerating factor for comple	SS,sushi	2.3
40	443986	AL381750	Hs.283437	HTGN29 protein	TM Contoxio	2.3 2.3
	443037 440516	AW500305 S42303	Hs.8906 Hs.161	syntaxin 7 cadherin 2, type 1, N-cadherin (neur	TM,Syntaxin HNH,cadherin,Cadherin	2.3
	404877	Al394145	Hs.18048	melanoma antigen MAGE-10	TM,MAGE	2.3
45	440704	M69241	Hs.162	insulin-like growth factor binding pr	SS,thyroglobulin_1,IGF	2.3
45	437952	D63209	Hs.5944	solute carrier family 11 (proton-coup	TM Comple	2.3 2.2
	418624 410434	AI734080 AF051152	Hs.104211 Hs.63668	ESTs toll-like receptor 2	Sema.ig SS,TIR,LRRCT,LRR	2.2
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,fn2,hemopexin,Pepli	2.2
50	431457	NM_012211	Hs.256297	integrin, alpha 11	TM,FG-GAP,vwa	2.2
50	407907	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5	SS,LysyLhydro	2.2
	400898 400303	AF220030 AA242758	Hs.125300 Hs.79136	Homo saplens tripartite motif protein Human breast cancer, estrogen regul	SPRY,7tm_1 SS,TM,	2.2 2.2
	411789	AF245505	Hs.72157	Homo saplens mRNA; cDNA DKFZ	ig,LRRCT	2.2
	414809	A1434699	Hs.77356	transferrin receptor (p90, CD71)	TM,PA,Ribosomal_S2	2.2
55	401131	NM_001651	Hs.298023	Homo saplens aquaporto 5 (AQP5),	ТММР	2.2
	400277 409317	Y00281 U20165	Hs.2280 Hs.53250	Human mRNA for ribophorin I bone morphogenatic protein recepto	TM TM.pkinase	2.1 2.1
	409956	AW103364	Hs.727	H.saplens activin bela-A subunit (ex	TGF-beta,TGFb_propep	2.1
60	451253	H48299	Hs.26126	claudin 10	TM,PMP22_Claudin	2.1
60	429638	AI916662	Hs.211577	Kinectin 1 (kinesin receptor)	TM .	21 21
	409267 418414	NM_012453 J04977	Hs.52515 Hs.84981	transducin (beta)-like 2 X-ray repair complementing defectiv	TM,WD40 SS	21
	449057	AB037784	Hs.22941	ESTs	TM	2.1
	417666	Al345001	Hs.82380	menage a trols 1 (CAK assembly fac	zf-C3HC4	21
65	428485	NM_002950	Hs.2280	ribophorin l	TM	2.1
	445798 430057	NM_012421 AW450303	Hs.13321 Hs.2534	rearranged L-myc fusion sequence bone morphogenetic protein recepto	TM,zf-C2H2 TM,Activin_recp,pkina	2.1 2.1
	425169	H16622	110.2004	gb:ym26c07.r1 Soares Infant brain 1	RasGEF,PH,fibrinogen_	21
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycopro	SS,Glyco_hydro_18	2.1
70	421343	BE246444	Hs.283685	hypothetical protein FLJ20396	. TM	21
	425627	AF019612	Hs.297007	ESTs peroxisomal famesylated protein	TM,Peplidase_M50	21 21
	426261 431638	AW242243 NM_000916	Hs.168670 Hs.2820	oxylocin receptor	E1-E2_ATPase,Cation_ TM,7tm_1	21
	456546	AI690321	Hs.203845	ESTs, Wealdy similar to TWIK-rela	TM	21
75	421685	AF189723	Hs.108778	calcium transport ATPase ATP2C1	TME1-E2_ATPase,Hy	2.1
	424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM_ABC_tran_ABC_m TM	21 21
	424800 41 00 07	AL035588 AW950887	Hs.153203 Hs.57813	MyoD family inhibitor zinc ribbon domain containing, 1	TFIIS	21
	436135	D85390	Hs.5057	carboxypeptidase D	SS,Zn_carbOpept	21
80	420633	NM_014581	Hs.99526	odorant-binding protein 2B	TMJipocalin	2.1
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase,ank,ArfGap,PH	2.1
	426156 442711	BE244537 AF151073	Hs.167382 Hs.8645	natriuretic peptide receptor Afguany hypothetical protein	TM,ANF_receptor,guan TM	2.0 2.0
	411872	AW327356	Hs.90918	chromosome 11 open reading frame	TM	20
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					1 / ()	

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5	427801 430268 431183 431846 404210 435640 447906 412666	AW979155 AK000737 NM_006855 BE019924 U02478 AF220053 AL050062 AL080116	Hs.234433 Hs.237480 Hs.250696 Hs.271580 Hs.100469 Hs.54960 Hs.19999 Hs.74420	hypothetical protein PRO1068 hypothetical protein FLI20730 KDEL (Ly3-Asp-Giu-Leu) endoplas Uroplaidn 18 Human AF-6 mRNA uncharacterized hematopoletic stern/ DKFZP566K023 protein origin recognition complex, subunit	TM,Aa_trans TM TM_ER_turnen_recept,I TM_transmembrans4 TM,RA,DIL_PDZ,FHA TM,SET_zf-CXXC,PHD SS TM	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	
10	417181 423945 411773 448350 401093	L10123 AA410943 NM_005799 L14561 AI955244	Hs.1071 Hs.72472 Hs.72026 Hs.78546 Hs.121520	surfactant protein A binding protein BMPR-lb; bone morphogenetic pro protease, serine, 21 (testish) Homo saplens clone 24411 mRNA s HYPOTHETICAL 16.4 KDa PROTE	TM TM_pkinase_Activin_rec SS,trypsin TM_E1-E2_ATPase,Hy TM_LRRCT	20 20 20 20 20	
15	415664 448165 416391 422926 446849	NM_004939 NM_005591 AI878927 NM_016102 AU076617	Hs.78580 Hs.202379 Hs.79284 Hs.121748 Hs.16251	DEAD/H (Asp-Glu-Ala-Asp/His) bo metrib recombination (s. cerevisiae mesoderm specific transcript (mouse ring finger protein 18 deavage and polyadenylation specif	DEAD,helicase_C,SPRY DNA_repair,Glyco_tran TM,abhydrolase SPRY,zi-C3HC4,zi-B_ TM	20 20 20 20 20 20	
20	427617 411678 432554	D42063 AI907114 AI479813	Hs.179825 Hs.71465 Hs.278411	RAN binding protein 2-like 1 squalene epoxidase NCK-associated protein 1	TM,Ran_BP1,zFRanBP TM,Monooxygenase TM	20 20 20	
25	CAT numb	B: que Eos probes er: Gene cluste : Genbank acce	er number	**			
30	Pkey 417742 425189	CAT Number 1696282_1 247825_1		4680 R12451 7322 AA351959			
35	TABLE 11C: Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495 Strand: Indicates DNA strand from which exons were predicted NL position: Indicates nucleotide positions of predicted exons						
40	Pkey 400534 401197	Ref 6981826 9719705	Strand Minus Plus	Nt_position 278637-279292 176341-176452			
45	small mole	cules. These w	rere selected as	for Table 10A, except that the ratio was g	reater than or equal to 2.0, and the	le either enzymes or proteins amenable to modulation predicted protein contained a structural domain that is rters). Predicted protein domains are noted.	
	TABLE 12	A: ABOUT 57 U	P-REGULATE	GENES ENCODING EXTRACELLULAR	CELL SURFACE PROTEINS, OVA	ARIAN CANCER VERSUS NORMAL ADULT TISSUES	

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TABLE 12A: ABOUT 57 UP-REGULATED GEN Pkey: Primekey Ex. Acon: Exemplar Accession UG ID: UniGene ID Title: UniGene title PFAM domains: predicted structural domains ratio; ratio tumor vs. normal 50

55	1800, 180	IO MINOI 42' INSII	I Idi			
	Pkey	Ex. Acen	UGID	Title	PFAM domains	ratio
	400292	AA250737 ·	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase,Activin_recp	30.0
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS, Peptidase_M10	25.2
	426427	M86699	Hs.169840	TTK protein kinase	pkinase	18.7
60	424905	NM 002497	Hs.153704	NIMA (never in mitosis gene a)-rela	pkinase	16.2
	433159	AB035898	Hs.150587	kinesin-like protein 2	kinestn	11.5
	453370	AI470523	Hs.182358	ESTs, Moderately similar to translat	ABC_tran	8.4
	418007	M13509	Hs.83169	Matrix metalloprolease 1 (Interstitia	SS. Peplidase_M10	7.2
	425465	L18964	Hs.1904	protein kinase C; lota	Skl_Sno,pkinase_C	6.1
65	409506	NM_006153	Hs.54589	NCK adaptor protein 1	SH2,SH3	5.2
	415539	Al733881	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase,Activin_recp	5.1
	424539	L02911	Hs.150402	activin A receptor, type I	Activin_recp,pkinase	4.8
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran	4.5
	431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis,	RhoGAP,FF,ras	3.9
70	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	C2,PLPLC-Y,PLPLC-X	3.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	ANF_receptor pkinase	3.6
	400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS, ,Peptidase_M10	3.5
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis.	EGF,fn3,pkinase	3.4
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SS,TM,trypsin	3.3
75	411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fn3,	3.2
	444755	AA431791	Hs.183001	ESTs	AAA	3.2
	418836	A1655499	Hs.161712	ESTs	pkinase,Acilvin_recp	3.2
	409178	BE393948	Hs.50915	kallikrein 5	SS, trypsin	3.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Pepiidase_M10, .lg	3.1
80	453920	AI133148	Hs.36602	I factor (complement)	kdl_recept_a,trypsin,SRCR	3.0
	404653	AA923729	Hs.26322	0 `	pkinase	2.9
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkinase,ig	29
	418848	AI820961	Hs.193465	ESTs	pklnase,Activin_recp	2.9
	428450	NM_014791	Hs.184339	KIAA0175 gene product	TM.pldnase,KA1	28

	401323	AL158037		predicted exon	lactamase B	2.7
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E	SH3,pkinase ,ABC_tran	2.7
	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protea	trefoll, trypsin	2.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras.arf	2.6
5	405671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	pkinase,Sema	2.5
•	453448	AL036710	Hs.209527	ESTs	CNH.pkinase	2.5
	414386	X00442	Hs.75990	haptoglobin	sushi,trypsin	2.5
	421270	H56037 ·	Hs.108146	ESTs	RhoGAP	2.4
	414695	BE439915	Hs.76913	proteasome (prosome, macropain) su	proteasome	2.4
10	431341	AA307211	Hs.251531	proteasome (prosome, macropain) su	proteasome	2.4
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (4	AAA Viral helicase1	2.2
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,fn2, ,Peptidase_M10	2.2
	416517	AA775987	Hs.79357	proteasome (prosome, macropain) 28 ·	AAA	2,2
	417601	NM_014735	Hs.82292	KIAA0215 gene product	PHD	2.1
15	400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan	pro_lsomerase	2.1
	430057	AW450303	Hs.2534	bone morphogenetic protein recepto	Activin_recp,pklnase	2.1
	421841	AA908197	Hs.108850	KIAA0936 protein	TPR pkinase	2.1
	453078	AF053551	Hs.31584	metaxin 2	pro_isomerase	21
	424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM_ABC_tran	2.1
20	411190	AA306342	Hs.69171	protein kinase C-like 2	pkinase,pkinase_C,HR1	2.1
	407740	AA295547	Hs.62666	ESTs	p450	2.1
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase ank AriGap ,ras	2.1
	420490	H69894	Hs.193041	ESTs	Pl3Ka,Pl3_Pl4_kinase	2.1
	426156	BE244537	Hs.167382	natriurelic peptide receptor Alguany	TM_ANF_receptor ,pkinase	2.0
25	423945	AA410943	Hs.72472	BMPR-lb; boge morphogenetic pro	TM,pkinase,Activin_recp	2.0
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	2.0
	447298	BE617527	Hs.180450	ribosomal protein S24	Pl3Ka, Pl4_kinase	2.0
	427617	D42063	Hs.179825	RAN binding protein 2-like 1	TPR.pro_isomerase	2.0
	453546	AF042385	Hs.33251	peptidylprolyl isomerase E (cycloph	pro_lsomerase,rrm	. 2.0
30						

TABLE 12C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22' Dunham, et al. (1999) Nature 402-489-495 Strand: Indicates DNA strand from which exons were predicted

35 Nt_position: Indicates nucleotide positions of predicted exons

Nt_position 401323 9212516 Plus 213509-214450 40

> Table 13A lists about 1086 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 10A, except that the ratio was greater than or equal to 10, and the denominator was the median value for various non-malignant ovary specimens.

45 TABLE 13A: About 1086 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY Pkey: Primekey

Ex. Acon: Exemplay Accession UG ID: UniGene ID

Title: UniGene title 50 ratio: ration tumor vs. normal ovary

Ex. Acon 109.2 107.8 439706 AW872527 Hs.59761 **ESTs** AU076643 AI868872 secreted phosphoprotein 1 (osteopontin, bone ceruloplasmin (ferroxidase) 446619 Hs.313 55 Hs.288966 104.4 422095 cysteine-rich protein 1 (intestinal) 447111 AI017574 Hs.17409 NM_006103 epididymis-specific; whey-acidic protein type secretory leukocyte protease inhibitor (antii 431130 Hs.2719 82.8 431369 BE184455 Hs.251754 81.9 AW992356 413859 Hs.8364 73.9 Hs.14623 interferon, gamma-inducible protein 30 E74-like factor 3 (ets domain transcription f 60 446291 BE397753 72.7 426050 AF017307 Hs.166096 68.1 411469 T09997 Hs.70327 cysteine-rich protein 2 66.6 lipocalin 2 (oncogene 24p3) uncoupling protein 2 (mitochondrial, proten c hypothetical protein FLJ20171 429504 X99133 Hs.204238 65.7 R34657 AW296454 Hs.80658 64.9 416971 65 62.5 Hs.24743 450273 hypothetical protein
Homo sapiens cDNA FLJ14303 fis, clone PLACE20
Homo sapiens cDNA FLJ10457 fis, clone NT2RP10
ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT
Homo sapiens mRNA; cDNA DKFZp5648076 60.7 59.7 446441 AK001782 Hs.15093 428758 AA433988 Hs.98502 57.8 56.7 55.7 441406 Z45957 Hs.7837 AW194364 AW772298 441859 448406 Hs.128022 70 Hs 21103 Homo saplens mRNA; cDNA DKFZp56481264 55.2 414602 AW630088 Hs.76550 54.8 53.4 51.4 50.7 AW971155 Hs.293902 ESTs. Weakly similar to prolyl 4-hydroxylase 418068 428330 L22524 Hs.2256 matrix metalloproteinase 7 (matritysin, uteri NM_004415 412636 Hs.74316 desmoplakin (DPI, DPII) 75 Al860651 430634 Hs.26685 **FSTs** 50.7 50.6 G protein-coupled receptor 56 AW837046 439318 Hs.6527 chondroitin sulfate proteoglycan 2 (versican) 417259 AW903838 Hs.81800 50.4 49.7 48.9 407786 AA687538 Hs.38972 tetraspan 1 vesicle-associated membrane protein 8 (endobr KIAA0101 gene product isocitrate dehydrogenase 2 (NADP+), mitochond 426836 N41720 Hs.172684 80 417308 H60720 Hs.81892 48.4 436876 Al124756 Hs.5337 Al393742 Hs.199067 v-erb-b2 avian erythroblastic leukemia viral 439180 M26301 complement component 2 46.3 428289 405484 46.1

	425371 403912	D49441	Hs.155981	mesothelin O	45.7 45.0
	443021	AA368546	Hs.8904	lg superfamily protein	44.6
	427697	T18997	Hs.180372	BCL2-like 1	44.3
5	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	44.0
_	404678			0	43.9
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	43.8
	451035	AU076785	Hs.430	plastin 1 (1 isoform)	43.8
10	440848	BE314650	Hs.7476	ATPase, H+ transporting, lysosomal (vacuolar	42.8
10	436278 413936	BE396290 AF113676	Hs.5097 Hs.75621	synaptogyrin 2	42.4 42.1
	420859	AW468397	Hs.100000	serine (or cysteine) proteinase inhibitor, cl S100 calcium-binding protein A8 (calgranulin	42.1
	428411	AW291464	Hs.10338	EST8	41.8
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin	41.5
15	412477	AA150864	Hs.790	microsomal glutathione S-transferase 1	40.7
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium prot	40.1
	424673	AA345051	Hs.294092	ESTs	39.8
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	39.7
20	443162 413719	T49951 BE439580	Hs.9029 Hs.75498	ESTs; Highly similar to KERATIN; TYPE I CYTO small inducible cytokine subfamily A (Cys-Cys	39.5 39.3
20	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase 8, 92k	38.9
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein-39	38.5
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	38.1
0.5	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid	37.9
25	415511	AI732617	Hs.182362	ESTs	37.7
	409453	Al885516	Hs.95612	ESTs	37.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	37.3 37.3
	442432 408243	BE093589 Y00787	Hs.38178 Hs.624	Homo sapians cDNA: FLJ23468 fis, clone HSI116 interleukin 8	37.3
30	419092	J05581	Hs.89603	mucin 1, transmembrane	36.7
50	444172	BE147740	Hs.104558	ESTs	36.0
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	. 35.8
	420440	NM_002407	Hs.97644	mammaglobin 2	35.7
26	414386	X00442	Hs.75990	haptoglobin	35.3
35	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	35.1
	440596	H13032	Hs.103378	ESTs, Weakly similar to DRR1 [H.saptens]	35.0 34.9
	413278 418506	BE563085 AA084248	Hs.833 Hs.85339	interferon-stimulated protein, 15 kDa G protein-coupled receptor 39	34.8
	445919	T53519	Hs.290357	ESTs	34.7
40	416854	H40164	Hs.80296	Purkinje cell protein 4	34.4
. •	414186	U33446	Hs.75799	prolease, serine, 8 (prostasin)	34.2
	434371	AA631362		gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	33.9
	421937	A1878857	Hs.109706	HN1 prolein	33.9
15	449722	BE280074	Hs.23960	cyclin B1	33.8
45	400965	V===00	11-400404	0 470 b) d) =	33.7
	452203	X57522 AL033527	Hs.158164 Hs.92137	ATP-binding cassetta, sub-family 8 (MDR/TAP), v-myc avian myelocytomatosis viral encogene h	33.5 33:5
	411945 425811	AL033327 AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin a	33.4
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	33.3
50	438461	AW075485	Hs.286049	phosphoserine aminotransferase	33.3
	422963	M79141	Hs.13234	ESTS	33.3
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	33.2
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	32.8
55	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	32.5
55	431211 436552	M86849 NM_014038	Hs.5566 Hs.5216	Homo saptens connexin 26 (GJB2) mRNA, complet HSPC028 protein	32.5 32.5
	442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subu	32.5
	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	32.4
	450353	Al244661	Hs.103296	ESTs	32.4
60	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	32.4
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (y	32.3
	441020	W79283	Hs.35962	ESTs	32.2 32.0
	432201 424125	AI538613 M31669	Hs.135657 Hs.1735	TMPRSS3a mRNA for serine protesse (ECHOS1) (T inhibin, beta B (activin AB beta polypeptide)	31.9
65	453309	Al791809	Hs.32949	defensin, bela 1	31.8
05	408380	AF123050	Hs.44532	diubiquitin	31.7
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	31.6
	409231	AA446644	Hs.692	GA733-2; epithelial glycoprotein (EGP) (KSA)	31.6
	423961	D13666	Hs.136348	Homo saplens mRNA for osteoblest specific fac	31.2
70	413840	AJ301558	Hs.290801	ESTs	30.8
•	440943	AW082298	Hs.146161	ESTs, Weakly similar to KIAA0859 protein [Hs Homo septens cDNA: FLJ23241 fis, clone COL013	30.8 30.4
	419239 410132	AA468183 NM_003480	Hs.184598 Hs.58882	Microfibril-associated glycoprotein-2	30.4 30.2
	410132 418203	X54942	Hs.83758	CDC28 prolein kinase 2	30.1
75	412719	AW016610	Hs.129911	EST8	30.0
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC10	30.0
	431563	A1027643	Hs.120912	ESTs	29.9
	431743	AW972642	Hs.293055	ESTs	29.8
00	443295	A1049783	Hs.241284	ESTs	29.7
80	413745	AW247252	Hs.75514	nucleoside phosphorylase	29.7
	441028	AI333660	Hs.17558	ESTs ESTs	29.6 29.6
	442315 452838	AA173992 U65011	Hs.7956 Hs.30743	ESTs Preferentially expressed entigen in melanoma	29.5
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	29.5
				•	

	432280	BE440142 ·	Hs.2943	signal recognition particle 19kD	29.4
	420158	AI791905	Hs.95549	hypothetical protein	29.3
	445033	AV652402	Hs.155145	EST8	29.2
-	452367	U71207	Hs.29279	eyes absent (Drosophila) homotog 2	29.1
5	432706	NM_013230	Hs.286124	CD24	29.0
	422163	AF027208	Hs.297332	prominin (mouse)-like 1	28.7
	447035	NM_004753	Hs.17144	short-chain dehydrogenase/reductase 1	28.6
	443958	BE241880	Hs.10029	cathepsin C	28.2 28.1
10	422956 450377	BE545072 AB033091	Hs.122579 Hs.24936	ESTs ESTs	28.0
10	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	28.0
	444725	AW952022	Hs.234174	Homo saplens cDNA FLJ13819 fis, clone THYRO10	27.8
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	27.7
	416305	AU076628	Hs.79187	coxsackle virus and adenovirus receptor	27.6
15	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	27.5
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cys-X-C	27.4
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	27.3
	427344	NM_000869 BE018682	Hs.2142 Hs.44343	5-hydroxytryptamine (serotonin) receptor 3A	27.2 27.2
20	442993 407137	T97307	Hs.199067	ESTs v-erb-b2 avian erythroblastic leukemia viral	27.0
20	419356	A1656166	Hs.7331	ESTs	27.0
•	433662	W07162	Hs.150826	CATX-8 protein	26.7
	422576	BE548555	Hs.118554	CGI-83 protein	26.4
0.0	423271	W47225	Hs.126256	interleukin 1, beta	26.3
25	443715	AI583187	Hs.9700	cyclin E1	26.1
	420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription factor	26.0
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus laevis) homolog	25.9
	443672 416889	AA323362 AW250318	Hs.9667	butyrobeteine (gamma), 2-oxoglutarate dioxyge	25.8 25.3
30	408474	AA188823	Hs.80395 Hs.83196	mal, T-cell differentiation protein Homo saplens cDNA: FLJ23597 fis, clone LNG152	25.3 25.3
50	411825	AK000334	Hs.72289	hypothetical protein FLJ20327	25.3
	400881	74,00000	110.7 2200	0	25.2
	440594	AW445167	Hs.126036	ESTs	25.1
	414586	AA306160	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)	25.1
35	411925	AW014588	Hs.72925	chromosome 11 open reading frame 13	25.1
	417869	BE076254	Hs.82793	proteasome (prosome, macropain) subunit, beta	25.0
	433447	U29195	Hs.3281	neuronal pentraxin II	25.0
	450858	C18458	Hs.25597	elongation of very long chain fatty acids (FE	24.8
40	410619 434094	BE512730 AA305599	Hs.65114 Hs.238205	keratin 18 hypothetical protein PRO2013	24.8 24.6
40	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	24.6
	446859	A1494299	Hs.16297	COX17 (yeast) homolog, cytochrome c oxidase a	24.5
	421451	AA291377	Hs.50831	ESTs	24.3
	433929	Al375499	Hs.27379	ESTs	24.3
45	438930	AW843633	Hs.81256	S100 calcium-binding protein A4 (calcium prot	24.2
	444212	AW503976	Hs.10649	basement membrane-induced gene	24.2
	441633	AW958544	Hs.112242	ESTS	24.2
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	24.2
50	417715 409361	AW969587	Hs.86366	ESTS	24.1 24.1
50	416984	NM_005982 H38765	Hs.54416 Hs.80706	sine oculis homeobox (Drosophila) homolog 1 diaphorase (NADH/NADPH) (cytochrome b-5 reduc	24.1
	430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	23.9
	434078	AW880709	Hs.283683 ~	EST	23.8
	408669	AM93591	Hs.78146	platetet/endothelial cell adhesion molecule (23.8
55	439413	A1598252	Hs.37810	ESTs	23.7
	449034	AI624049	Hs.277523	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	23.7
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR150	23.6
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	23.6
60	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated prot	23.5 23.4
UU	451267 450101	A1033894 AV649989	Hs.117865 Hs.24385	solute carrier family 17 (anton/sugar transpo Human hbc647 mRNA sequence	23.4 23.4
	419693	AA133749	Hs.92323	FXYD domain-containing ion transport regulato	23.4
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth factor 8	23.4
	451110	A1955040	Hs.301584	ESTs	23.3
65	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	23.2
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to sign	23.1
	424670	W81215	Hs.116651	epithelial V-like antigen 1	23.1
	417847	A1521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fls, clone HRC052	23.1
70	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	23.1 23.1
70	424969 433159	AW950928 AB035898	Hs.153998 Hs.150587	creatine kinase, mitochondrial 1 (ubiquitous) kinesin-like protein 2	23.1
	411393	AW797437	Hs.69771	B-factor, properdin	23.0
	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamine-alp	22.8
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	22.7
75	445721	H92136	Hs.13144	HSPC160 protein	22.6
	448258	BE386983	Hs.85015	ESTs, Weakly similar to A4P_HUMAN INTESTINAL	22.6
	456844	AJ264155	Hs.152981	COP-diacylglycerol synthase (phosphatidate cy	22.6
	452698	NM_001295	Hs.301921	ESTs	22.5
80	418693	AJ750878	Hs.87409	thrombospondin 1 eukaryotic translation initiation factor 5A	22.4 22.4
50	414880 401519	AW247305	Hs.119140	eukaryouc translation invalion factor SA 0	22.3
	402496			ŏ	22.3
	420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	22.3
	403022			. 0	22.2

	121012	41000044	11-0054	humathadianal annatala DECORRE	22.4
	434042	Al589941	Hs.8254	hypothetical protein PRO0899	22.1 22.1
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	
	406545	AB018249	Hs.10458	small inducible cytokine subfamily A (Cys-Cys	22.1
_	447362	AW176120	Hs.9061	ESTs .	22.0
5	429547	AW009166	Hs.99376	ESTs .	22.0
	427954	J03060	Hs.247551	metaxin 1	22.0
	423161	AL049227	Hs.124776	Homo saptens mRNA; cDNA DXFZp564N1116 (from c	22.0
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (21.9
10	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polypeplide	21.7
10	414421-	Al521130	Hs.55567	ESTs, Weakly similar to LAK-4p [H.saplans]	21.5
	412589	R28660	Hs.24305	ESTs	21.5
	446525	AW967069	Hs.211556	Homo saplens cDNA: FLJ23378 fis, clone HEP162	21.5
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like docking	21.5
	436972	AA284679	Hs.25640	claudin 3	21.5
15	428698	AAB52773	Hs.297939	ESTs; Wealthy similar to neogenin (H.sapiens)	21.5
	421340	F07783	Hs.1369	decay accelerating factor for complement (CD5	21.4
	413966	AA133935	Hs.173704	ESTs	21.4
	448243	AW369771	Hs.77496	ESTs	21.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	21.3
20	403399			0	21.3
	435793	AB037734	Hs.4993	ESTs	21.3
	432629	AW860548	Hs.280658	ESTs	21.2
	449057	AB037784	Hs.22941	ESTs	21.2
	437575	AW954355	Hs.36529	ESTs ·	21.2
25	401131	A11307000	110.00023	0	21.0
25		T03651	Hs.179661	tubulin, bela polypeptide	20.8
	407207 444783	AK001468	Hs.62180	ESTs	20.8
					20.8
	426230	AA367019	Hs.241395	prolease, serine, 1 (typsin 1) EST:: Violar typical to LOW DENSITY LIPOPROTE	20.6
30	447343	AA256641	Hs.236894	ESTs; Highly similar to LOW-DENSITY LIPOPROTE	20.7
30	409041	AB033025	Hs.50081	KIAA1199 protein	
	421305	BE397354	Hs.289721	diptheria toxin resistance protein required f	20.6
	411704	Al499220	Hs.71573	hypothetical protein FLJ10074	20.5
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related oncog	20.5
~ ~	432827	Z68128	Hs.3109	Rho GTPase activating protein 4	20.4
35	410174	AA306007	Hs.59461	DKFZP434C245 protein	20.4
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen incl	20.4
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	20.3
	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemota	20.2
	447335	BE617695	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	20.2
40	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	20.1
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating e	20.1
	429083	Y09397	Hs.227817	BCL2-related protein A1	20.0
	410173	AA706017	Hs.119944	ESTs	19.8
	433047	M86135	Hs.279946	methionine-tRNA synthetase	19.8
45	419088	A1538323	Hs.77496	ESTs	19.7
	403381	1400000	110.11110	0	19.6
	409162	H25530	Hs.50868	solute carrier family 22 (organic cation tran	19.5
	426150	NM_003658	Hs.167218	Bart-Hike homeobox 2	19.4
	449292	A1990292	Hs.225457	ESTs	19.4
50			Hs.155120	rho/rac guanine nucleotide exchange factor (G	19.4
50	425207	AB014551			19.3
	419950	AK001645	Hs.93871	hypothetical protein FLJ10783	19.3
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	
	445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	19.2 19.1
55	446608	N75217	Hs.257846	ESTs	
55	425222	M85430	Hs.155191	villin 2 (ezrin)	19.1
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	19.1
	420005	AW271106 .		ESTs	19.1
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0
C 0	407142	AA412535	Hs.55235	sphingomyelin phosphodlesterase 2, neutral me	19.0
60	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood Leuke	18.9
	446293	AI420213	Hs.149722	ESTs	18.9
	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase kinas	18.9
	407634	AW016569	Hs.301280	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosami	18.9
	445200	AA084460	Hs.12409	somatostatin	18.9
65	418917	X02994	Hs.1217	adenosine deaminase	18.8
	435777	AW419202	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	18.8
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene	18.7
	426427	M86699	Hs.169840	TTK protein kinase	18.7
	436281	AW411194	Hs.120051	ESTS	18.6
70	425907	AA365752	Hs.155965	ESTs	18.6
	459720			ESTs	18.6
	421242	AW161386	Hs.13561	ESTs, Wealdy similar to dJ37E16.5 [H.sapiens]	18.5
	457715	AA642402	Hs.59142	ESTs	18.5
	451668	Z43948	Hs.26789	ASPIC (acidic secreted protein in cartilage)A	18.4
75	437142	AI791617	Hs.145068	ESTs	18.4
	418588	BE387040	Hs.182476	ESTs. Weakly similar to similar to alpha/beta	18.3
	433068		Hs.288215	slalyltransferase	18.3
		NM_006456	Hs.87836	Homo saplens PAC done RP5-1097M19 from 7q11.	18.3
	419854	AW664873	Hs.11801	interferon regulatory factor 6	18.3
80	444726	NM_006147		ESTs, Highly stmilar to A2AD_HUMAN ALPHA-2C-2	18.2
30	423011	NM_000683		ESTs, Weakly similar to K02E10.2 [C.elegans]	18.2
	451428	AW083384	Hs.11067	lymphocyta antigen 75	18.2
	424865	AF011333	Hs.153563	EST8	18.1
	418742	AW451197	Hs.113418	ESTS: hypothetical protein SBBI48	18.1
	446627	A1973016	Hs.15725	Costs, Hypothonous protest opens	10.1

	10.1000				
	424885 402926	AI333771	Hs.82204	ESTs	18.1
	405452			0	18.0 18.0
	428641	AA431367	Hs.234546	GMPR2 for guanosine monophosphate reductase i	18.0
5	454390	AB020713	Hs.56966	KIAA0906 protein	18.0
	441784	AJ522132	Hs.28700	ESTs	18.0
	418758	AW959311	Hs.87019	ESTs	17.9
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	17.9
10	426201	AW182614	Hs.128499	ESTs	17.8
10	410442 456423	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta polype	17.8
	422867	AW748920 L32137	Hs.1584	gb:CM2-BT0306-171199-034-g02 BT0306 Homo sapi cartilage oligomeric matrix protein	17.8 17.8
	448110	AA626937	Hs.181551	ESTs	17.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	17.7
15	405224			0	17.7
	447630	AI660149	Hs.44865	lymphold enhancer-binding factor 1	17.7
	407663	NM_016429	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP	17.7
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	17.6
20	414812	X72755	Hs.77367	monokine induced by gamma interferon	17.6
20	427691	AW194426	Hs.20726	ESTs	17.6
	420650 439841	AA455706 AF038961	Hs.44581	heat shock protein hsp70-related protein mannose-P-dolichol utilization defect 1	17.5 17.5
	425810	AP036301 AI923627	Hs.6710 Hs.31903	ESTs	17.5
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	17.5
25	456098	AW747800	Hs.55016	hypothetical protein FLJ21935	17.4
	428579	NM_005756	Hs.184942	G protain-coupled receptor 64	17.4
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	17.4
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	17.4
20	411734	AW374954	Hs.71779	Homo sepiens DNA from chromosome 19, cosmid F	17.3
30	405295		11. 44000	0	17.3
	408340	AB037762	Hs.44268	myelin gene expression factor 2	17.3 17.3
	456068 448571	A1677897 AA486794	Hs.76640 Hs.66915	RGC32 protein ESTs, Weakly similar to 16.7Kd protein [H.sap	17.3
	441829	AL117482	Hs.7978	DKFZP434C131 protein	17.2
35	418004	U37519	Hs.87539	akdehyde dehydrogenase 8	17.2
55	412078	X69699	Hs.73149	paired box gene 8	17.2
	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD), mem	17.1
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	17.0
40	426805	AB032945	Hs.172506	myosin VB	17.0
40	410247	AF181721	Hs.61345	RU2S	17.0
	434516	AA807814	Hs.70582	ESTs, Moderately similar to AF144056 1 apopto	16.9
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B	16.9
45	454163 415402	AW175997 AA164687	Hs.297889	gb:QV0-BT0078-190899-005-E02 8T0078 Homo sapi ESTs	16.9 16.9
73	420309	AW043637	Hs.21766	ESTS	16.9
	419201	M22324	Hs.1239	alanyl (membrane) aminopeptidase (aminopeptid	16.9
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	16.9
	457705	AW974668		gb:EST386757 MAGE resequences, MAGM Homo sapl	16.8
50	412723	AA648459	Hs.179912	ESTs	16.8
	435774	R88066	Hs.4992	tumor suppressing subtransferable candidate 1	16.8
	408753	Al337192	Hs.47438	SH3 domain binding glutamic acid-rich protein	16.8
	447783	AF054178	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alpha subco	16.8
55	418085	R40328	Hs.258822	ESTS	16.7
22	452472	AW957300	Hs.294142	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	16.7
	409112 410250	BE243971 Al082777	Hs.50649 Hs.61384	quinone oxidoreductase homolog KIAA1445 protein	16.7 16.7
	446219	AI287344	Hs.149827	ESTs	16.6
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
60	425812	AA364128	Hs.245633	ESTs	16.6
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor 4E b	16.6
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	18.6
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
65	440667	8E076969	Hs.7337	hypothetical protein FLJ10936	16.6
65	430375	AW371048	Hs.93758	H4 histone family, member H	16.6
	419607	R52557	Hs.91579	Homo saplens clone 23783 mRNA sequence	16.6 16.5
	410328 405426	BE080190	Hs.62275	CGI-141 protein 0	16.5
	432636	AA340864	Hs.278562	claudin 7	16.5
70	434725	AK000796	Hs.4104	hypothetical protein	16.5
, -	414683	S78296	Hs.76888	internexin neuronal intermediate filament pro	16.5
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	16.5
	449944	AF290512	Hs.58215	Homo sapiens rhotekin mRNA, partial cds	16.4
75	400666			0	16.4
75	421536	BE250690	Hs.105509	CTL2 gene	16.4
	436032	AA150797	Hs.109276	latexin protein	16.4
	418196	AJ745649	Hs.26549	ESTs, Weakly similar to T00066 hypothetical p ESTs, Weakly similar to C43H8.1 [C.elegans]	16.4 16.4
	452323 407699	W44356 AAB25974	Hs.292812 Hs.32646	Homo saplens cDNA: FLJ21901 fis, clone HEP034	16.4
80	414617	AI339520	Hs.20524	ESTs, Moderately similar to hexokinase I [H.s	16.3
-	408204	AA454501	Hs.43666	protein tyrosine phosphalase type IVA, member	16.3
	452650	AW270150	Hs.254516	ESTs	16.3
	432906	BE265489	Hs.3123	tethal glant larvae (Drosophilia) homolog 2	16.3
	402408			. 0	16.3
				104	

	408805	H69912	Hs.48269	vaccinia related kinase 1	16.3
	447155	AA100605	Hs.121557	ESTs, Weakly similar to AF251041 1 SGC32445 p	16.3
	405699			0	16.2
_	406893	M22406		gb:Human Intestinal mucin mRNA, partial cds,	16.2
5	418629	BE247550	Hs.86859	growth factor receptor-bound protein 7 (GRB7)	16.2
	424905	NM_002497	Hs.153704	NIMA (never in miliosis gene a)-related kinase	16.2
	424243	AI949359	Hs.301837	ESTs, Highly similar to cis Golgi-localized c	16.2
	418462	BE001596	Hs.85266	Integrin, beta 4	16.1
	457205	Al905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	16.1
10	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal t	16.1
	449845	AW971183	Hs.60054	ESTs	16.1
	406429			0	16.1
	407375	AA091354		gb:li0815.seq.F Human fetal heart, Lambda ZAP	16.1
	448377	Al494514	Hs.171380	ESTs	16.1
15	431156	NM_002220	Hs.2722	inositol 1,4,5-trisphosphate 3-kinase A	16.0
13	450043	AA885699	Hs.24332		16.0
		AA003033	113.24332	CGI-26 protein	16.0
	403121			0	15.9
	400214	200400	11-045705	0 .	
20	453252	R02436	Hs.215725	ESTs	15.9
20	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate, RC3)	15.9
	416855	AA188763	Hs.36793	Homo saplens cDNA: FLJ23188 ffs, clone LNG120	15.9
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interacting pro	15.9
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
05	428187	AI687303	Hs.285529	ESTs	15.9
25	438817	AI023799	Hs.163242	ESTs	15.9
	425692	D90041	Hs.155956	NAT1; arylamine N-acetyltransferase	15.9
	421674	T 10707	Hs.296355	neuronal PAS domain protein 2	15.9
	439999	AA115811	Hs.6838	ras homolog gene family, member E	15.9
	411351	W02919	Hs.283476	peroxisomal acyl-CoA thioesterase	15.9
30	413027	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	15.9
	453884	AA355925	Hs.36232	KIAA0186 gene product	15.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase C-bet	15.8
	422748	AA316266	Hs.129349	ESTs	15.8
	414591	AI888490	Hs.55902	ESTs	15.8
35	421877	AW250380	Hs.109059	milochondrial ribosomal protein L12	15.8
55		A11230300	15.103033	0	15.8
	404780			·	15.8
	401192	1145050	11- 00440	0	15.8
	447519	U45258	Hs.23448	ESTs .	
40	434262	AF121858	Hs.12169	sorting nextin 8	15.7
40	451253	H48299	Hs.26126	daudin 10	15.7
	435499	R89344	Hs.14148	ESTs	15.7
	422424	AI186431	Hs.116577	prostate differentiation factor; placental bo	15.7
	424834	AK001432	Hs.153408	Homo saptens cDNA FLJ10570 fls, clone NT2RP20	15.7
4.5	424562	Al420859	Hs.150557	basic transcription element binding protein 1	15.7
45	443247	BE614387	Hs.47378	ESTs	15.7
	430696	AA531276	Hs.59509	ESTs	15.6
	437044	AL035864	Hs.69517	ESTs, highly similar to differentially expres	15.6
	428237	AF175206	Hs.183125	killer cell lectin-like receptor F1	15.6
	440048	AA897461	Hs.158469	ESTs, Wealdy similar to envelope protein [H.s	· 15.6
50	414922	D00723	Hs.77631	glycine cleavage system protein H (aminomethy	15.6
	422030	X51416	Hs.110849	estrogen-related receptor alpha	15.6
	408716	Al567839	Hs.151714	ESTs	15.5
	410258	X52638	Hs.739	6-phosphofructo-2-ktnase/fructose-2,6-blphosp	15.5
	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR A	15.5
55	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	15.5
	409015	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S protein	15.5
	447549		Hs.231265	ESTs :	15.5
	449704	AK000733	Hs.23900	GTPase activating protein	15.4
	427337	Z46223	Hs.176663	Fo fragment of IgG, low affinity lilb, recept	15.4
60	421630	NM_001956	Hs.1407	endothelin 2	15.4
00	433018	AI669760	Hs.188881	ESTs	15.4
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	15.3
			ns.1354		15.2
	407014 429311	U38268	Un 400000	gb:Human cytochrome b pseudogene, partial cds	15.2
65		AF080157	Hs.198998	conserved helix-loop-helix ubiquitous kinase	
UJ	431842	NM_005764	Hs.271473	epitheliai protein up-regulated in cardinoma,	15.2
	406907	Z25427	11s 4 40F0F	gb:H.sapiens protein-serine/threonine kinase	15.2
	458495	Al202029	Hs.148593	ESTs	15.2
	420551	AL137692	Hs.98790	Homo sapiens mRNA; cDNA DKFZp434P182 (from cl	15.1
70	448443	AW167128	Hs.231934	ESTs	15.1
70	443646	AI085198	Hs.298699	ESTs	15.1
	431538	AL137547	Hs.259619	Homo saplens mRNA; cDNA DKFZp434B1120 (from c	15.1
	436687	AA868643	Hs.120461	ESTs	15.1
	420917	AW135716	Hs.117330	ESTs	15.0
	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibitor, d	15.0
75	403482			0	15.0
	421499	A1271438	Hs.105022	Homo saplens PAC clone RP4-701016 from 7q33-q	15.0
	401047			0	14.9
	417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	14.9
	416693	AJ373204	Hs.79531	Homo sapiens TTF-I Interacting peptide 20 mRN	14.9
80	428474	AB023182	Hs.184523	KIAA0965 protein	14.9
- •	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (campome	14.9
	430271	T06199	Hs.237506	heat shock cognate 40	14.9
	414328	Z21666	Hs.75900	aconitase 2, mitochondrial	14.9
	415314	N88802	Hs.5422	glycoprotein M6B	14.8
	110017			. •• ••	

	453735	Al066629	Hs.125073	ESTs .	14.8
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 ffs, clone NT2RP20	14.8
	423575	C18863	Hs.163443	ESTs	14.8
_	438081	H49546	Hs.298964	ESTs	14.8
5	403485			0	14.8
_	452114	N22687	Hs.8236	ESTs	14.8
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system 4	14.8
	412869	AA290712	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	14.8
	452101	T60298		gb:yb87f12.r1 Stratagene liver (937224) Homo	14.7
10	420505	AW967984	Hs.291612		14.7
10				ESTS	
	426125	X87241	Hs.166994	FAT turnor suppressor (Orosophila) homolog	14.7
	433336	AF017986	Hs.31386	ESTs; Highly similar to FRIZZLED PROTEIN PRE	14.7
	428977	AK001404	Hs.194698	cyclin B2	14.7
		H82114			
1.5	429785	H02114	Hs.301769	ESTs	14.7
15	402424			0	14.7
	424971	AA479005	Hs.154036	turnor suppressing subtransferable candidate 3	14.7
	433037	NM_014158	Hs.279938	HSPC067 protein	14.6
	421670	BE207318	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy	14.6
	438598	A1805943	Hs.5723	Homo saplens cDNA: FLJ23439 fis, clone HSI001	14.6
20	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation initi	14.6
20					
	410561	BE540255	Hs.6994	Homo saplens cDNA: FLJ22044 ffs, clone HEP091	14.6
	402287			0	14.6
	419741	NM_007019	Hs.93002	ubliquitin cerrier protein E2-C	14.6
	442047	AA974598	Hs. 150324	ESTs	14.5
25					
23	428582	BE336699	Hs.185055	BENE protelin	14.5
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	14.5
	406851	AA609784	Hs.180255	major histocompatibility complex, class II, D	14.5
	457316	Al123657	Hs.127264	ESTs	14.5
	420453	AL157500	Hs.97840	Homo saplans mRNA; cDNA DKFZp434G015 (from d	14.5
30	436406	AW105723	Hs.125346	ESTs .	14.5
50					
	420736	AI263022	Hs.82204	ESTs	14.5
	419743	AW408762	Hs.127478	ESTs .	14.5
	429113	D28235	Hs.196384	Prostaglandin-endoperoxide synthase 2 (COX-2)	14.5
25	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-rich tan	14.5
35	424906	Al566086	Hs.153716	Homo saplens mRNA for Hmob33 protein, 3' untr	14.5
	427414	F11750	Hs.6647	Homo saplens cDNA FLJ13088 fis, clone NT2RP30	14.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activat	14.4
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	14.3
40	424669	AA417181	Hs.120858		14.3
70				Homo saptens cDNA FLJ13945 fis, clone Y79AA10	
	408989	AW361666	Hs.49500	KIAA0746 protein	14.3
	406788	AI911841	Hs.5184	TH1 drosophila homolog	14.3
	417861	AA334551	Hs.82767	sperm specific antigen 2	14.3
		777007001	113.02101	spenn specific anagen z	
4.0	402104			U	14.3
45	416368	R88849		gb:ym98a06.r1 Soares adult brain N2b4HB55Y Ho	14.2
	405802			0	14.2
		1100400	11- 400000	· .	
	448357	N20169	Hs.108923	ESTs	14.2
	444261	AA298958	Hs.10724	MDS023 protein	14.2
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	14.2
50					
50	425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain 2	14.1
	402520			0	14.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	14.1
	430044	AA464510	Hs.152812		14.1
				EST cluster (not in UniGene)	
	429663	M68874	Hs.211587	Human phosphalidylcholine 2-acylhydrolase (cP	14.1
55	427036	AA397625	Hs.163913	ESTs .	14.1
	444381	BE387335	Hs.283713	ESTs	14.1
	432090	AW972855	Hs.292853	ESTs	14.0
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (from cl	14.0
	404961	AW972195	Hs.284236	aldo-keto reductase family 7, member A3 (afla	14.0
60	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	14.0
00					
	452355	N54926	Hs.29202	G protein-coupled receptor 34	14.0
	429942	A1338993	Hs.134535	ESTs	14.0
	403165			0	13.9
		A12004E0	Ne 400004	ESTs .	
CF	442150	Al368158	Hs.128864		13.9
65 ·	439709	AW401433	Hs.6649	hypothetical protein FLJ20128	13.9
	456799	AC004923	Hs.135187	Homo sapiens clone CDABP0025 mRNA sequence	13.9
	427356	AW023482	Hs.97849	ESTs	13.9
	448982	A1638164	Hs.225520	ESTs	13.9
	432025	BE407132	Hs.111286	hypothetical protein FLJ22512	13.8
70		AA361562			13.8
, 0	427505	MM30 1302	Hs.178761	26S proteasome-associated pad1 homolog	
	402965			U	13.8
	418601	AA279490	Hs.86368	calmegin	13.8
	436954	AA740151	Hs.130425	ESTs	13.8
		INTERIOR	110.130123		
76	405024			0	13.8
75	453976	BE463830	Hs.163714	ESTs	13.8
	431921	N46466	Hs.58879	ESTs	13.8
		1710100	110.00013		
	401735			0	13.8
	445496	AB007860	Hs.12802	development and differentiation enhancing fac	13.8
	425007	AA456483	Hs.172081	phosphodiesterase 4D, cAMP-specific (dunce (D	13.7
80					
OU	409463	AI458165	Hs.17296	EST8	13.7
	430193	A1826653	Hs.102928	Homo sapiens cDNA FLJ13479 fis, clone PLACE10	13.7
		AI637934	HS.224978	ESIS	1.1.7
	458869	A1637934	Hs.224978	ESTs	13.7
	458869 426769	AA075598	Hs.172153	glutathlone peroxidase 3 (plasma)	13.7
	458869				

	439901	N73885	Hs.124169	ESTs	13.7
	431374	BE258532	Hs.251871	CTP synthase	13.7
	432861 441172	- AA339526 Al279652	Hs.279593 Hs.132879	HSPC171 protein ESTs	13.7 13.7
5	410001	AB041036	Hs.57771	kallikrein 11; serine protease (TLSP)	13.7
•	430315	NM_004293	Hs.239147	guanine deaminase	13.6
	422769	AA938905	Hs.289112	CGI-43 protein	13.6
	402389			0	13.6
10	448977	X91809	Hs.22698	regulator of G-protein signalling 19	13.6
10	459648			gb:IL3-CT0220-150200-070-B02 CT0220 Homo sapl	13.6
	452972	M31732	Hs.31210	B-cell CLL/tymphoma 3	13.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	13.6 13.6
	448585 428385	AB020676 AF112213	Hs.21543 Hs.184062	KIAA0869 protein putative Rab5-interacting protein	13.6
15	426363 434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEM8B10	13.6
13	447238	AW451676	Hs.158564	ESTs	13.6
	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HS1009	13.6
	425749	AW328587	Hs.159448	surfelt 2	13.5
•	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	13.5
20	413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin (140	13.5
	419034	NM_002110	Hs.89555	hemopoletic cell kinase	13.5
	448361	H82028	Hs.238707	Homo sapiens cDNA: FLJ22457 fis, clone HRC099	13.5
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein 1	13.5 13.5
25	419081 407732	AJ798863 AW138839	Hs.87191 Hs.24210	ESTs :	13.5
23	423329	AF054910	Hs.127111	tektin 2 (testicular)	13.5
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68k	13.4
	439636	AF086467	110.110.01	gb:Homo sapiens full length insert cDNA clone	13.4
	417605	AF006609	Hs.82294	regulator of G-protein signalling 3	13.4
30	445861	BE293423	Hs.11809	single ig IL-1R-related molecule	13.4
	447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
	451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	13.4
25	422443	NM_014707	Hs.116753	histone deacetylase 7B	13.4
35	412504	Z44496	Hs.26039	Homo saplens cDNA FLJ13937 fis, clone Y79AA10	13.4
	453344	BE349075	Hs.44571	ESTs 0	13.4 13.4
	402885 438712	AW978161	Hs.169877	ESTs	13.4
	421774	AL050374	Hs.108169	DKFZP586C1619 protein	13.3
40	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific protein 1	13.3
	401897			0	13.3
	425601	AW629485	Hs.293352	ESTs	13.3
	450779	AW204145	Hs.156044	ESTs	13.3
4.00	444858	AJ199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	13.3
45	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 protein x	13.3
	434263	N34895	Hs.44648	ESTs	13,3
	426059	BE292842	Hs.166120	Interferon regulatory factor 7	13.3 13.3
	407467	D55638 R24601	Hr 108300	gb:Human B-cell PABL (pseudoautosomal boundar CCR4-NOT transcription complex, subunit 3	13.3
50	412560 442986	AI025990	Hs.108300 Hs.285520	ESTs	13.2
50	420317	AB006628	Hs.96485	KIAA0290 protein	13.2
	443211	Al128388	Hs.143655	ESTs	13.2
	434361	AF129755	Hs.117772	ESTs	13.2
	423493	AI815965	Hs.129683	ubiquitin-conjugating enzyma E2D 1 (homologou	13.2
55	414183	AW957446	Hs.301711	ESTs	13.2
	447778	BE620592	Hs.71190	ESTs	13.2
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box prot	13.1
	439490	AW249197	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	• 13.1
60	409606	AW444594	Hs.2387	transglutaminase 4 (prostate)	13.1
OU	421308	AA687322	Hs.192843	ESTS	13.1 13.1
	414950 416783	C15407 AA206186	Hs.79889	gb:C15407 Clontech human aorta polyA+ mRNA (6 monocyte to macrophage differentiation-associ	13.1
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod phenotype)	13.1
	422605	H16646	Hs.118666	Human clone 23759 mRNA, partial ods	13.0
65	430427	AA296701	Hs.241413	opticin	13.0
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	13.0
	421693	X71490	Hs.106876	ATPase, H+ transporting, lysosomal (vacuolar	13.0
	407727	AW411148	Hs.38044	DKFZP564M082 protein	13.0
70	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	13.0
70	406709	Al355761	Hs.242463	keratin 8	13.0
	405353	COOK OC181A	Un 24E04	0 ESTs	13.0 13.0
	453060 459299	AW294092 BE094291	Hs.21594 Hs.155651	hepatocyte nuclear factor 3, beta	13.0
	459299 447843	AW337186	Hs.224891	ESTs	13.0
75	446576	A1659477	Hs.51820	ESTs, Moderately similar to ALU7_HUMAN ALU SU	13.0
. 5	449700	L02867	Hs.78358	ESTs	13.0
	436476	AA326108	Hs.53631	ESTs	13.0
	432532	AW058459	Hs.162248	ESTs	13.0
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	13.0
80	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40 co-ch	129
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mitoc	12.9
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase A1a	12.9
	427923	AW274357	Hs.268384	Fzr1 protein	12.9 12.9
	437395	AL365408	Hs.10632	hypothetical protein DKFZp762M136	123

	441697	AA947552	Hs.58086	ESTs	12.9
	441627 419084	AA496539	Hs.179902	transporter-like protein .	12.9
	423067	AA321355	Hs.285401	ESTs	12.9
_	423070	R55677	Hs.155569	ESTs	12.8
5	441344	BE250144	Hs.41514	ESTs	12.8
	423527	A1206965	Hs.105861	Homo saplens cDNA FLJ13824 fts, clone THYRO10	12.8
	417006	AW673606	Hs.80758	aspartyl-IRNA synthetase	12.8
	453552	AL041941	Hs.154729	3-phospholnositide dependent protein kinase-1	12.8
10	453657 434414	W23237 Al798376	Hs.298162	ESTs gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA	12.8 12.7
10	456051	T85626	Hs.76239	hypothelical protein FLJ20608	12.7
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
	418216	AA582240	Hs.283099	AF15q14 protein	12.7
	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-recog	12.7
15	424275	AW673173	Hs.144505	DKFZP566F0546 protein	12.7
	440062	Al350518	Hs.129692	ESTs	12.7
	444371	BE540274	Hs.239	Forkhead box M1	12.7
	412520	AA442324	Hs.795	H2A histone family, member O	12.7
20	413349	BE086692	Hs.76285	gb:QV1-BT0678-130400-156-g07 BT0678 Homo sapl	12.7 12.6
20	414500 429261	W24087 AW176254	Hs.143475	DKFZP564B167 protein ESTs	12.6
	402238	ATT110234	110.170773	0	12.6
	400280			Ŏ	12.6
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pro	12.6
25	442029	AW956698	Hs.14456	neural precursor cell expressed, developmenta	12.6
	435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl D-as	12.6
	409964	AW368226	Hs.67928	ESTs	12.6
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	12.5
30	452117	AI421760	Hs.77870	Homo saplens cDNA FLJ12750 fis, clone NT2RP20	12.5
30	448074	BE621355	Hs.27160	ESTs	12.5 12.5
	442655 409928	AW027457 AL137163	Hs.30323 Hs.57549	ESTs hypothetical protein dJ473B4	12.5
	400240	AL13/103	NS.37343	O O	12.5
	413048	M93221	Hs.75182	mannose receptor, C type 1	12.5
35	426215	AW963419	Hs.155223	ESTs	12.5
	430024	AI808780	Hs.227730	integrin, alpha 6	12.5
	445655	AA873830	Hs.167746	B cell linker protein	12.5
	419941	X98654	Hs.93837	phosphalidylinositol transfer protein, membra	12.5
40	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (soluble)	12.5
40	427767	AI879283	Hs.180714	cytochrome c oxidase subunit VIa polypeptide	12.4
	450243	AW119084	Hs.201037	ESTs	12.4
	408930	AA146721	Hs.49005	hypothetical protein	12.4 12.4
	418783	T41368 BE394901	Hs.226785	gb:ph1d1_19/1TV Outward Alu-primed hncDNA lib ESTs	12.4
45	452096 424513	BE385864	Hs.149894	mitochondrial translational initiation factor	12.4
-13	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	12.4
	409031	AA376836	Hs.76728	ESTs	12,4
	435515	N40080	Hs.6879	DC13 protein	12.4
	429583	NM_006412	Hs.209119	1-acylglycerol-3-phosphate O-acyltransferase	12.3
50	449643	R05989	Hs.19603	ESTs	12.3
	440313	AL050060	Hs.7158	DKFZP566H073 protein	12.3
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	12.3
	447357	Al375922	Hs.159367	ESTs	12.3
55	405089	0000000	U. 7700E	O MARRONS compression	12.3 12.3
25	414972	BE263782	Hs.77695	KIAA0008 gene product ESTs	12.3
	435039 447033	AW043921 Al357412	Hs.130526 Hs.157601	EST - not in UniGene	12.3
	427521	AW973352	Hs.299056	ESTs	12.3
	409377	AA300274	Hs.115659	Homo saplens cDNA: FLJ23461 fis, clone HS1077	12.3
60	400116			0	12.3
	445806	AL137516	Hs.13323	hypothelical protein FLJ22059	12.2
	457817	AA247751	Hs.79572	cathepsin D (lysosomal aspartyl protease)	12.2
	442410	AW996503	Hs.197680	ESTs	12.2
65	445404	AJ261687	Hs.145541	ESTs, Weakly similar to JC4974 sodium todide	12.2
65	403372	AW249152	Hs.44017	SIR2 (silent mating type information regulati	12.2
	427082	AB037858	Hs.173484	hypothetical protein FLJ10337	12.2 12.2
	433764 400268	AW753676	Hs.39982	ESTs ·	12.2
	433190	M26901	Hs.3210	renin	12.2
70	444863	AW384082	Hs.301323	ESTs	12.2
. •	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, subfam	12.2
	451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein (leu	12.2
	430262	AA218780	Hs.237323	N-acetylgtucosamine-phosphate mutase	12.2
-	421071	Al311238	Hs.104476	ESTs	12.2
75	426773	NM_015556	Hs.172180	KIAA0440 protein	12.1
	409178	BE393948	Hs.50915	keliikrein 5	12.1
	400250	MA 64 1951	Un 40 4000	U NAAAATE aana amdust	12.1
	428450	NM_014791	Hs.184339	KIAA0175 gene product	12.1 12.1
80	414531 448210	T69387 AW247775	Hs.76364 Hs.7393	allografi Inflammatory factor 1 hypothetical protein from EUROIMAGE 1987170	12.1
30	440081	AW247775 AA863389	Hs.135643	ESTs	12.1
	413179	N99692	Hs.75227	NADH dehydrogenase (ubiquinone) 1 alpha subco	12.1
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	12.1
	400517	AF242388	Hs.149585	lengsin	12.1
				100	

	401610			0	12.0
	454381	A1935093	Hs.193428	ESTs	12.0
	443997	AW081465	Hs.299644	ESTs	12.0
•	402944			0	12.0
5	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin	12.0
	415099	Al492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3 (ubiq	12.0 12.0
	445422 416667	AV653731 AK000526	Hs.282829 Hs.79457	ESTs hypothetical protein FLJ20519	12.0
	442611	BE077155	Hs.177537	ESTs	12.0
10	443271	BE568568	Hs.195704	ESTs	12.0
	415120	N64464	Hs.34950	ESTs	12.0
	439574	AJ469788	Hs.165190	ESTs	12.0
	405804			0	12.0
1.5	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	12.0
15	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	12.0 12.0
	447075 416841	AV662037 N33878	Hs.124740 Hs.249495	ESTs heterogeneous nuclear ribonucleoprotein A1	12.0
	402943	100010	110,270700	0	11.9
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypeptide A	11.9
20	439744	AL389994	Hs.301272	ESTs, Weakly similar to homologue of Drosphil	11.9
	405762			0	11.9
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductance reg	11.9
	455102	BE005496		gb:CM1-BN0117-110400-183-b09 BN0117 Homo sapi	11.9
25	402840	414445000	13- 400000	U analogo aDMA: F1 194425 for alogo CACO72	11.9 11.9
23	449183 439273	AW445022 AW139099	Hs.196985 Hs.269701	Homo saplens cDNA: FLJ21135 fis, clone CAS072 ESTs	11.9
	450484	BE220675	113.203701	gb:hi98f11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA	11.9
	445431	AF137386	Hs.12701	plasmolipin	11.9
	401888			Ò	11.9
30	426037	AW160780	Hs.166071	cyclin-dependent kinase 5	11.9
	416742	R38644	Hs.248420	ESTs	11.9
	418324	AW246273	Hs.84131	threonyl-IRNA synthetase	11.8
	412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	11.8
35	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	11.8 11.8
33	421478 426635	A1683243 BE395109	Hs.97258 Hs.129327	ESTs ESTs	11.8
	420523	AA262999	Hs.42788	ESTs	11.8
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mRNA; 3	11.8
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachned	11.8
40	441816	AI401807	Hs.149997	ESTs	11.8
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	11.8
	400640			0	11.8
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	11.8 11.8
45	401532 400161			0	11.8
70	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (from c	11.7
	451002	AA013299	Hs.8018	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	11.7
	401879			0	11.7
	415989	Al267700	Hs.111128	ESTs	11.7
50	416434	AW163045	Hs.79334	nuclear factor, Interleukin 3 regulated	11.7
	410616	AW873401	Hs.273599	ESTs	11.7
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1 Homo saplens mRNA; cDNA DKFZp564E122 (from cl	11.7 11.7
	447669 436877	AL049985 AA931484	Hs.19180 Hs.121255	ESTs, Wealdy similar to cDNA EST EMBL:D67419	11.7
55	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	11.7
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	11.7
	400279			0	11.6
	440497	AA887266	Hs.144979	ESTs	11.6
~	451260	AW750773		gb:CM0-CN0044-260100-164-h03 CN0044 Homo sapl	11.6
60	429175	A1953040	Hs.127714	ESTs, Moderately similar to SOX30 protein [H.	11.6
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule)	11.6 11.6
	428856	AA436735 N22120	Hs.183171 Hs.75277	Homo saplans cDNA: FLJ22002 fis, clone HEP066 hypothetical protein FLJ13910	11.6 11.6
	420153 428760	AI351459	Hs.192398	ESTs	11.6
65	421401	AW410478	Hs.104019	transforming, acidic coiled-coll containing p	11.6
•-	404502		,	0	11.6
	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical protein	11.6
	405192			0	11.6
70	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	11.6
70	401714	117/0007	N= 50400	0 ESTs, Wealdy similar to S59856 collagen alpha	11.5 11.5
	439335	AA742697	Hs.62492 Hs.82927	adenosine monophosphate deaminase 2 (isoform	11.5
	406082 401010	S47833	136361	0	11.5
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	11.5
75	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodiester	11.5
	459684			gb:ao86a08.x1 Schiller meningioma Homo saplen	11.5
	451051	BE254309	Hs.125262	DKFZP586G1624 protein	11.5
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chronic	11.5
00	412153	R87934		gb:yo47b10.r1 Soares adult brain N2b4HB55Y Ho	11.5
80	427256	AL042436	Hs.97723	ESTs	11.5 11.4
	408708	A1282759 AA770080	Hs.242463 Hs.144962	keratin 8 ESTs, Moderately similar to 159365 ubiquitin	11.4
	457644 422848	Z25884	Hs.121483	chloride channel 1 , skeletal muscle (Thomsen	11.4
	424134	AF070637	Hs.140950	hypothetical protein	11.4

	451931	AK000208	Un 27267	Homo sapiens cDNA FLJ20201 fis, clone COLF121	11.4
	400438	AF185611	Hs.27267 Hs.115352	growth hormone 1	11.4
	412994	D32257	Hs.75113	general transcription factor IIIA	11.4
_	408124	U89337	Hs.42853	cAMP responsive element binding protein-like	11.4
5	452249	BE394412	Hs.61252	ESTs	11.4
	424627	AA344555		gb:EST50715 Gall bladder I Homo sapiens cDNA	11.4
	405626 436690	AA373970	Hs.183098	0 ESTs	11.4 11.4
	415862	R51034	Hs.144513	ESTs	11.4
10	406755	N80129	Hs.94360	metallothlonein 1L	11.4
	433657	AI24436B	Hs.8124	PH domain containing protein in retina 1	11.4
	429612	AF082649	Hs.252587	pituitary tumor-transforming 1	11.4
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	11.4
15	433053	BE301909	Hs.279952 Hs.184276	glutathione S-transferase subunit 13 homolog solute canter family 9 (sodium/hydrogen exch	11.4 11.3
13	428423 442353	AU076517 BE379594	Hs.49136	ESTs	11.3
	447700	AJ420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	402077			0	11.3
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypeptide 1	11.3
20	405145			0	11.3
	428248	AJ126772	Hs.40479	ESTs	11.3
	425508	AA991551	Hs.97013	ESTs	11.3 11.3
	428340 431452	AF261088 Al073641	Hs.154721 Hs.152372	aconitase 1, soluble ESTs	11.3
25	446651	AA393907	Hs.97179	ESTs	11.3
25	443755	C18397	Hs.9730	tachykinin 3 (neuromadin K, neurokinin beta)	11.3
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	11.3
	401020			0	11.3
20	456724	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	11.2
30	407227	H94949	Hs.171955	trophinin associated protein (tastin)	11.2 11.2
	402066 442721	AI015892	Hs.101282	0 Homo sapiens mRNA; cDNA DKFZp434B102 (from cl	11.2
	401025	AU13032	113.101202	0	11.2
	452423	AA991724	Hs.180535	Homo sapiens cDNA: FLJ22711 fis, clone HSI133	11.2
35	431685	AW296135	Hs.267659	vav 3 oncogene	11.2
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-relate	11.2
	409079	W87707	Hs.82065	Interlaukin 6 signal transducer (gp130; onces	11.2
40	456995	T89832	Hs.170278	ESTs CD0 college (n24)	11.2 11,2
40	419223 407788	X60111 BE514982	Hs.1244 Hs.38991	CD9 antigen (p24) S100 calcium-binding protein A2	11.2
	407604	AW191962	Hs.288061	actin, beta	11.2
	437929	T09353	Hs.106642	ESTs, Weakly similar to hypothetical protein	11.1
	415789	H01581		gb:yj33f08.r1 Soares placenta Nb2HP Homo sapi	11.1
45	424447	AL137376	Hs.147368	Homo saplens mRNA; cDNA DKFZp434J0226 (from c	11.1
	436034	AF282693	Hs.150185	inflammation-related G protein-coupled recept	11.1
	404931	41000047	11- 202205	0	11.1 11.1
	445979 446733	A1695047 AA863360	Hs.202395 Hs.26040	ESTs ESTs; Highly similar to CYTOCHROME P45 IVA2	11.1
50	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
50	445258	AI635931	Hs.147613	ESTs	11.1
	417251	AW015242	Hs.99488	ESTs; Wealty similar to ORF YKR074w [S.cerevi	11.1
	421041	N36914	Hs.14691	ESTs	11.1
	425537	AB007913	Hs.158291	KIAA0444 protein	11.1
55	435763	Al243929	Hs.190419	ESTs	11.1 11.1
	444790	AB030506 AL080235	Hs.11955 Hs.35861	B9 protein DKFZP586E1621 protein	11.1
	453857 433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxyge	11.1
	405358	030111	12.0022	0	11.1
60	435814	AW615179	Hs.152870	ESTs	11.0
	422809	AK001379	Hs.121028	hypothetical protein FU10549	11.0
	446772	AW294404	Hs.144515	Homo sepiens cDNA FLJ11672 fis, clone HEMBA10	11.0
	456694	AW016382	Hs.105642	Homo sapiens cDNA: FLJ23271 fis, clone HEP001 ESTs	11.0 11.0
65	441128 432677	AA570256 NM_004482	Hs.54628 Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypepiid	11.0
05	412576	AA447718	Hs.107057	ESTs	11.0
	411122	F00809	Hs.143696	coactivator-associated arginine mathyltransfe	11.0
	427225	AA432391	Hs.258903	Homo saplens mRNA for KIAA1640 protein, parti	11.0
	426260	NM_002541	Hs.168669	oxoglutarate dehydrogenase (lipoamide)	11.0
70	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A	11.0
	431947	AL359613	Hs.49933	hypothetical protein DKFZp762D1011 Homo sapiens clone CDABP0005 mRNA sequence	11.0 11.0
	414432 458627	BE378174 AW088642	Hs.26508 Hs.97984	ESTs; Wealdy similar to WASP-family protein [10.9
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	10.9
75	447827	AF090922	Hs.285902	CGI-113 protein	10.9
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of 55 kD	10.9
	454227	AW963897	Hs.44743	KIAA1435 protein	10.9
	402927	4 / 000000	11, 4000 10	0	10.9 10.9
80	422380	AA309881	Hs.136248	ESTs gb:RC1-HT0598-140300-021-g06 HT0598 Homo sapi	10.9
30	455986 410962	BE177736 BE273749	Hs.752	FK506-binding protein 1A (12kD)	10.9
	450361	BE327108	Hs.202512	ESTs	10.9
	457484	H57645		gb:yr21e01.r1 Soares fetal liver spieen 1NFLS	10.9
	407903	Al287341	Hs.154029	. bHLH factor Hes4	10.9

				•	
	403398			0	10.9
	401405			0	10.9
	405570			0	10.9
5	421240	R72730	Hs.29283	ESTs, Weakly similar to PLK_HUMAN PROTEOGLYCA	10.9
J	403649			0	10.9
	447824	BE620800		gb:601483379T1 NIH_MGC_69 Homo sapiens cDNA c	10.9
	450935	BE514743	Hs.25664	turnor suppressor deteted in oral cancer-relat	10.9
	439853	AL119566	Hs.6721	lysophospholipase-like	10.9
10	451852	R51928		gbtyj71c05.r1 Soares breast 2NbHBst Homo sapi	10.9
10	431218	NM_002145	Hs.2733	homeo box B2	10.9
	457794	AA689292	Hs.246850	ESTs	. 10.9
	444374	AA009841	Hs.11039	Homo saptens cDNA FLJ12798 fis, clone NT2RP20	10.9
	456566	AW235317	Hs.259214	ESTs	10.8
4 ~	405552			0	10.8
15	439436	BE140845	Hs.57868	ESTs	10.8
	435310	AA705075	Hs.169536	Rhesus blood group-essociated glycoprotein	10.8
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	10.8
	415807	H03139	Hs.24683	ESTs	10.8
~~	409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5	10.8
20	417033	H83784	Hs.40532	ESTs, Wealtly similar to PEBP MOUSE PHOSPHATID	10.8
	418464	R87580		gb:ym89h07.r1 Soares edull brein N2b4HB55Y Ho	10.8
	404567			0	10.8
	418384	AW149266	Hs.25130	ESTs	10.8
	421971	U63127	Hs.110121	SEC7 homolog	10.8
25	428769	AW207175	Hs.106771	ESTs .,	10.8
	459104	R19238	Hs.282057	ESTs	10.8
	410896	AW809637		gb:MR4-ST0124-261099-015-b07 ST0124 Homo sapi	10.8
	416969	AI815443	Hs.283404	organic callon transporter	10.8
	408796	AA688292	Hs.118553	ESTs	10.8
30	426298	AW965058	Hs.111583	ESTs	10.8
	421595	AB014520	Hs.10595B	Homo saplens cDNA: FLJ22735 fis, clone HUV001	10.8
	408007	AW135965	Hs.246783	ESTs	10.8
	400167			0	10.7
	445243	AJ217439	Hs.109854	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	10.7
35	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	10.7
	412241	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapl	10.7
	425827	W28316		gb:45b6 Human retina cDNA randomly primed sub	10.7
	420255	NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral endop	10.7
	430891	U22492	Hs.248118	G protein-coupled receptor 8	10.7
40	402883	OLLIDE	(10.210110	0	10.7
	423811	AW299598	Hs.50895	homeo box C4	10.7
	447078	AW885727	Hs.301570	ESTs	10.7
	414343	AL036166	Hs.75914	coated vesicle membrane protein	10.7
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	10.7
45	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	10.7
73	401220	707200044	113.01200	0	10.7
	459259	AJ003294		gb:AJ003294 Selected chromosome 21 cDNA libra	10.7
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	10.7
	448449	BE314567	Hs.211440	ESTs	10.7
50	429670	L01087	Hs.211593		10.7
50	448759	R61463	Hs.16165	protein kinase C, theta expressed in activated T/LAK lymphocytes	10.7
	400776	NO 1405	ris. 10103	0	10.7
	428093	AW594506	Hs.104830	ESTs	10.7
	412801	AA121055	NS. 104030	gb:zm22b01.r1 Stratagene pancreas (937208) Ho	10.7
55			Un 100550		10.6
	440545 434540	AW183201	Hs.190559 Hs.5184	ESTs TH1 drosophila homolog	10.6
	414273	NM_016045 BE269057	FIS. 0 104	gb:601184231F1 NIH_MGC_8 Homo sapiens cDNA cl	10.6
		DE203031		80:001104231F1 MIN_MOC_0 HOULD SAPERIS COMM CI	
	401817	4141400100	Un 00400	U ambala himalaa ahaashalaa aasa saasataa bi	10.6
60	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-receptor ty	10.6
60	430590	AW383947	Hs.246381	CD68 anligen	10.6
	426580	AA320160	HS.1/1811	adenylate kinase 2	10.6
	445413	AA151342	Hs.12677	CGI-147 protein	10.6
	402947	414074440			10.6
65	457426	AW971119	Un 4744	gb:EST383206 MAGE resequences, MAGL Homo sapi	10.6
UJ	424148	BE242274 ·	Hs.1741	integrin, beta 7	10.6
	404944			0	10.6 10.6
	405421	41722070	Un 70700	0 and and hade 4 feedbade (file 4)	
	416772	AJ733872	Hs.79769	protocadherin 1 (cadherin-like 1)	10.6
70	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.6
70	457588	AI571225	Hs.284171	KIAA1535 protein	10.6
	406038	Y14443	Hs.88219	zinc finger protein 200	10.6
	404790	Alemerene	Un sacon	O Three-becondin 1 (No 97400)	10.6
	418922	AW956580	Hs.42699	Thrombospondin-1 (Hs.87409)	10.6
75	425940	AB023184	Hs.163990	KIAA0967 protein	10.6
75	448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	10.6
	418870	AF147204	Hs.89414	CXCR4; chemokine CXC receptor 4 (fusin)	10.5
	417933	X02308	Hs.82962	thymidylate synthetase	10.5
	45053B	AW297396	Hs.227052	ESTs	10.5
oΛ	427928	AA417662	Hs.119217	ESTs	10.5
80	432721	AL121478	Hs.3132	steroidogenic acute regulatory protein	10.5
	429267	AA299290	Hs.245857	ESTs, Highly similar to S71100 protein kinase	10.5
	439190	AW978693	Hs.293811	ESTs	10.5
	408975	AW958693	Hs.49391	hypothetical protein LOC54149	10.5
	415130	W85893	Hs.249867	. ESTs	10.5
				101	

	425738	H29630	Hs.159408	Homo saplens clone 24420 mRNA sequence	10.5
	440232 425065	A1766925	Hs.112554	ESTs	10.5
	420003 420829	AA371906 AW665612	Hs.294151 Hs.221969	ESTs, Moderately similar to KIAA0544 protein ESTs	10.5 10.5
5	430466	AF052573	Hs.241517	polymerase (DNA directed), thata	10.5
•	407771	AL138272	Hs.62713	ESTs	10.5
	444611	AK002180	Hs.11449	DXFZP564Q123 protein	10.5
	444665	BE613126	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	10.5
10	448030	N30714	Hs.20161	HDCME31P protein	10.5
10	438982	AW979101	Hs.291980	ESTs	10.5
	446224	AW450551	Hs.13308	ESTs	10.5
	405108 438233	W52448	Hs.56147	0 ESTs	10.5 10.5
	401799	1132440	115.00 141	0	10.5
15	454038	X06374	Hs.37040	platelet-derived growth factor alpha polypept	10.5
	414222	AL135173	Hs.878	sorbitol dehydrogenase	10.5
	421828	AW891965	Hs.289109	dimethylarginine dimethylaminohydrolase 1	10.5
	422626	AA344932	Hs.118786	metallothioneln 2A	10.5
20	449261	A1637592	Hs.224958	ESTs	10.4
20	416218	R21499	Hs.23213	ESTs	10.4
	457848 442577	W26524 AA292998	Hs.125682 Hs.163900	ESTs; Wealdy similar to D2092.2 [C.elegans] ESTs	10.4 10.4
	406505	AF016272	Hs.115418	cadherin 16, KSP-cadherin	10.4
	412258	AA376768	Hs.288977	Homo sapiens cDNA: FLJ22622 fis, clone HSI056	10.4
25	429224	AI905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	10.4
	447774	8E018118	Hs.19554	chromosome 1 open reading frame 2	10.4
	403914			0	10.4
	406329			0	10.4
30	402423	4.4.00430	11- 440040	0	10.4
30	431986 423145	AA536130 BE264548	Hs.149018 Hs.222190	ESTs Woolds challes to secretary source man	10.4 10.4
	414402	BE294186	F13.22213U	ESTs, Weakly similar to secretory carrier mem gb:601172959F1 NiH_MGC_17 Homo saptens cDNA c	10.4
	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	10.4
	426095	AJ278023	Hs.89986	ESTs	10.4
35	434577	R37316	Hs.179769	Homo saplens cDNA: FLJ22487 fis, clone HRC109	10.4
	442415	Al005101	Hs.129550	ESTs	10.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	10.3
	435084	D17516	Hs.301607	adenylate cyclase activating polypeptide 1 (p	10.3
40	431724	AA514535	Hs.283704	ESTs .	10.3
40	456798 417370	AJ006422 T28651	Hs.135183 Hs.82030	centaurin-alpha tryptophanyl-IRNA synthetase	10.3 10.3
	422596	AF083611	Hs.118633	2-5'oligoadenylate synthetase-like	10.3
	435226	AI248938	Hs.270106	ESTs	10.3
	433192	AB040880	Hs.225594	ESTs, Moderately similar to KIAA1447 protein	10.3
45	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	10.3
	416228	AW505190	Hs.79089	sema domain, immunoglobulin domain (lg), tran	10.3
	453403	BE466639	Hs.61779	Homo saplens cDNA FLJ13591 fis, clone PLACE10	10.3
	447906	AL050062	Hs.19999	DKFZP566K023 protein	10.3
50	401782	NM_012434	Hs.117865	solute carrier family 17 (anion/sugar transpo	10.3
50	453927 450737	AA082465 AW007152	Hs.301751 Hs.203330	ESTs, Weakly similar to /prediction ESTs	10.3 10.3
	421633	AF121860	Hs.106260	sorting nextn 10	10.3
	409881	AF139799	Hs.202830	ESTS	10.3
	432883	U48936	Hs.3112	sodium channel, nonvoltage-gated 1, gamma	10.3
55	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.3
	419024	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi polype	10.3
	401835			0	10.3
	408896	AI610447	Hs.48778	nlban protein	10.3
60	443120	AW402677	Hs.290801	ESTs 0	10.3 10.2
00	400208 416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	10.2
	400166	~~~~	113.00727	0	10.2
	434642	W25739	Hs.135287	ESTs	10.2
	424837	BE276113	Hs.153436	N-acetyltransferase, homolog of S. cerevislae	10.2
65	435075	R51094	Hs.12400	ESTs	10.2
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pleckst	10.2
	435080	A1831760	Hs.155111	ESTs	10.2
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin-like	10.2
70	410020	T86315 R20693	Hs.728 Hs.69954	ribonuclease, RNase A family, 2 (liver, eosin	10.2 10.2
, 0	411410 450294	H42587	Hs.238730	taminin, gamma 3 ESTs	10.2
	421154	AA284333	Hs.287631	Homo saplens cDNA FLJ14269 fis, clone PLACE10	10.2
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	10.2
	400812			0	10.2
75	425843	BE313280	Hs.159627	death associated protein 3	10.2
	449392	Z41698	Hs.26039	Homo saplens cONA FLJ13937 fis, clone Y79AA10	10.2
	409089	NM_014781	Hs.50421	KIAA0203 gene product	10.2
	401383	V EUJSELJO	Un 152002	0 MAD (methors sections description)s Describ	10.2
80	456855 442912	AF035528 A1088060	Hs.153863 Hs.131450	MAD (mothers against decapentaplegic, Drosoph ESTs	10.2 10.2
55	400954	D25969	Hs.78325	Homo septens cDNA: FLJ23125 fis, clone LNG082	10.2
	401029	BE382701	Hs.25960	v-myc avian myelocytomatosis viral related on	10.2
	416602	NM_006159	Hs.79389	net (chicken)-like 2	10.2
	421905	AJ660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein (H.sapi	10.2

	405094			0	10.2
	450832	AW970602	Hs.105421	ESTs	10.2
	440076	R32052	Hs.178617	ESTs, Wealty similar to AF151840 1 CGI-82 pro	10.2
5	447563	BE536115	Hs.160983	ESTs	10.2
3	421238 400882	AB033101	Hs.102796	KIAA1275 protein 0	10.2 10.2
	415738	BE539367	Hs.295953	ESTs, Wealthy similar to AF220049 1 uncharacte	10.1
	445464	AW172389	Hs.249999	ESTs	10.1
10	459042	AW272058	Hs.210338	ESTs	10.1
10	414469	R51952	Hs.32587	steriod receptor RNA activator 1 (complexes w	10.1
	434732	AI078443	No 174494	gb:oz05g05.x1 Soares_fetal_liver_spleen_1NFLS	10.1
	441030 446855	AW204139 BE616767	Hs.174424 Hs.16269	ESTs, Weakly similar to p140mDia [M.muscutus] B-cell CLL/lymphoma 7B	10.1 10.1
	456785	AF151074	Hs.132744	hypothelical protein	10.1
15	404182			0	10.1
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	10.1
	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, beta po	10.1
	442152 436354	R39246 A1879252	Hs.239666 Hs.5151	Homo saplens cDNA FLJ13495 fls, clone PLACE10 Homo saplens mRNA; cDNA DKFZp564C2163 (from c	10.1 10.1
20	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	10.1
	450599	AA460865	Hs.48516	ESTs	10.1
	454393	BE153288		gb:PM0-HT0335-180400-008-c08 HT0335 Homo sapi	10.1
	403383	1101015	11- 2000 (0	10.1
25	415947	U04045 NM_006799	Hs.78934 Hs.72026	mutS (E. coli) homolog 2 (colon cancer, nonpo	10.1 10.1
23	411773 412116	AW402166	Hs.784	protease, serine, 21 (testisin) Epstein-Barr virus Induced gene 2 (tymphocyte	10.1
	413808	J00287	Hs.182183	caldesmon 1	10.0
	458572	Al223423	Hs.292794	ESTs	10.0
20	403295			0	10.0
30	403910			0	10.0
	453400	Al991901	Hs.82590	ESTs, Moderately similar to ALU7_HUMAN ALU SU 0	10.0 10.0
	406502 404743			Ö	10.0
	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo saplens cDNA cl	10.0
35	402679			0	10.0
	455864	BE148970		gb:CM0-HT0245-031199-085-h05 HT0245 Homo sapi	10.0
	425734	AF056209	Hs.159396	peplidylglycine alpha-amidating monooxygenase	10.0
	419280	W07506	Hs.283725	Homo sapiens cDNA FLJ12627 fis, clone NT2RM40	10.0
40	443503 423165	AV645438 A1937547	Hs.282927 Hs.124915	ESTs Human DNA sequence from clone 380A1 on chromo	10.0 10.0
70	450206	A1796450	Hs.201600	ESTs	10.0
	459052	AA298812	Hs.98539	ESTs	10.0
	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5	10.0
4.5	428438	NM_001955	Hs.2271	Endothelin 1	10.0
45	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	10.0
	426127	L36983	Hs.167013	dynamin 2	10.0
	TABLE 13	B:			
			et identitier num	ber	
50		ber: Gene cluste			
	Accession	: Genbank acco	ession numbers		
	Die	CAT Number	According		
	Pkey 410896	CAT Number 1226053_1			0 AW810088 AW809742 AW809816 AW809749 AW809639 AW809722
55	410000	122000_1			0 AW809728 AW809768 AW809951 AW809657 AW809954
• •	412153	1279701_1		W898205 AW896020 AW896035	
	412241	1284681_1	AW94834	3 AW948341 AW902855 AW984737	
	412517	130281_1		AA112511	
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00	413349 414273	1363558_1 1431911_1		2 BE087077 BE087072 7 BE513434 BE396654	
	414402	1443240_1		BE298975	
	414950	1509777_1		81769 D61133	·
~~	415789	1555357_1		12850 R65905 H13053	
65	416368	1591066_1		84573 H50890	
	418464	17590382	R87580	413C0 T41304	
	418783 424627	1789791_1 241724_1		41369 T41294 5 AA344312 AW963070	
	425827	256834_1		N26507 AA364334	
70	434371	384839_1	AA63136	2 AA631438	
	434414	38585_1			8232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
					173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
					267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 /882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
75					65 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
, 5				5 AW817703 AW817659 BE081531 H59570	TO THE PARTY OF TH
	434732	392447_1		AA648102 AI765577 AW974381	
	439092	468554_1	AA83014	9 AW978407 MB5983 AW503637	
00	439635	47467_1		7 W81444 W81445	
80	447824	738611	BE62080		
	450484	83645_1 863912_1		5 AA345621 AA009992 73 A1768154	
	451260 451852	888359_1		3 A1706154 \1820698 R48360 A1820694	•
	452101	898742_1		N858257 T69667 T67634 T61224 T71537 T68933	
		_		193	•

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AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
BE153288 BE153151 BE152925 AA078302
BE005496 BE005494 AW856324 AW900199
BE148970 BE148975 BE148957 BE148937
BE177735 BE177735 BE177734
AW748920 AA487506 AA248914 AA780494
AW971119 AA574265 AA513268
H57645 T19302 AA527038 Z24851 H93171
AW974668 AA661959 AA649572 AA640401 AA640402
AJ003294 AJ003315 AJ003293
                                                                                          1048369_1
115888_1
1253524_1
1377038_1
1397521_1
187241_1
336189_1
242113_1
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457484
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459259
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389383_1
966269_1
10
                                            TABLE 13C:
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Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495

Strand: Indicates DNA strand from which exons were predicted

NL position: Indicates nucleotide positions of predicted exons 15

20	Pkey	Ref	Strand	Nt_position
20	400640	8117686	Plus	144324-144429
	400666	8118496	Plus	17982-18115,20297-20456
	400776	8131651	Plus	103576-103720
	400812	8568711	Plus	71708-72153
25	400881	2842777	Minus	91446-91603,92123-92265
25	400882	2842777	Minus	110431-110708
	400965	7770576	Minus	173043-173564
	401010	8117391	Minus	83967-84180
	401020	8117458	Minus	59085-60227
20	401025	8117518	Minus	179287-179483,181044-181166,181844-182039
30	401047	6705887	Minus	4804-5035,5133-5314
	401131	8699812	Minus	94802-94987,95804-95887,96323-96487,97596-97826
	401192	9719502	Minus	69559-70101
	401220	9929324	Minus	48079-48279
25	401383	6721135	Minus	155543-157381
35	401405	7768126	Minus	69278-69452,69548-69958
	401519	6649315	Plus	157315-157950
	401532	7798785	Plus	124414-124950,125050-125418
	401610	7705041	Minus	18921-19505
40	401714	6715702	Plus	96484-96681
40	401735	3252819	Plus	217235-217356,217621-217873
	401799	7331447	Plus	147802-148251
	401817	7417850	Minus	45888-46535
	401835	7139700	Plus	142257-142742
45	401879	8099914	Minus	101064-102827
45	401888	8516069	Minus	189498-190514
	401897	8569218	Plus	604-767
	402066	6649269	Plus	135543-136031
	402077	8117414	Plus	65014-65195
50	402104	8119072	Plus	122409-122600
50	402238	7690126	Plus	24726-24880,26791-27021
	402287	4559317	Plus ·	40811-42447
	402389	9885999	Minus	771-972,1571-1683
	402408	9796239	Minus	110326-110491
<i>E E</i>	402423	9796344	Minus	62487-62664
55	402424	9796344	Minus	64925-65073
	402496	9797769	Minus	8615-9103
	402520	7596899	Minus	171761-171996
	402679	8113438	Plus	132079-132216
60	402840	9369121	Minus	57118-57306
60	402883	9926562	Plus	38666-38803,38885-39019,39097-39231,39308-39445
	402885	9926751	Plus	71919-72049
	402926	8217647	Minus	41261-41443
	402927	8217647	Minus	47247-47396
65	402943	6456831	Plus	38467-39068
65	402944	9368423	Plus	110411-110716,111173-111640
	402947	9368458	Minus	101629-101991
	402965	9581599	Minus	· 46865-46941,47032-47148
	403022	3132351	Plus	92097-92864
70	403121	9180223	Plus	4059-4258
70	403165	9838098	Minus	90595-91848
	403295	8096528	Plus	22386-22708
	403381	9438267	Minus	26009-26178
	403383	9438267	Minus	119837-121197
75	403398	6862689	Minus	13685-14699
13	403399	6684178	Plus	61841-62145,62367-62758
	403482	9966050	Plus	196964-197135
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403649	8705159	Minus	27141-27247
0Λ	403910	7710710	Minus	5761-6188
80	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	403914	7417588	Minus	7431-8472
	404182	4775644	Plus	18163-18444
	404502	7229863	Minus	56277-56819
	404567	7249169	Minus	101320-101501
				104

	404678	9797204	Phus	115196-115448
	404743	8894169	Minus	120556-120999
	404780	9887810	Minus	175708-175871
	404790	7230958	Plus	38611-38761
5	404931	7342203	Plus	44226-44382
-	404944	6899705	Plus	4256-4581
	405024	7107727	Plus	88500-88697
	405089	8072523	Plus	103182-103973
	405094	8072579	Plus	135587-135758
10	405108	7107890	Minus	135020-135472
	405145	9438278	Plus	37883-38052.38138-38332
	405192	7230070	Plus	115629-116071
	405224	6731245	Minus	14413-15979
	405295	3818412	Plus	56933-57099
15	405353	2811095	Plus	118525-118892
	405358	2341017	Minus	18016-18315
	405421	7243869	Minus	97411-97687
	405426	7243900	Minus	37640-37817
	405452	7656638	Minus	93876-94275
20	405484	5922025	Plus	199214-199579,199672-199920,200262-200495
	405552	1552506	Plus	45199-45647
	405570	2808656	Plus ·	98208-98331
	405626	4508116	Minus	89275-89384,92450-92629,97091-97279,98546-98666
	405699	4165331	Plus	100727-100859
25	405762	5931935	Plus	160502-161110
	405802	5924004	Minus	27743-28264
	405804	7274891	Minus	122557-123551
	406329	6982072	Minus	.607903-608271
	406429	9256476	Minus	83206-83365,94051-94193
30	406502	7711350	Minus	63430-63602

Table 14A lists about 695 genes up-regulated in ovarian cancer compared to normal adult lissues. These were selected from 59680 probesets on the Aflymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult lissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarians cancers. The "average" normal adult lissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. 35

TABLE 14A: ABOUT 695 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES 40

Pkey: Primekey Ex. Accn: Exemplar Accession UG ID: UniGene ID

Title: UniGene title

45

ratio: ratio of tumor vs. normal tissues

	Ot	Pr. Annu	UGID	Trd-	ratio
	Pkey	Ex. Acon		Title	
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	70.4
	438817	AJ023799	Hs.163242	ESTs	62.8
50	432938	T27013	Hs.3132	steroldogenic acute regulatory protein	57.8
50	421478	AI683243	Hs.97258	ESTs	45.7
	415989	Al267700	Hs.111128	ESTs	42.7
	418179	X51630	Hs.1145	Wilms tumor 1	36.0
	449034	A1624049		gb:ts41a09.x1 NCL_CGAP_Ut1 Homo sapiens cDNA clone	34.0
55	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
55	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-box c	30.1
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix protei	29.4
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal chon	27.0
	435094	Al560129	Hs.277523	EST	26.2
~	430691	C14187	Hs.103538	ESTs	26.2
60	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clone EU	26.1
	415511	AJ732617	Hs.182362	EST8	24.8
	448243	AW369771	Hs.77496	ESTs	24.7
	428187	AI687303	Hs.285529	ESTs	23.9
	408081	AW451597	Hs.167409	ESTs	21.9
65	418007	M13509	Hs.83169	Matrix metalloprotease 1 (Interstitial collagenase	20.6
	400292	AA250737	Hs.72472	BMPR-lb; bone morphogenetic protein receptor; typ	20.6
	422956	BE545072	Hs.122579	ESTs	20.0
	413335	AI613318	Hs.48442	ESTs	19.9
	423739	AA398155	Hs.97600	ESTs	18.9
70	410929	H47233	Hs.30643	ESTs	18.5
	424086	Al351010	Hs.102267	tysyl oxidase	17.7
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	17.4
	427356	AW023482	Hs.97849	ESTs	17.4
	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Homo sapien	17.1
75	407638	AJ404672	Hs.288693	EST	17.1
-	427469	AA403084	Hs.269347	ESTs	17.0
	438993	AA828995		Integrin; beta 8	16.7
	428684	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.5
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clone EU	16.5
80	421155	H87879	Hs.102267	lysyl oxidase	16.1
	426635	BE395109	Hs.129327	ESTs	15.9
	431989	AW972870	Hs.291069	ESTs	15.9
	422805	AA436989	Hs.121017	H2A histone family; member A	15.9
	444783	AK001458	Hs.62180	. ESTs	15.8
				•	

	40.4504	Lectors	11. 450047	and the face of the control of the O	40.7
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), alpha 2	15.7
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAMIL	15.7
	459325	AW088369	Hs.282184	ESTs	15.6
_	428976	AL037824	Hs.194695	ras homolog gene family, member I	15.1
5	416209	AA236776	Hs.79078	MAD2 (mitotic errest deficient, yeast, homolog)-li	15.0
	408660	AA525775	Hs.292523	ESTs	15.0
	410247	AF181721	Hs.61345	RU2S	15.0
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	15.0
	459583	AI907673		gb:lL-BT152-080399-004 BT152 Homo sapiens cDNA, mR	14.8
10	413623	AA825721	Hs.246973	EST8	14.8
	439706	AW872527	Hs.59761	ESTs	14.7
	409041	AB033025	Hs.50081		14.6
				KIAA1199 protein	
	451110	AI955040	Hs.301584	ESTs	14.5
15	436775	AA731111	Hs.291891	EST ₈	14.3
15	443211	AI128388	Hs.143655	ESTs	14.3
	445258	AI635931	Hs.147613	ESTs	14.2
	447350	A1375572	Hs.172634	ESTs; HER4 (c-erb-B4)	14.2
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	14.1
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.9
20	447033	Al357412	Hs.157601	EST - not in UniGene	13.7
	423811	AW299598	Hs.50895	homeo box C4	13.7
	452461	N78223	Hs.108106	transcription factor	13.7
	451106	BE382701	Hs.25960	N-myc	13.6
	416208	AW291168	Hs.41295	ESTs	13.5
25	452249	BE394412		COTA	13.4
25			Hs.61252	ESTs -	
	452055	Al377431	Hs.293772	ESTs	13.2
	439243	AA593254	Hs.191349	ESTs	13.1
	420149	AA255920	Hs.88095	ESTs	12.9
	429125	AA446854	Hs.271004	ESTs	12.9
30	413597	AW302885	Hs.117183	ESTs	12.8
	416566	NM_003914	Hs.79378	cydin A1	12.8
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo saplens cDNA clon	12.7
	407710	AW022727	Hs.23616	ESTs	12.6
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.6
35	428392	H10233	Hs.2265	secretary granule, neuroendocrine protein 1 (782 p	12.4
55					
	431725	X65724 .	Hs.2839	Norte disease (pseudoglioma)	12.3
	447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serine/threonin	12.2
	458027	L49054	Hs.85195	ESTs, Highly similar to 1(3;5)(q25.1;p34) fusion g	12.2
40	408460	AA054726	Hs.285574	ESTs	12.2
40	424735	U31875	Hs.152677	short-chain alcohol dehydrogenase family member	12.0
	415263	AA948033	Hs.130853	ESTs	11.9
	400298	AA032279	Hs.61635	STEAP1	11.8
	452096	BE394901	Hs.226785	ESTs	11.7
	421451	AA291377	Hs.50831	ESTs	11.6
45	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-related pro	11.6
73					
	443715	AI583187	Hs.9700	cyclin E1	11.5
	402606	#(NOCAT)			11.5
	436954	AA740151	Hs.130425	ESTs	11.5
50	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity gluta	11.5
50	410102	AW248508	Hs.279727	ESTs;	11.4
	408562	A1436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, partial cd	11.4
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	11.4
	442353	BE379594	Hs.49136	ESTs	11.3
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.2
55	453160	Al263307	Hs.146228	ESTs	11.2
-	426427	M86699	Hs.169840	TTK protein kinase	11.1
			Hs.9012	·	11.1
	449433	AI672096		ESTs	
	412723	AA648459	Hs.179912	ESTs	11,1
60	400250			0	11.1
60	419752	AA249573	Hs.152618	ESTs	11.1
	438167	R28363	Hs.24286	ESTs	11.1
	434539	AW748078	Hs.214410	ESTs	10.9
	429918	AW873986	Hs.119383	ESTs	10.8
_	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (mel	10.8
65	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	10.B
	420900	AL045633 .	Hs.44269	EST8	10.8
	428758	AA433988	Hs.98502	Homo saplens cDNA FLJ14303 fis, clone PLACE2000132	10.8
					10.5
	446142	AI754693	Hs.145968	ESTS	
70	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid 17-alpha-	10.6
10	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	10.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	10.5
	433447	U29195	Hs.3281	neuronal pentraxin II	10.4
	424188	AW954552	Hs.142634	zinc finger protein	10.4
	414245	BE148072	Hs.75850	WAS protein family, member 1	10.3
75	426462		Hs.169993	dermatan sulphate proteoglycan 3	10.3
	418601	AA279490	Hs.86368	calmegin	10.3
			Hs.102408	ESTs	10.3
	444170				10.3
	453816		Hs.33848	dynein, axonemal, light intermediate polypeptide	
00	407378			gb:EST11752 Uterus Homo sapiens cDNA 5' end simila	10.2
80	440901		Hs.128612	ESTs	10.2
	407366			gb:Homo sapiens cig33 mRNA, partial sequence.	10.2
	415227	AW821113	Hs.72402	ESTs	10.2
	409269		Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone OVARC1002165	10.1
	450480		Hs.25040	zinc finger protein 239	10.1
				•	

	440000	A1E20202	11. 77400	FOT.	40.0
	419088	AI538323	Hs.77496	ESTs	10.0
	453922 428253	AF053306	Hs.36708	budding uninhibited by benzimidazolas 1 (yeast hom	9.9
	426471	AL133640 M22440	Hs.183357 Hs.170009	Homo sapiens mRNA; cDNA DXFZp586C1021 (from clone transforming growth factor, alpha	9.8 9.8
. 5	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-0-sulfotransferase	9.7
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, 8, cerevisiae, homolo	9.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	9.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.6
	423992	AW898292	Hs.137206	Homo saplans mRNA; cDNA DKFZp564H1663 (from clon	9.6
10	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	9.6
- •	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation regu	9.6
	438209	AL120659	Hs.6111	KIAA0307 gene product	9.5
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding p	9.5
	424945	Al221919	Hs.173438	hypothetical protein FLJ10582	9.5
15	414972	BE263782	Hs.77695	KIAA0008 gene product	9.4
	439262	AA832333	Hs.124399	ESTs	9.4
	403381	#(NOCAT)		0	9.3
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.3
20	435509	A1458679	Hs.181915	ESTs	9.3
20	445413	AA151342	Hs.12677	CGI-147 protein	9.2
	414083	AL121282	Hs.257786	ESTs	9.2
	421373	AA808229	Hs.167771	ESTs	9.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	9.1
25	446999	AA151520	Hs.279525	hypothetical protein PRO2605	9.1
23	459587	AA031958	11- 440050	gb:zk15e04.ş1 Soares_pregnant_uterus_NbHPU Homo sa	9.1
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	9.1
	406687	M31126 Y00272	Hs.272620 Hs.184572	pregnancy specific bela-1-glycoprotein 9	9.0 9.0
	428479			cell division cycle 2, G1 to S and G2 to M	9.0
30	408908	BE296227 Al834273	Hs.48915 Hs.9711	serine/threonine kinase 15	9.0
50	431548 433764	AW753676	Hs.39982	Homo sapiens cDNA FLJ13018 fis, clone NT2RP3000685 ESTs	9.0
	434636	AA083764	Hs.241334	ESTs .	
	451807	W52854	Hs.27099	DKFZP564J0863 protein	8.8
	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.8
35	443054	AI745185	Hs.8939	yes-essociated protein 65 kDa	8.8
"	420092	AAB14043	Hs.88045	ESTs	8.8
	420159	AI572490	Hs.99785	ESTs	8.8
	447164	AF026941	Hs.17518	Homo saplens cig5 mRNA, partial sequence	8.8
	451254	AI571016	Hs.172967	ESTs	8.8
40	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a	8.7
	450434	AA166950	Hs.18645	ESTs, Wealdy similar to partial CDS [C.elegans]	8.7
	400301	X03635	Hs.1657	Estrogen receptor 1	8.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransferase	8.7
4.5	434891	AA814309	Hs.123583	ESTs	8.7
45	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Homo s	8.7
	438885	A1886558	Hs.184987	ESTs	8.7
	449765	N92293	Hs.206832	EST, Moderately similar to ALUS_HUMAN ALU SUBFAM	8.7
	447342	Al199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARNI	8.6
εΛ .	434424	AIB11202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone LNG05548	8.6
50 、	438078	A1016377	Hs.131693	ESTs	8.6
	437212	AI765021	Hs.210775	EST8	8.5
	417728	AW138437	Hs.24790	KIAA1573 protein	8.5
	438081	H49546	Hs.298964	ESTs	8.5
55	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	8.4
55	435663	AI023707	Hs.134273 Hs.152213	ESTs wingless-type MMTV integration site family, member	8.4 8.4
	424717 425734	H03754 AF056209	Hs.159396		8.4
	450505	NM_004572	Hs.25051	peptidylglycine alpha-amidating monooxygenase COOH plakophilin 2	8.4
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	8.3
60	436396	A1683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA1001323	8.3
	425695	NM_005401	Hs.159238	protein tyrosine phosphatese, non-receptor type 14	8.3
	438180	AA808189	Hs.272151	ESTs	8.2
	447268	Al370413	Hs.36563	Homo saplens cDNA: FLJ22418 fls, clone HRC08590	8.2
	433159	AB035898	Hs.150587	kinesin-like protein 2	8.1
65	400195			0	8.1
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untransia	8.1
	438202	AW169287	Hs.22588	ESTs	8.1
	438915	AA280174	Hs.23282	ESTs	8.1
	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	8.1
70	453884	AA355925	Hs.36232	KIAA0186 gene product	8.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; t	8.0
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clone EU	8.0
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	8.0
75	424001	W67883	Hs.137476	KIAA1051 protein	8.0
75	434415	BE177494	11- 00000	gb:RC6-HT0596-270300-011-C05 HT0596 Homo sapiens c	8.0
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransferase, phosp	7.9
	438968		U. 97050	gb:EST391184 MAGE resequences, MAGP Homo sapiens c	7.9
	415245		Hs.27252	ESTs	7.9 7.9
80	422352		Hs.99200	ESTs	7.9 7.8
00	425492 442655		Hs.158174 Hs.30323	zinc finger protein 184 (Kruppel-like) ESTs	7.8 7.8
	442655 445657	AW612141	Hs.279575	ESTs	7.8
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.8
	426320		Hs.169300	transforming growth factor, beta 2	7.8
	720020	11 11 330	1	· acronamenta Statute recent ages a	110

	414142	AW368397	Hs.150042	ESTs	77
	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.7 7.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinese 1	7.6
_	436476	AA326108	Hs.53631	ESTs	7.6
5	414132	AIB01235	Hs.48480	ESTs	7.6
	437789	AI581344	Hs.127812	ESTs, Wealty similar to AF141326 1 RNA helicase HD	7.6
	450192 449328	AA263143	Hs.24596	RAD51-Interacting protein	7.6
	440238	AI962493 AW451970	Hs.197647 Hs.155644	ESTs paired box gene 2	7.5 7.5
10	403657	#(NOCAT)	113.100044	0	7.5
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	7.5
	418735	N48769	Hs.44609	ESTs	7.5
	413627	BE182082	Hs.246973	EST8	7.4
15	446293	AI420213	Hs.149722	ESTs	7.4
15	441627 425465	AA947552 L18964	Hs.58086	ESTs	7.4
	409242	AL080170	Hs.1904 Hs.51692	protein kinase C; iota DKFZP434C091 protein	7.3 7.3
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	7.3
	440250	AA876179	Hs.134650	ESTs	7.3
20	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAMIL	7.3
	458861	A1630223		gb:ad06g08.r1 Proliferating Erythroid Cells (LCB:a	7.3
•	435032	AA150797	Hs.109276	latexin protein	7.2
	407771 435039	AL138272 AW043921	Hs.62713	ESTs :	7.2
25	444342	NM_014398	Hs.130526 Hs.10887	similar to lysosome-associated membrane glycoprote	7.2 7.2
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, done NT2RP3004451	7.2
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma cells	7.2
	404253	#(NOCAT)		0	7.1
20	424120	T80579	Hs.290270	ESTs	7.1
30	429126	AW172356	Hs.99083	ESTs	7.1
	413573	A1733859	Hs.149089	ESTs	7.1
	421464 430388	AA291553 AA356923	Hs.190086	ESTs nuclear cap binding protein subunit 2, 20kD	7.0 7.0
	437938	A#950087	Hs.240770	ESTs; Weakly similar to Gag-Pol polyprotein [M.mus	7.0
35	420362	U79734	Hs.97206	huntingtin interacting protein 1	7.0
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked molety X)-typ	7.0
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP12	6.9
	410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	6.9
40	429418	Al381028	Hs.99283	ESTs	6.9
40	409178 446608	BE393948 N75217	Hs.50915 Hs.257846	kallikrein 5 ESTs	6.9
	425905	AB032959	Hs.161700	KIAA1133 protein	6.9 6.9
	428532	AF157326	Hs.184786	TBP-Interacting protein	6.9
	433426	H69125	Hs.133525	ESTa	6.9
45	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapiens	6.8
	437960	A1669586	Hs.222194	ESTs	6.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif, Y is	6.8
	424085 448674	NM_002914 W31178	Hs.139226	replication factor C (activator 1) 2 (40kD) ESTs	6.8
50	438122	A1620270	Hs.154140 Hs.129837	ESTs	6.8 6.8
•	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.saplen	6.7
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (metanoma, p1	6.7
	407162	N63855	Hs.142634	zinc finger protein	6.7
55	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxia 3,	6.7
55	424639	AI917494	Hs.131329	ESTs	6.7
	432415 421470	T16971	Hs.289014	ESTs annexin A3	6.7 6.7
	445459	R27496 A1478629	Hs.1378 Hs.158465	ESTs	6.7
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.6
60	432809	AA565509	Hs.131703	ESTs	6.6
	409234	Al879419	Hs.27206	ESTs	6.6
	438394	BE379623	Hs.27693	CGI-124 protein	6.6
	452097	AB002364	Hs.27916	ADAM-TS3; a distintegrin-like and metalloproteas	6.6
65	453745 414136	AA952989 AA812434	Hs.63908 Hs.178227	Homo sapiens HSPC316 mRNA, partial cds ESTs	6.6 6.6
05	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.6
	454018	AW016892	Hs.241652	ESTs	6.6
	452281	T93500	Hs.28792	ESTs	6.5
70	424620	AA101043	Hs.151254	kallikrein 7 (chymotyptic; stratum comeum)	6.5
70	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter), me	6.5
	434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subunit [H.sap	6.5
	425776 418677	U25128 S83308	Hs.159499 Hs.87224	parathyroid hormone receptor 2 SRY (sex determining region Y)-box 5	6.4 6.4
	409517	X90780	Hs.54668	troponin I, cardiac	6.4
75	432666	AW204069	Hs.129250	ESTs, Wealdy similar to unnamed protein product (H	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo saplens cDN	6.4
	413582	AW295647	Hs.71331	Homo saplens cDNA: FLJ21971 fis, clone HEP05790	6.4
80	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from clone	6.4
ov.	424153 434265	AA451737 AA846811	Hs.141496 Hs.130554	MAGE-like 2 Homo sepiens cDNA: FLJ23089 fis, clone LNG07061	6.4 6.4
	434265	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone THYRO1000187	6.4
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H.sapi	6.4
	443539	AI076182	Hs.134074	ESTs	6.4

	443830	Al142095	Hs.143273	ESTs	6.4
	452606	N45202	Hs.90012	Homo sapiens cDNA: FLJ23441 fis, clone HSI00612	6.4
	418384	AW149266	Hs.25130	ESTs	6.3
	425371	D49441	Hs.155981	mesothelin	6.3
5	429441	AJ224172	Hs.204096	Spophilin B (uteroglobin family member), prostate	6.3
-	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced gene	6.3
	437117	AL049256	Hs.122593	ESTs	6.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	6.3
	453370	A1470523	Hs.182356	ESTs, Moderately similar to translation initiation	6.3
10	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1	6.3
10				guanylate cyclase 1, soluble, beta 3	6.3
	415076	NM_000857	Hs.77890		6.2
	408155	AB014528	Hs.43133	KIAA0628 gene product	6.2
	452904	AL157581	Hs.30957	Horno sapiens mRNA; cDNA DKFZp434E0626 (from clone	
1.5	439138	Al742605	Hs.193696	ESTs .	6.2
15	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	6.2
	436281	AW411194	Hs.120051	ESTS	6.1
	407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	6.1
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferase	6.1
20	430437	AJ768801	Hs.169943	Homo saplens cDNA FLJ13569 ffs, clone PLACE1008369	6.1
20	428743	AL080060	Hs.301549	Homo saplens mRNA; cDNA DXFZp564H172 (from clone	6.1
	415139	AW975942	Hs.48524	ESTs	6.1
	417404	NM_007350	Hs.B2101	.pleckstrin homology-like domain, family A, member	6.1
	433527	AW235613	Hs.133020	ESTs	6.1
0.5	449448	D60730	Hs.57471	ESTs ·	6.1
25	457733	AW974812	Hs.291971	ESTs	6.1
	457979	AA776655	Hs.270942	ESTs	6.1
	422857	L32137	Hs.1584	cartilage oligomeric matrix protein	6.0
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1	6.0
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), membe	6.0
30	412733	AA984472	Hs.74554	KIAA0080 protein	6.0
	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	6.0
	449347	AV649748	Hs.295901	ESTs	6.0
	440870	Al687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO1000085	6.0
	437478	AL390172	Hs.118811	ESTs	6.0
35	411598	BE336654	Hs.70937	H3 histone family, member K	6.0
55		AA397769	Hs.86617	ESTs	6.0
	418134	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	6.0
	418845	AI922988		ESTs	6.0
	452039		Hs.172510	a disintegrin and metalloproteinase domain 17 (turn	5.9
40	410555	U92649	Hs.64311		5.9
40	412719	AW016610	Hs.129911	ESTS	
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PLACE1009150	5.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN LAMININ ALPH	5.9
	453431	AF094754	Hs.32973	glycine receptor, beta	5.9
4.5	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	5.9
45	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	5.9
	420440	NM_002407	Hs.97644	mammaglobin 2	5.9
	430291	AV660345	Hs.238126	CGI-49 protein	5.9
	405547	#(NOCAT)		0	5.9
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypeptide	5.9
50	435793	AB037734	Hs.4993	ESTs	5.8
	427975	A1536065	Hs.122460	ESTs	5.8
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 (H.sapie	5.8
	452693	T79153	Hs.48589	zinc finger protein 228	5.8
	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.8
55	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 protein	5.8
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	5.8
	448186	AA262105	Hs.4094	Homo saplens cDNA FLJ14208 fis, clone NT2RP3003264	5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.7
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP2004081	5.7
60	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapiens	5.7
	431924		Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone ADKA01954	5.7
	446868	AV660737	Hs.135100	ESTs	5.7
	452971	AI873878	Hs.91789	ESTs	5.7
	428927		Hs.90250	ESTs	5.7
65	425282		Hs.155485	huntingtin interacting protein 2	5.7
UJ	419247		Hs.89764	fragile X mental retardation 1	5.7
	445640		Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	5.7
					5.6
	422938		Hs.1594 Hs.301570	centromere protein A (17kD) ESTs	5.6
70	447078			general transcription factor IIH, polypeptide 4 (5	5.6
70	421247		Hs.102910	Zic family member 1 (odd-paired Drosophila homolog	5.6
	407896		Hs.41154		5.6
	436556		Hs.7572	ESTS	5.6
	417830		Hs.132808	epithelial cell transforming sequence 2 oncogene	5.6
75	429826		Hs.40747	ESTs	
75	432030		Hs.143789	ESTs	5.6
	443270		Hs.9192	Homer, neuronal immediate early gene, 18	5.5
	453900		Hs.226414	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAMIL	5.5
	411098		Hs.68583	mitochondrial intermediate peptidase	5.5
00	419558		Hs.278394	ESTs	5.5
80	427386		Hs.177486	armyloid beta (A4) precursor protein (protease next	5.5
	427961		Hs.143134	ESTs	5.5
	404561			0	5.5
	429682		Hs.211602	SMC1 (structural maintenance of chromosomes 1, yea	5.5
	407216	N91773	Hs.102267	lysyl oxidase	5.5

	410658	AW105231	Hs.192035	ESTs	5.5
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	5.5
	414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal muscle cD	5.5
5	427878	C05768	Hs.181022	CGI-07 protein	5.5
,	431041 441645	AA490967 A1222279	Hs.105276 Hs.201555	ESTs	5.5 5.5
	428071	AF212848	Hs.182339	transcription factor ESE-38	5.4
	436406	AW105723	Hs.125346	ESTs .	5.4
10	429181	AW979104	Hs.294009	ESTS	5.4 5.4
10	410909 424345	AW898161 AK001380	Hs.53112 Hs.145479	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAMIL Homo saplens cDNA FLJ10518 fts, clone NT2RP2000814	5.4 5.4
	451996	AW514021	Hs.245510	EST8	5.4
	449318	AW235021	Hs.108788	ESTs, Weakly similar to zeste [D.melanogaster]	5.4
15	441433	AA933809	Hs.42746	ESTs	5.4
15	445495 410153	BE622641 BE311926	Hs.38489 Hs.15830	ESTs Homo sapiens cDNA FLJ12691 fis, clone NT2RM4002571	5.4 5.4
	442611	BE077155	Hs.177537	ESTs	5.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6	5.4
20	453161	AA628608	Hs.61656	ESTs	5.4
20	419948	AB041035	Hs.93847	NAOPH oxidase 4	5.3 5.3
	427718 453867	A1798680 A1929383	Hs.25933 Hs.108196	ESTs HSPC037 protein	5.3
	422634	NM_016010	Hs.118821	CGI-62 protein	5.3
0.5	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.3
25 ·	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapiens cDNA c	5.3
	443486 451177	NM_003428 AI969716	Hs.9450 Hs.13034	zinc finger protein 84 (HPF2) ESTs	5.3 5.3
	408298	AI745325	Hs.271923	ESTs; Moderately similar to IIII ALU SUBFAMILY SB2	5.3
	435867	AA954229	Hs.114052	ESTs	5.3
30	423698	AA329796	Hs.1098	DKFZp434J1813 protein	5.3
	448543	AW897741	Hs.21380	Homo saplens mRNA; cDNA DKFZp586P1124 (from clone	5.3 5.3
	427660 430345	AI741320 AK000282	Hs.114121 Hs.239681	Homo saplens cDNA: FLJ23228 fis, clone CAE06654 hypothetical protein FLJ20275	5.3 5.3
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFA	5.3
35	449532	W74653	Hs.271593	ESTs	5.3
	452822	X85689	Hs.288617	Homo saplens cDNA: FLJ22621 fis, clone HSI05658	5.3
	437641 418379	AA811452 AA218940	Hs.291911 Hs.137516	ESTs fidgetin-like 1	5.2 5.2
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.2
40	433589	AA886530	Hs.188912	ESTs	5.2
	409143	AW025980	Hs.138965	ESTs .	5.2
	410303	AA324597	Hs.21851	Homo saplens cDNA FLJ12900 fis, clone NT2RP2004321	5.2 5.2
	413384 424698	NM_000401 AA164366	Hs.75334 Hs.151973	exostoses (multiple) 2 hypothelical protein FLJ10378	5.2
45	431229	AA496479	110.101010	gb:zv37h05.r1 Soares ovary turnor NbHOT Homo sapien	5.2
	433377	Al752713	Hs.43845	ESTs	5.2
	445236	AK001676	Hs.12457	hypothetical protein FLI 10814	5.2
	406367 442500	#(NOCAT) AJB1906B	Hs.209122	0 ESTs	5.2 5.2
50	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	5.2
	419140	Al982647	Hs.215725	ESTs	5.2
	411078	AJ222020	Hs.182364	ESTs, Wealdy similar to 25 kDa trypsin inhibitor [5.2
	423020 427061	AA383092 AB032971	Hs.1608 Hs.173392	replication protein A3 (14kD) KIAA1145 protein	5.2 5.2
55	439042	AW979172	(15.115532	gb:EST391282 MAGE resequences, MAGP Homo saplens c	5.2
	452930	AW195285	Hs.194097	ESTs	5.2
	417791	AW965339	Hs.111471	ESTs	5.1
	433277 447835	W27266 AW591623	Hs.151010 Hs.164129	ESTs ESTs	5.1 5.1
60	434401	AV551023 AI864131	Hs.71119	Pulative prostate cancer tumor suppressor	5.1
	437496	AA452378	Hs.170144	Homo saplens mRNA; cDNA DKFZp547J125 (from clone D	5.1
	418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [Celegans]	5.1
	428093 408621		Hs.104830 Hs.46638	ESTs chromosome 11 open reading frame 8; fetal brain (5.1 5.1
65	453096		Hs.11325	ESTs	5.1
	418852		Hs.273294	hypothetical protein FLJ20069	5.1
	436787		Hs.192756	ESTs	5.1
	446577 437267		Hs.15420 Hs.258110	KIAA1500 protein ESTs	5.1 5.0
70	419423		Hs.90315	KIAA0007 protein	5.0
	404939			0	5.0
	439052		Hs.37921	ESTs	5.0
	447020		Hs.16986 Hs.19025	hypothetical protein FLJ11046	5.0 5.0
75	453878 410824		Hs.33264	ESTs ESTs	5.0
. •	427701		Hs.221750	ESTs	5.0
	424602	AK002055	Hs.301129	Homo saplens clone 23859 mRNA sequence	5.0
	430044		Hs.152812	EST cluster (not in UniGene)	5.0 5.0
80	417423 421477		Hs.111164 Hs.104650	ESTs hypothetical protein FLJ10292	5.0 5.0
50	433384		Hs.124244	ESTs	5.0
	434160	BE551196	Hs.114275	ESTs	5.0
	443555		Hs.21398	ESTs, Moderately similar to GNP1_HUMAN GLUCOSAM	5.0
	416198	H27332	Hs.99598	, ESTs	4.9

	424530	102014	Un 150100	cellide A connector from I	4.9
	424539 436645	L02911 AW023424	Hs.150402 Hs.156520	activin A receptor, type I ESTs	4.9
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevisiae]	4.9
_	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.9
5	416565	AW000960	Hs.44970	ESTs	4.9
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.9
	435420 435532	AI928513 AW291488	Hs.59203 Hs.117305	ESTs ESTs	4.9 4.9
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.9
10	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP03830	4.9
	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.saplens]	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type; fou	4.9
	408938	AA059013	Hs.22607	ESTS	4.9
15	432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.9 4.9
13	436754 442573	A1061288 H93366	Hs.133437 Hs.7567	ESTs, Moderately similar to gonadotropin inducible Branched chain aminotransferase 1, cytosofic, U215	4.9
	409049	AI423132	Hs.146343	ESTs	4.9
	422475	AL359938	Hs.117313	Mels (mouse) homolog 3	4.9
	447112	H17800	Hs.7154	ESTs	4.9
20	458627	AW088642	Hs.97984	ESTs; Wealdy similar to WASP-family protein [H.sap	4.8
	431689	AA305688	Hs.267695	UDP-GathetaGlcNAc bela 1,3-galactosyltransferase,	4.8
	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR AT	4.8 4.8
	429414 418882	AI783656 NM_004996	Hs.202095 Hs.89433	empty spiracles (Drosophila) homolog 2 ATP-binding cassette, sub-family C (CFTR/MRP), mem	4.8
25	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell death 9;	4.8
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.8
	428555	NM_002214	Hs.184908	Integrin, beta 8	4.8
	452909	NM_015368	Hs.30985	pannexin 1	4.8
20	449535	W15267	Hs.23672	low density lipoprotein receptor-related protein 6	4.8
30	452232	AW020603	Hs.271698	ESTs	4.8
	409732	NM_016122	Hs.56148	NY-REN-58 anligen	4.8 4.7
	415115 423161	AA214228 AL049227	Hs.127751 Hs.124776	hypothetical protein Homo sapiens mRNA: cDNA DKFZp564N1116 (from clon	4.7
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200	4.7
35	423575	C18863	Hs.163443	ESTs	4.7
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN SP1	4.7
	418804	AA809632		gb:nz17h04.s1 NCI_CGAP_GCB1 Homo saplens cDNA do	4.7
	428405	Y00762	Hs.2266	cholinergic receptor, nicolinic, alpha polypeptide	4.7
40	432865	AI753709	Hs.152484	ESTS	4.7 4.7
40	433330 453047	AW207084 AW023798	Hs.132816 Hs.286025	ESTs ESTs	4.7
	421308	AA687322	Hs.192843	ESTs	4.7
	456273	AF154846	Hs.1148	zinc finger protein	4.7
	443933	Al091631	Hs.135501	Homo sapiens two pore potassium channel KT3.3	4.7
45	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR PRO	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.7
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.7
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	4.7 4.7
50	446102 420547	AW168067 AF155140	Hs.252956 Hs.98738	ESTs gonadotropin-regulated testicular RNA helicase	4.7
50	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	4.7
	429944	R13949	Hs.226440	Homo saplens clone 24881 mRNA sequence	4.7
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HEMBA1004610	4.7
c	434988	Al418055	Hs.161160	ESTs	4.6
55	452571	W31518	Hs.34665	ESTs	4.6
	434361	AF129755	Hs.117772	ESTs 0	4.6 4.6
	406400 410227	#(NOCAT) AB009284	Hs.61152	exostoses (multiple)-like 2	4.6
	419945	AW290975	Hs.118923	ESTs	4.6
60	428301	AW628666	Hs.98440	ESTs	4.6
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo saplens c	4.6
	431349	AA503653	Hs.156942	ESTs, Moderately similar to ALU2_HUMAN ALU SUBFA	4.6
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 ffs, clone NT2RP2003137	4.6 4.6
65	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from clone	4.6
U)	448027 449611	AI458437 AI970394	Hs.177224 Hs.197075	ESTs ESTs	4.6
	459574		Hs.101810	Homo saplens cDNA FLJ14232 fts, clone NT2RP4000035	4.6
	409928		Hs.57549	hypothetical protein dJ473B4	4.6
	409387		Hs.123526	EŜTs	4.6
70	424078	AB006625	Hs.139033	paternally expressed gene 3	4.6
	435244		Hs.187824	ESTs	4.6
	404996		13- 252005	0 ECTo	4.6 4.6
	407905 411560		Hs.252905	ESTs gb:IL3-CT0220-150200-071-H05 CT0220 Homo sepiens c	4.6
75	424341			gb:EST98673 Thyroid Homo sapiens cDNA 5 end simil	4.6
. •	441675		Hs.5461	ESTs	4.6
	452172		Hs.133207	Homo sapiens mRNA for KIAA1230 protein, partial od	4.6
	420276		Hs.190561	ESTs, Highly similar to mosaic protein LR11 (H.sap	4.5
οΛ	402820		11. 04040	0	4.5
80	419699		Hs.31246	ESTs	4.5 4.5
	422529 438018		Hs.256703 Hs.5999	ESTs hypothetical protein FLJ10298	4.5
	441826		Hs.129915	phosphotriesterase related	4.5
	453931		Hs.25144	ESTs	4.5

	435538	AB011540	Hs.4930	low density lipoprotein receptor-related protein 4	4.5
	457465	AW301344	Hs.195969	ESTs	4.5
	418848	A1820961	Hs.193465	ESTs	4.5
5	408321 447499	AW405882 AW262580	Hs.44205 Hs.147674	cortistatin KIAA1621 protein	4.5 4.5
-	424513	BE385864	Hs.149894	mitochondrial translational initiation factor 2	4.5
	432731	R31178	Hs.287820	fibroneclin 1	4.5
	448275 430371	BE514434 D87466	Hs.20830 Hs.240112	synaptic Ras GTPase activating protein 1 (homolog KIAA0276 protein	4.5 4.5
10	448693	AW004854	Hs.228320	Homo sepiens cDNA: FLJ23537 fis, clone LNG07690	4.5
	407289	AA135159	Hs.203349	Homo saplens cDNA FLJ12149 fis, done MAMMA100042	4.4
	448141	AJ471598	Hs.197531	ESTS	4.4
	434699 417718	AA643687 T86540	Hs.149425 Hs.193981	Homo septens cDNA FLJ11980 fis, clone HEM8B1001304 ESTs	4.4 4.4
15	436464	AI016176	Hs.269783	ESTs, Wealthy similar to ALU1_HUMAN ALU SUBFAMIL	4.4
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cerevisia	4.4
	409092	AI735283	Hs.172608	ESTs	4.4
	416241 432005	N52639 AA524190	Hs.32683 Hs.120777	ESTs, Wealty similar to ELL2_HUMAN RNA POLYMER	4.4 4.4
20	440234	AW117264	Hs.126252	ESTs	4.4
	448743	AB032962	Hs.21896	KIAA1136 protein	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	4.4
	453331 454036	A1240665 AA374756	Hs.8895 Hs.93 5 60	ESTs ESTs, Wealdy similar to unnamed protein product (H	4.4 4.4
25	448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.4
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (melt	4.4
	453279	AW893940	Hs.59698	ESTs	4.4
	409459 431708	D86407 Al698136	Hs.54481 Hs.108873	low density lipoprotein receptor-related protein 8 ESTs	4.4 4.4
30	433906	AI167816	Hs.43355	ESTs	4.4
	437958	BE139550	Hs.121668	ESTs	4.4
	441423	Al793299	Hs.126877	ESTs	4.4
	429876 446770	AB028977 AV660309	Hs.225974 Hs.154986	KIAA1054 protein ESTs, Weakly similar to AF137386 1 plasmolipin [H.	4.3 4.3
35	412078	X69699	Hs.73149	paired box gene 8	4.3
	422093	AF151852	Hs.111449	CGI-94 protein	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium	4.3
	448390 453628	AL035414 AW243307	Hs.21068 Hs.170187	hypothetical protein ESTs	4.3 4.3
40	449722	BE280074	Hs.23960	cyclin B1	4.3
	436679	Al127483	Hs.120451	ESTs, Weakly similar to unnamed protein product [H	4.3
	431592	R69016	Hs.293871	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.3
	432383 419926	AK000144 AW900992	Hs.274449 Hs.93798	Homo saplens cDNA FLJ20137 fis, clone COL07137 DKFZP586D2223 protein	4.3 4.3
45	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.3
	401644	#(NOCAT)		0	4.3
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine heptad	4.3
	413775 424296	AW409934 Al631874	Hs.75528 Hs.169391	nucleolar GTPase ESTs	4.3 4.3
50	431118	BE264901	Hs.250502	carbonic anhydrase VIII	4.3
	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protease (ECHOS1) (TADG-1	4.3
	451073	AI758905	Hs.206063	ESTs	4.3
	451592 452453	Al805416 Al902519	Hs.213897	ESTs gb:QV-8T009-101198-051 BT009 Homo sapiens cDNA, m	4.3 4.3
55	441020	W79283	Hs.35962	ESTs	4.2
-	439024	R96696	Hs.35598	ESTa	4.2
	453619	H87648	Hs.33922	H.saplens novel gene from PAC 117P20, chromosome 1	4.2
	453459 408427	BE047032 AW194270	Hs.257789 Hs.177236	ESTs ESTs	4.2 4.2
60	419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	4.2
-	426460	D79721	Hs.183702	Homo sepiens cDNA FLJ11752 fis, clone HEMBA1005582	4.2
	444540	AI693927	Hs.265165	ESTs	4.2
	452943 453913	BE247449 AW004683	Hs.31082 Hs.233502	hypothelical protein FLJ 10525 ESTs	4.2 4.2
65	417847	AI521558	Hs.288312	Homo saplens cDNA: FLJ22316 fis, clone HRC05262	4.2
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP05638	4.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sapiens cDNA	4.2
	441006	AW605267	Hs.7627 Hs.254020	CGI-60 protein ESTs, Moderately similar to unnamed protein produc	4.2 4.2
70	436209 446936	AW850417 H10207	Hs.47314	ESTs	4.2
	406076	AL390179	Hs.137011	Homo saptens mRNA; cDNA DKFZp547P134 (from clone	4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	4.2
	406671 418432	AA129547 M14156	Hs.285754 Hs.85112	met proto-oncogene (hepatocyte growth factor recep insulin-like growth factor 1 (somatomedia C)	4.2 4.2
75	417048		Hs.55498	geranylgeranyl diphosphate synthase 1	4.2
. •	431750		Hs.283705	ESTs	4.2
	439314	AA382413	Hs.178144	ESTs	4.2
	448582		Hs.94812	ESTs	4.2
80	449554 455700		Hs.59982	ESTs gb:CM1-8T0368-061299-060-g07 BT0368 Homo sapiens c	4.2 4.2
00	409073			gb:zf71a07.s1 Soares_pineal_gland_N3HPG Homo sapie	4.1
	433929		Hs.27379	ESTs	4.1
	415457		Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.1 •
	444381	BE387335	Hs.283713	, ESTs	4.1

	451024 415539	AA442176 AI733881	Hs.72472	gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_9w Homo sa BMPR-lb; bone morphogenetic protein receptor; typ	4.1 4.1
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialytransferase L long form	4.1
	420736	AI263022	Hs.82204	ESTs	4.1
5	453293 409564	AA382267 AA045857	Hs.10653	ESTs frecture callus 1 (rat) homolog	4.1 4.1
	418378	AW962081	Hs.54943	gb:EST374154 MAGE resequences, MAGG Homo seplens	4.1
	429628	H09604	Hs.13268	ESTs	4.1
10	439635 440452	AA477288 Al925136	Hs.94891 Hs.55150	Homo sepiens cDNA: FLJ22729 fis, clone HSI15685 ESTs, Weakly similar to CAYP_HUMAN CALCYPHOSIN	4.1 4.1
10	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal short-c	4.1
	448816	AB033052	Hs.22151	KIAA1226 protein	4.1
	452795 443171	AW392555 BE281128	Hs.18878 Hs.9030	hypothetical protein FLJ21620 TONDU	4.1 4.1
15	425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic polypepti	4.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	4.1
	414747 417300	U30872 Al765227	Hs.77204 Hs.55610	centromere protein F (350/400kD, mitosin) solute carrier family 30 (zinc transporter), membe	4.1 4.1
	417389	BE260964	Hs.82045	Midkine (neurile growth-promoting factor 2)	4.1
20	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	4.1
	419131 406348	AA406293 #(NOCAT)	Hs.301622	ESTs 0	4.1 4.1
	419750	AL079741	Hs.183114	Homo saplens cDNA FLJ14236 fis, ctona NT2RP4000515	4.1
25	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitochondria	4.1
25	420908 421039	AL049974 NM_003478	Hs.100261 Hs.101299	Homo sapiens mRNA; cDNA DKFZp564B222 (from clone cutlin 5	4.1 4.1
	426890	AA393167	Hs.41294	ESTs	4.1
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease, autosomal	4.1
30	452834 428771	A1638627 AB028992	Hs.105685 Hs.193143	ESTs KIAA1069 protein	4.1 4.0
•	437949	U78519	Hs.41654	ESTs	4.0
	450568	AL050078	Hs.25159	Homo sapiens CDNA FLJ10784 fis, clone NT2RP4000448	4.0
	424081 418375	NM_006413 NM_003081	Hs.139120 Hs.84389	ribonuclease P (30kD) synaptosomal-associated protein, 25kD	4.0 4.0
35	447204	Al366881	Hs.157897	ESTs, Moderately similar to ALUC_HUMAN IIII ALU CL	4.0
	407910 412314	AA650274 AA825247	Hs.41296 Hs.250899	fibronectin teucine rich transmembrane protein 3 heat shock factor binding protein 1	4.0 4.0
	436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulating cytokin	4.0
40	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.0
40	426991 409365	AK001536 AA702376	Hs.285803 Hs.226440	Homo sapiens cDNA FLJ12852 fis, clone NT2RP2003445 Homo sapiens clone 24881 mRNA sequence	4.0 4.0
	410784	AW803201	113,220770	gb:lL2-UM0077-070500-080-E06 UM0077 Homo sapiens c	4.0
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.0
45	413425 417655	F20956 AA780791	Hs.14014	gb:HSPD05390 HM3 Homo sapiens cDNA clone 032-X4-1 ESTs, Weakly similar to KIAA0973 protein [H.sapien	4.0 4.0
43	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated factor,	4.0
	425024	R39235	Hs.12407	ESTs	4.0
	445941 448595	A1267371 AB014544	Hs.172636 Hs.21572	ESTs KIAA0644 gene product	4.0 4.0
50	453448	AL036710	Hs.209527	ESTs	4.0
	458944	N93227	Hs.98403	ESTs	4.0
	400284 441134	W29092	Hs.7678	Estrogen receptor 1 cellular retinoic acid-binding protein 1	4.0 4.0
	408796	AA688292	Hs.118553	ESTs	4.0
55	408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.0
	438913 402408	Al380429	Hs.172445	ESTs O	4.0 4.0
	411630	U42349	Hs.71119	Putative prostate cancer turnor suppressor	4.0
۲۸	450701	H39960	Hs.288467	Homo saplens cDNA FLJ12280 fis, clone MAMMA100174	4.0
60	439780 418301	AL109688 AW976201	Hs.187618	gb:Homo saplens mRNA full length insert cDNA clone ESTs	4.0 4.0
	420077	AW512260	Hs.87767	ESTs	4.0
	426572	AB037783	Hs.170523	hypothetical protein FLJ11183	4.0
65	403721 411945	AL033527	Hs.92137	v-myc avian myelocytomatosis virat oncogene homoto	4.0 4.0
-	408684		Hs.12727	hypothetical protein FLJ21610	4.0
	414869	AA157291	Hs.72163	ESTs	4.0 4.0
	-437980 451050	R50393 AW937420	Hs.278436 Hs.69662	KIAA1474 protein ESTs	4.0
70					
	TABLE		al idealifes sur	shore	
		Inique Eos probes mber: Gene cluste		ioci	
95		on; Genbank acc		•	
75	Mean	CAT N	Accession		
	Pkey 409073	CAT Number 109851_1		1 B AA063018 A1444822	
	410784		AW80320	1 BE079700 BE062940	
80	411560			6 AW996967 BE143456	
OU	413425 414315			A129374 AA133740 AYV819878 AA94098 F13654 AA494040 AA143127	
	418378	174656_1	AW96208	31 AA218925 AA354237	
	418804			2 A1917245 A1701732 AA228406 14 AW074361 AA238240 A1077451 AA631300 AW074262	
	419311	183793_1	AADUSSS	1 AW974261 AA236240 AI077451 AA631399 AW974262	

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195241_1
                                                       AW976153 AA278945 AA747691
AA385074 AA339054 AA339115 AW956359
AA418703 AA418711 BE071915 BE071920 BE071912
               420637
               424341
                              238294_1
               428002
                               285602_1
               428579
                               294049_1
                                                        AA431765 AA432015
   5
                                                        AA884766 AW974271 AA592975 AA447312
AW968128 AA468102 AA468165
AA496479 T89859 AW020056 AW135251 AI221100 AA628705 AI263148 T79074
                              300543_1
               429163
               430153
                               313709 1
               431229
                               330060_1
               431322
                               331543_1
                                                        AW970622 AA503009 AA502998 AA502989 AA502805 T92188
                              385931 1
                                                        BE177494 AW276909 AA632849
               434415
                                                        AW298067 AA731645 AA810101 AW194180 Al690673 AW978773
10
                               427323 1
               436812
                                                        AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
               437938
                               44573_2
                                                       ASSOLOF M 10206 1870-0 NS803 AUS0113 AV88101 17 AV88101 17 NS302 M25173 NS303 M491137 SS397 AV891137 AV89101 1
AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328511 T75102 R34725 AA884922 BE328517 AI219788 AA88444 N92578
F13493 AA927794 AI560251 AW874068 AL 134043 AW233363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346
AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813
AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538
15
                                                       AA180009 AA337499 AW961101 AA251669 AA251874 AB19225 AW205862 AI68333B AI659509 AW276905 AI633008 AA972584 AA908741
AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456
AI373032 AI564269 F00531 H83488 W37181 W78802 R66058 AI002839 R67840 AA300207 AW959581 T63226 F04005
                                                       AW979074 AA834841 AA828650
AA828995 AA834879 AI926361
                              467436 1
               438966
20
               438993
                               467651_1
                                                       AM0799172 AA829595 R95050
AL109588 R23655 R256578
AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
AI624049 AW117770 AI858360
               439042
                               468079_1
               439780
                               47673_1
                              542469_1
               442438
                              794817_1
85565_1
               449034
25
               451024
                                                        AA442176 AA259181
                                                        Al902519 Al902518 Al902516
               452453
                               918300_1
                                                        BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
               455700
                               1351264_1
                                                        Al630223 Al630470
               458861
                              798085 1
30
               TABLE 14C:
               Pkey: Unique number corresponding to an Eos probeset
              Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402489-495

Strand: Indicates DNA strand from which exons were predicted
35
               Nu position: Indicates nucleofide positions of predicted exons
               Pkey
401644
                                                   Strand
                                                                      Nt_position
82655-83959
                                 8576138
                                                   Plus
                                 9796239
                                                                      110326-110491
               402408
                                                   Minus
40
                                                                      81747-82094
82274-82443
26009-26178
               402606
                                 9909429
                                                   Minus
                                 6456853
               402820
                                                   Minus
                                 9438267
                                                   Minus
               403381
                                  8843996
                                                                      156223-156370
               403657
                                                   Minus
                                  7528046
                                                                       156647-157366
               403721
                                                    Minus
45
               404253
                                  9367202
                                                    Minus
                                                                      55675-56055
                                                                      69039-70100
175318-175476
               404561
                                 9795980
6862697
                                                   Minus
               404939
                                                   Plus
               404996
                                  6007890
                                                   Plus
                                                                      37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
               405547
                                  1054740
                                                   Plus
                                                                       124361-124520,124914-125050
50
               406348
                                  9255985
                                                   Minus
                                                                      71754-71944
                                                                      58313-58489
1553-1712,1878-2140,4252-4385,5922-6077
               406367
                                 9256126
                                                   Minus
               406400
                                 9256298
                                                   Plus
```

Table 15A lists about 499 genes up-regulated in ovarian cancer compared to normal adult itssues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 14A, except that the ratio was greater than or equal to 3.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., ig, fin3, egf, 7tm domains). Predicted protein domains are noted.

TABLE 15A: ABOUT 499 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Primekey

UG ID: UniGene ID

Prot. Dom.: Predicted protein structural domains

ratio: ration turnor vs normal tissues

Ex. Accn Al267700 NM_005756 AW513143	UG ID Hs.111128 Hs.184942	Title ESTs Goratein-counted recentor 64	Prot. Dom. TM	ratio 42.7
NM_005756				42.7
	Hs.184942	G protein-counted recentor 64	man t	
AW513143		O proton soupled toocpan or	TM	30.5
	Hs.98367	similar to SRY-box containing gene 17	TM	30.1
AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix	SS	29.4
D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphy	C1q,Collagen	27.0
C14187	Hs.103538	ESTs	TM	26.2
M13509	Hs.83169	Matrix metalloprotease 1 (Interstitial collag	SS,,Peptidase_M10	20.6
AA250737	Hs.72472	BMPR-lb; bone morphogenetic protein rec	TM	20.6
Al351010	Hs.102267	lysyl oxidase	Lysyl_oxidase	17.7
NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kin	pidse,pkinase	17.4
AW023482	Hs.97849	ESTs	TM	17.4
AJ404872	Hs.288693			17.1
AA403084	Hs.269347	ESTs		17.0
AA828995		Integrin; beta 8		16.7
H87879	Hs.102267			16.1
AW972870	Hs.291069	ESTs	SS	15.9
AL037824	Hs.194695	ras homolog gene family, member I	res	15.1
AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, hom	TM	15.0
	AB018305 D31152 C14187 M13509 AA250737 A1351010 NM_002497 AW023482 AJ404872 AA403084 AA628995 H87879 AW972870 AL037824	AW513143 Hs.98367 AB018305 Hs.5378 D31152 Hs.179729 C14187 Hs.103538 M13509 Hs.83169 AA250737 Hs.72472 AJ351010 Hs.102267 NM_002497 Hs.153704 AW023482 Hs.97849 AJ404672 Hs.28693 AA403884 Hs.269347 AA828995 H87879 Hs.102267 AW972870 Hs.291069 AL037824 Hs.194695	AW513143 Hs.98367 similar to SRY-box containing gene 17 AB018305 Hs.5378 spondin 1, (Fapondin) actracellular matrix D31152 Hs.179729 collagen; type X; alpha 1 (Schmid metaphy EST5 M13509 Hs.83169 Matrix metalloprotease 1 (Interstitial collag AA250737 Hs.102267 hs.102267 NM_002497 Hs.153704 AW0023482 Hs.97849 EST5 AJ404672 Hs.28693 EST AA403084 Hs.269347 EST5 AA403084 Hs.269347 EST5 AA828995 Hs.102267 hs.102267 AW972870 Hs.291069 EST5 AL037824 Hs.194695 ras homolog gene family, member I	AW513143 Hs.98367 similar to SRY-box containing gene 17 AB018305 Hs.5378 spondin 1, (Fepondin) autracellular matrix SS D31152 Hs.179729 collagen; type X; alpha 1 (Schmild metaphy C1q.Collagen TM M13509 Hs.83169 Matrix metalloprotease 1 (Intersitial collag AA250737 Hs.72472 BMPR-lb; bone morphogenetic protein rec AJ351010 Hs.102267 lysyl oxidase Lysyl_oxidase Usyl_oxidase Usyl_oxi

	413623	AA825721	Hs.246973	ESTs	TM	14.8
	447350	AL375572	Hs.172634	ESTs; HER4 (c-erb-B4)	SS,TM,Furin-like,pkinase	14.2
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PRO	11.8	14.1
5	452461	N78223	Hs.108106	transcription factor	G9a,PHD	13.7
)	451106 416208	BE382701 AW291168	Hs.25960 Hs.41295	N-myc ESTs	Myc_N_term TM	13.6 13.5
	452249	BE394412	Hs.61252	ESTs	homeobox	13.4
•	416566	NM_003914	Hs.79378	cyclin A1	cyclin	12.8
10	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	TM	12.6
10	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	12.3 12.2
	458027	L49054	Hs.85195 Hs.285574	ESTs, Highly similar to t(3;5)(q25.1;p34) f ESTs	TM TM	12.2
	408460 415263	AA054726 AA948033	Hs.130853	ESTs	histone	11.9
	400298	AA032279	Hs.61635	STEAP1	TM	11.8
15	421451	AA291377	Hs.50831	ESTs	TM	11.6
	443715	AJ583187	Hs.9700	cyclin E1	cyclin	11.5
	413472	BE242870	Hs.75379	solute carrier family 1 (gilal high affinity gi	TM,SDF SS	11.5 11.4
	410102 408562	AW248508 AJ436323	Hs.279727 Hs.31141	ESTs; Homo sapiens mRNA for KIAA1568 prote	TM	11.4
20	442353	BE379594	Hs.49136	ESTs	TM	11.3
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3	TM,neur_chan	11.2
	453160	AL263307	Hs.146228	ESTs	histone	11.2
	412723	AA648459	Hs.179912	ESTs	TM	11.1
25	400250	D202C2	U= 24206	O . ESTs	Hist_deacetyl+F105 7tm_1	11.1 11.1
23	438167 434539	R28363 AW748078	Hs.24286 Hs.214410	ESTs	TM	10.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	TM	10.8
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2	SS,hemopexin	10.8
	446142	A1754693	Hs.145968	ESTs	Cadherin_C_term	10.7
30	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	TM,p450	10.6
	433496	AF064254	Hs.49765 Hs.85339	VERY-LONG-CHAIN ACYL-COA SYNT	SS,TM TM	10.6 10.5
	418506 433447	AA084248 U29195	Hs.3281	G protein-coupled receptor 39 neuronal pentraxin li	SS	10.4
	414245	BE148072	Hs.75850	WAS protein family, member 1	TM	10.3
35	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	SS,LRRNT	10.3
	418601	AA279490	Hs.86368	calmegin	SS	10.3
	415227	AW821113	Hs.72402	EST6	TM	10.2 10.1
	409269	AA576953 M22440	Hs.22972 Hs.170009	Homo saptens cDNA FLJ13352 fis, clone O transforming growth factor, alpha	TM SS,EGF	9.8
40	426471 407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	9.7
70	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	9.7
•	414972	BE263782	Hs.77695	KIAA0008 gene product	TM	9.4
	435509	AI458679	Hs.181915	ESTa	TM	9.3
45	445413	AA151342	Hs.12677	CGI-147 protein	UPF0099	9.2 9.1
43	446999	AA151520	Hs.279525	hypothelical protein PRO2605 Prostate cancer associated protein 1	TM TM	9.1
	414569 405687	AF109298 M31126	Hs.118258 Hs.272620	pregnancy specific beta-1-glycoprotein 9	hemopexin	9.0
	408908	BE296227	Hs.48915	serine/threonine kinese 15	pklse,TM	9.0
	451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	8.8
50	420159	AI572490	Hs.99785	ESTs	TM	8.8
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:poly	TM,Ricin_B_lectin	8.7 8.7
	408829	NM_006042 AI886558	Hs.48384 Hs.184987	haparan sulfate (glucosamine) 3-O-sulfotran ESTs	TM TM	8.7
	438885 447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAM	TM	8.6
55	437212	Al765021	Hs.210775	ESTs	UDPGT	8.5
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	8.4
	450505	NM_004572	Hs.25051	plakophilin 2	TM	8.4
	436398	A1683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone H	wnt	8.3 8.3
60	425695	NM_005401	Hs.159238 Hs.36563	protein tyrosine phosphatase, non-receptor Homo sapiens cDNA: FLJ22418 fis, clone	Y_phosphatase Ribosomal_S8	8.2
00	447268 400195	Al370413	H3.30303	0	TM	8.1
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein,	TM	8.1
	438202	AW169287	Hs.22588	ESTs	· TM	8.1
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	TM	8.0
65	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	TM,Fz,Frizzled	8.0 8.0
	424001	W67883	Hs.137476	KIAA1051 protein ESTs	TM TM	7.8
	442655 445657	AW027457 AW612141	Hs.30323 Hs.279575	ESTs	7tm_1	7.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	SS,TGF-beta	7.8
70	412170	D16532	Hs.73729	very low density lipoprotein receptor	TM,ldl_recept_b,EGF	7.6
	436476	AA326108	Hs.53631	ESTs	TM	7.6
	414132	AI801235	Hs.48480	ESTS	TM TM	7.6 7.6
	437789 450192	Al581344 AA263143	Hs.127812 Hs.24596	ESTs, Wealdy similar to AF141326 1 RNA RAD51-Interacting protein	TM	7.6
75	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	TM	7.5
, ,	413627	BE182082	Hs.246973	ESTs	TM	7.4
	446293	Al420213	Hs.149722	ESTs	LIM,homeobox	7.4
	409242	AL080170	Hs.51692	DKFZP434C091 protein	TM,7tm_1	7.3
00	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA	TM	7.3 7.3
80	451659	8E379761	Hs.14248	ESTs, Wealdy similar to ALU8_HUMAN A similar to lysosome-essociated membrane g	TM TM	7.3 7.2
	444342 429126	NM_014398 AW172356	Hs.10887 Hs.99083	ESTs	7tm_1	7.1
	421464		Hs.190086	EST8	TM	7.0
-	420362		Hs.97206	huntinglin interacting protein 1	TM	7.0
				205		

	11/7/19	44045540				
	444743 415138	AA045648 C18356	Hs.11817	nudix (nucleoside diphosphate linked moiet fissue factor pathway inhibitor 2 TFP12	TM Kunih ROTI C namma	7.0
	429418	AJ381028	Hs.78045 Hs.99283	ESTs	Kunitz_BPTI,G-gamma AAA	6.9 6.9
_	409178	BE393948	Hs.50915	kellikrein 5	SS,trypsin	6.9
5	425905	AB032959	Hs.161700	KIAA1133 protein	TM	6.9
	428532	AF157326	Hs.184786	TBP-Interacting protein	TM	6.9
	433426	H69125 W31178	Hs.133525	ESTs	TM	6.9
	448674 432415	T16971	Hs.154140 Hs.289014	ESTs ESTs	TM TM	6.8 6.7
10	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM	6.6
	438394	BE379623	Hs.27693	CGI-124 protein	pro_lsomerase	6.6
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metal	Reprolysin	6.6
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cd	TGFb_propeptide	6.6
15	423248 452281	AA380177 T93500	Hs.125845 Hs.28792	ribulose-5-phosphate-3-epimerase ESTs	filament TGF-beta	6.6 6.5
13	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum	SS,trypsin	6.5
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter)	TM, Sulfate_transp	6.5
	434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subun	pkinase,fn3	6.5
20	425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	6.4
20	409517	X90780	Hs.54668	troponin I, cardiac	Y_phosphatase	6.4
	432666 448706	AW204069 AW291095	Hs.129250 Hs.21814	ESTs, Weakly similar to unnamed protein p class II cytokine receptor ZCYTOR7	TM SS	6.4 6.4
	413582	AW295647	Hs.71331	Homo saptens cDNA: FLJ21971 fis, clone	TM	6.4
	424153	AA451737	Hs.141496	MAGE-like 2	TM	6.4
25	441081	Al584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	6.4
	443539	AJ076182	Hs.134074	ESTs	TM	6.4
	418384	AW149266	Hs.25130	ESTs	TM	6.3
	425371 449048	D49441 Z45051	Hs.155981 Hs.22920	mesothelin similar to \$68401 (cattle) glucose induced g	SS SS	6.3 6.3
30	437117	AL049256	Hs.122593	ESTs	TM	6.3
-	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation init	ABC_tran	6.3
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic p	SS,TGF-beta	6.3
	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E	TM	6.2
35	457030	AJ301740	Hs.173381	dihydropyrimidinase-like 2	TM.	6.2
22	436281 415139	AW411194 AW975942	Hs.120051 Hs.48524	ESTs ESTs	TM TM	6.1 6.1
	449448	D60730	Hs.57471	EST\$	TM	6.1
	457979	AA776655	Hs.270942	ESTs	TM	6.1
40	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	SS,EGF,tsp_3	6.0
40	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate)	TM	6.0
	412733	AA984472	Hs.74554	KIAA0080 protein	C2	6.0
	422095 418845	A1868872	Hs.288966 Hs.89232	ceruloplasmin (ferroxidase)	SS Chromo chodow	6.0
	410555	AA852985 U92649	Hs.64311	chromobox homolog 5 (Drosophila HP1 alp a disintegrin and metalloproteinase domain	Chromo_shadow TM,dlsintegrin,Reprolysin	6.0 5.9
45	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	5.9
	453431	AF094754	Hs.32973	glycine receptor, beta	TM,neur_chan	5.9
	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	TSPN, Collagen, COLFI	5.9
	430291	AV660345	Hs.238126	CGI-49 protein	TM	5.9
50	405547	#(NOCAT)	Un 4002	0	TM.ABC_membrane	5.9
50	435793 440138	AB037734 AB033023	Hs.4993 Hs.6982	ESTs hypothetical protein FLJ10201	TM .	5.8 5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	SS,Collagen,TSPN	5.7
	419335	AW960146	Hs.284137	Homo saplens cDNA FLJ12888 fls, clone N	TM	5.7
	452971	AI873878	Hs.91789	ESTs	TM	5.7
55	428927	AA441837	Hs.90250	ESTs ·	TM	5.7
	419247	S65791	Hs.89764	fragila X mental retardation 1	TM	5.7
	445640 447078	AW959526 AW885727	Hs.31704 Hs.301570	ESTs, Weakly similar to KIAA0227 [H.sap ESTs	TM kazai	5.7 5.6
	421247	BE391727	Hs.102910	general transcription factor (IH, polypeptid	TM.	5.6
60	432030	Al908400	Hs.143789	ESTs	SS	5.6
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	TM	5.5
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	Peptidase_M3	5.5
	419558	AW953679	Hs.278394	ESTs	SS	5.5
65	427386 427961	AW836261 AW293165	Hs.177486 Hs.143134	amyloid beta (A4) precursor protein (protea ESTs	TM TM	5.5 5.5
05	407216	N91773	Hs.102267	lysyl oxidase	TM	5.5
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	ras,TM	5.5
	414315	Z24878		gb:HSB65D052 STRATAGENE Human sk	TM	5.5
70	441645	A1222279	Hs.201555	ESTs	SS	5.5
70	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanoga	TM	5.4
	441433 445495	AA933809 BE622641	Hs.42746 Hs.38489	ESTs ESTs	TM LLWEQ.ENTH	5.4 5.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone N	Glycos_transf_2	5.4
	442611	BE077155	Hs.177537	ESTs	TM	5.4
75	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced protein	XIInk, CUB	5.4
	419948	AB041035	Hs.93847	NADPH oxidase 4	TM	5.3
	427718	AI798680	Hs.25933	ESTs	histone	5.3
	453867 408298	A1929383 A1745325	Hs.108196 · Hs.271923	HSPC037 protein ESTs; Moderately similar to IIII ALU SUB	TM Glycos_transf_2,DSPc	5.3 5.3
80	448543	AV/45325 AW897741	Hs.21380	Homo saplens mRNA; cDNA DKFZo586P	TM	5.3
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALUS_HUMA	TM	5.3
	449532	W74653	Hs.271593	ESTs	TM.	5.3
	452822	X85689	Hs.288617	Homo saplens cDNA: FLJ22521 fis, done	TM,EGF,fn3	5.3
	418379	AA218940	Hs.137516 .	fidgetin-like 1	AAA	5.2

	416530	U62801	Hs.79361	kaliikrein 6 (neurosin, zyme)	TM, trypsin	5.2
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.2
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	TM	5.2
5	406367 442500	#(NOCAT)	11- 000122	0 FCT-	proteasome,trypsin	5.2
9	450101	AI819068 AV649989	Hs.209122 Hs.24385	ESTs Human hbc647 mRNA sequence	SS TM	5.2 · 5.2
	419140	AI982647	Hs.215725	ESTs	TM	5.2
	417791	AW965339	Hs.111471	ESTs	Ald_Xan_dh_C	5.1
10	437496	AA452378	Hs.170144	Homo saplens mRNA; cDNA DKFZp547J1	TSPN,Folate_carrier	5.1
10	418849 428093	AW474547 AW594506	Hs.53565 Hs.104830	ESTs, Weakly similar to B0491.1 [C.elegan ESTs	TM TM .	5.1 5.1
•	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; feta	TM .	5.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.1
1.	404939			0	TM	5.0
15	447020	T27308	Hs.16986	hypothetical protein FLJ11046	TM	5.0
	410824 417423	AW994813 AA197341	Hs.33264 Hs.111164	ESTs ESTs	TM TM	5.0 5.0
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	TM	5.0
••	443555	N71710	Hs.21398	ESTs, Moderately similar to GNP1_HUMA	Glucosamine_iso	5.0
20∙	424539	L02911	Hs.150402	activin A receptor, type t	SS,Activin_recp,pkinase	4.9
	416565	AW000960	Hs.44970	ESTS	TM	4.9
	431130 408938	NM_006103 AA059013	Hs.2719 Hs.22607	epididymis-specific; whey-acidic protein ty ESTs	SS TM	4.9 4.9
	436754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin i	TM	4.9
25	409049	AI423132	Hs.146343	ESTs	TM	4.9
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro	TM	4.8
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM,ABC_membrane	4.8
	422505 428555	AL120862 NM_002214	Hs.124165 Hs.184908	ESTs; (HSA)PAP protein (programmed ce integrin, beta 8	TM SS,integrin_B	4.8 4.8
30	452909	NM_015368	Hs.30985	pannexin 1	TM	4.8
- •	449535	W15267	Hs.23672	low density (ipoprotein receptor-related pro	SS,ldl_recept_a,EGF	4.8
	452232	AW020603	Hs.271698	ESTs	TM	4.8
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N	Cadherin_C_term	4.7
35	428405 433330	Y00762 AW207084	Hs.2266 Hs.132816	cholinergic receptor, nicotinic, alpha polype ESTs	TM,neur_chan TM	4.7 4.7
33	443933	A1091631	Hs.135501	Homo saptens two pore potassium channel	TM	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	TM	4.7
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	4.7
40	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	AAA,DEAD,helicase_C	4.7
40	429944 434988	R13949 Al418055	Hs.226440 Hs.161160	Homo sapiens clone 24881 mRNA sequenc ESTs	TM TM	4.7 4.6
	406400	#(NOCAT)	113.101100	0	trypsin,TM	4.6
•	428301	AW628666	Hs.98440	ESTs	TM	4.6
A E	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone N	TM	4.6
45	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone N	TM TM	4.6 4.6
	409928 435244	AL137163 N77221	Hs.57549 Hs.187824	hypothetical protein dJ47384 ESTs	pkinase,In3	4.6
	404996	#(NOCAT)	110.101024	0	Peptidase_C1	4.6
	407905	AW103655	Hs.252905	ESTs	SS,Ephrin	4.6
50	441675	Al914329	Hs.5461	ESTs	TM	4.6
	420276 422529	AA290938 AW015128	Hs.190561	ESTs, Highly similar to mosaic protein LR1 ESTs	TM,fn3,ldi_recept_a TM	4.5 4.5
	438018	AK001160	Hs.256703 Hs.5999	hypothetical protein FLJ10298	TM	4.5
	457465	AW301344	Hs.195969	ESTs	Pribosyltran	4.5
55	418848	AJ820961	Hs.193465	ESTa	TM.pkise	4.5
	447499	AW262580	Hs.147674	KIAA1621 protein	TM	4.5
	432731	R31178	Hs.287820	fibroneciin 1	SS Nucleoside_tra2	4.5 4.4
	434699 427528	AA643687 AU077143	Hs.149425 Hs.179565	Homo sapiens cDNA FLJ11980 fis, clone H minichromosome maintenance deficient (S.	TM	4.4
60	409092	AI735283	Hs.172608	ESTs	TM	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	TM	4.4
	453331	A1240665	Hs.8895	ESTs	TM	4.4
	448133 429597	AA723157 NM_003816	Hs.73769 Hs.2442	folate receptor 1 (adult) a disintegrin and metalloproteinase domain	TM TM	4.4 4.4
65	453279	AW893940	Hs.59698	ESTs	TM	4.4
•	409459	D86407	Hs.54481	low density lipoprotein receptor-related pro	TM,EGF,Id1_recept_a	4.4
	431708	A1698136	Hs.108873	ESTs	TM	4.4
	433906	A1167816	Hs.43355	ESTs	TM	4.4
70	441423 446770	A1793299 AV660309	Hs.126877 Hs.154986	ESTs ESTs, Wealdy similar to AF137386 1 plasm	TM TM	4.4 4.3
70	412078	X69699	Hs.73149	paired box gene 8	TM	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS	4.3
	448390	AL035414	Hs.21068	hypothetical protein	TM	4.3
75	453628	AW243307	Hs.170187	ESTs	TM	4.3
13	452367 413775	U71207 AW409934	Hs.29279 Hs.75528	eyes absent (Orosophila) homolog 2 nucleolar GTPase	TM MMR_HSR1	4.3 4.3
	451592	AVV409934 AI805416	Hs.213897	ESTs	TM	4.3
	419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GC81 Homo s	TM	4.2
00	452943	BE247449	Hs.31082	hypothetical protein FLJ 10525	TM	4.2
80	428679	AA431765	II- ecteas	gb:zw80c03.s1 Soares_testis_NHT Home s	TM	4.2
	436209 406076	AW850417 AL390179	Hs.254020 Hs.137011	ESTs, Moderately similar to unnamed prote Homo sapians mRNA; cDNA DKFZp547P	TM TM	4.2 4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	TM	4.2
	406871	AA129547	Hs.285754 .		F-ectin_cap_A	4.2
				•		

	4217EA	AA514986	11- 000705	FOT-	714	40
	431750 449554	AA514300 AA682382	Hs.283705 Hs.59982	ESTs ESTs	TM TM	4.2 4.2
	409073	AA063458	NS.33302	gbzf71a07.s1 Soares_pineat_gland_N3HP	SEA	4.1
_	433929	Al375499	Hs.27379	ESTs	TM.	4.1
5	415457	AW081710	Hs.7369	ESTs, Wealty similar to ALU1_HUMAN A	TM	4.1
	444381	BE387335	Hs.283713	ESTs	TM	4.1
	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic protein rec	TM	4.1
	421515	Y11339	Hs.105352	GaiNAc alpha-2, 6-sialyltransferase I, long	TM	4.1
10	453293 409564	AA382267 AA045857	Hs.10653 Hs.54943	ESTS	TM TM	4.1
10	429628	H09604	Hs.13268	fracture callus 1 (rat) homolog ESTs	TM	4,1 4,1
	440452	Al925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN	TM	4.1
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retina	TM	4.1
	425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic po	TM	4.1
15	417300	A1765227	Hs.55610	solute carrier family 30 (zinc transporter), m	TM	4.1
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM	4.1
	452834	AI638627	Hs.105685	ESTs	kinesin	4.1
	428771	AB028992	Hs.193143	KIAA1069 protein	PI-PLC-X,PI-PLC-Y	4.0
20	412314	AAB25247	Hs.250899	heat shock factor binding protein 1	TM	4.0
20	436291	8E568452	Hs.5101	ESTs; Highly similar to protein regulating c	TM	4.0
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	KRAB	4.0
	409365 413374	AA702376 NM_001034	Hs.226440 Hs.75319	Homo sapiens clone 24881 mRNA sequenc ribonucleotide reductase M2 polypeptide	TM Change and	4.0 4.0
	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	ribonuc_red TM	4.0
25	445941	Al267371	Hs.172636	ESTs	TM,lectin_c	4.0
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	lipocalin	4.0
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	TM	4.0
	418301	AW976201	Hs.187618	ESTs	TM	4.0
20	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	TGF-beta,Myc_N_term	4.0
30	408684	R61377	Hs.12727	hypothetical protein FLJ21610	TM	4.0
	414869	AA157291	Hs.72163	ESTS	TM	4.0
	420281	A1623693	Hs.191533	ESTs	Cation_efflux	3.9
	416658	·U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	EGF,TB	3.9
35	411274 437222	NM_002776 AL117588	Hs.69423 Hs.299963	kalikrein 10 ESTs	typsin,TM	3.9
55	431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	TM TM,cadherin,	3.9 3.9
	430634	AIB60651	Hs.26685	ESTs	TM	3.9
	415716	N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fis, clone H	NAP_family	3.9
	420179	N74530	Hs.21168	ESTs	TM	3.8
40	451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone N	TM	3.8
	429496	AA453800	Hs.192793	ESTs	TM	3.8
	421764	Al681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN C	TM	3.8
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Hom	TM,SDF	3.8
45	422939	AW394055	Hs.98427	ESTs ·	TM.	3.8
43	414737	Al160386	Hs.125087	ESTs	TM CC to make	3.8
	411773 425247	NM_006799 NM_005940	Hs.72026 Hs.155324	protease, serine, 21 (testisin) matrix metalloproteinase 11 (stromelysin 3)	SS,trypsin SS,Peptidase_M10	3.8 3.7
	424433	H04607	Hs.9218	ESTs	TM	3.7
	431846	BE019924	Hs.271580	Uroplakin 18	TM,transmembrane4	3.7
50	407792	AJ077715	Hs.39384	putative secreted ligand homologous to fix1	SS	3.7
••	417531	NM_003157	Hs.1087	serine/threonine kinase 2	pkise,pkinase	3.7
	434836	AA651629	Hs.118088	ESTs	TM	3.7
	439810	AL109710	Hs.85568	EST	TM	3.7
	418693	Al750878	Hs.87409	thrombospondin 1	SS,EGF,TSPN	3.7
55	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM	3.7
	436304	AA339622	Hs.108887	ESTs	TM	3.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transloco	TM	3.7
	453468 428943	W00712 AW086180	Hs.32990	DKFZP566F084 protein	TM TM	3.6
60	411402	BE297855	Hs.37636 Hs.69855	ESTs, Weakly similar to KIAA1392 protein NRAS-related gene	CSD,ras,CSD	3.6 3.6
00	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMA	TM	3.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR	ABC_tran	3.6
	407340	AA810168	Hs.232119	ESTs	TM	3.6
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	TM	3.6
65	438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMA	TM	3.6
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	AAA,AAA	3.6
	441111	A1806867	Hs.126594	ESTs	· TM	3.6
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM	3.6
70	409542	AA503020	Hs.36563	ESTs	Ribosomal_S8	3.6
70	425441	AA449644	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone N	Aa_trans	3.6
	428137	AA421792	Hs.170999	ESTS	AAA	3.6
	433692 438689	AI805860 AW129261	Hs.208675	ESTs, Wealdy similar to neuronal thread pr	TM TM	3.6 3.6
	438669	AW129261 AW631480	Hs.250565 Hs.8688	ESTS ESTS	TM	3.6 3.6
75	446261	AA313893	Hs.13399	hypothetical protein FLJ12615 similar to m	ATP-synt_D,PH	3.6
. •	414343	AL036166	Hs.75914	coated vesicle membrane protein	TM	3.5
	414812	X72755	Hs.77367	monokine induced by gamma interferon	SS,IL8	3.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-Indu	· TM	3.5
	415786	AW419196	Hs.257924	ESTs	TM	3.5
80	427177	AB006537	Hs.173880	Interleukin 1 receptor accessory protein	TMig	3.5
	427687	AW003867	Hs.112403	ESTs	7tm_1	3.5
	444619	BE538082	Hs.8172	ESTs	TM	3.5
	447336	AW139383	Hs.245437	ESTs	AhpC-TSA	3.5
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	TM	3.5

	418792	AB037805	Hs.88442	KIAA1384 protein	TH	9.5
	408031	AAD81395	Hs.42173	Homo saplens cDNA FLJ10366 fis, clone N	TM TM	3.5 3.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	TM	3.5
5	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (pro	EGF	3.5
,	448089 422278	A1467945	Hs.173696	ESTs	S\$	3.5
	442133	AF072873 AW874138	Hs.114218 Hs.129017	ESTS ESTS	TM,Fz,Frizzled TM	3.5 3.5
	410908	AA121686	Hs.10592	ESTs	GTP_EFTU	3.5
10	452198	AI097560	Hs.61210	ESTs	TM	3.5
10	408730	AV660717	Hs.47144	DKFZP586N0819 protein	pkinase	3.4
	436488	BE620909	Hs.261023	hypothetical protein FLJ20958	TM	3.4
	409745 445870	AA077391 AW410053	Hs.13406	gb:7814E12 Chromosome 7 Fetal Brein cD syntaxin 18	TM TM	3.4 3.4
	451743	AW074266	Hs.23071	ESTs	TM	3.4
15	407846	AA426202	Hs.40403	Cbp/p300-Interacting transactivator, with G	TM	3.4
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	3.4
	412848 413625	AA121514	Hs.70832 Hs.71371	ESTs	TM	3.4
	417801	AW451103 AA417383	Hs.82582	ESTs integrin, beta-like 1 (with EGF-like repeat d	filament SS	3.4 3.4
20	422972	N59319	Hs.145404	ESTs	TM	3.4
	429170	NM_001394	Hs.2359	dual specificity phosphatese 4; MAP kinas	DSPc,Rhodanese	3.4
	450377	AB033091	Hs.24936	ESTa	TM	3.4
	443475	AI066470	Hs.134482	· ESTs	TM	3.4
25	419452 409744	U33635 AW675258	Hs.90572 Hs.56265	PTK7 protein tyrosine kinase 7 Homo sapjens mRNA; cDNA DKFZp586P	TM,pkise,ig,SRF-TF TM	3.4 3.4
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	TM	3.4
	404440	#(NOCAT)		0	TM,neur_chan	3.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,Ig	3.4
30	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	wnt	3.4
30	417177 421013	NM_004458 M62397	Hs.81452 Hs.1345	fatty-acid-Coenzyme A ligase, long-chain 4	SS TM	3.4
	427072	H38046	113-13-13	mutated in colorectal cancers gb:yp58c10.r1 Soares fetal liver spleen 1NF	Ribosomal_L22e	3.4 3.4
	433703	AA210863	Hs.3532	nemo-like kinase	pkinase	3.4
25	434294	AJ271379	Hs.21175	ESTs	TM	3.4
35	444188	Al393165	Hs.19175	ESTs	TM	3.4
	446109	N67953	Hs.145920	ESTs	TM Assertance 7	3.4
	400881 450236	AW162998	Hs.24684	KIAA1376 protein	Asparaginase_2 TM	3.3 3.3
	418836	AI655499	Hs.161712	ESTs	TM	3.3
40	437951	T34530	Hs.4210	Homo sapiens cDNA FLJ13069 fis, clone N	TM	3.3
	446896	T15767	Hs.22452	Homo sapiens cDNA: FLJ21084 fis, clone	TM	3.3
	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to rat	mn ee	3.3
	410060 419546	NM_001448 AA244199	Hs.58367	glypican-4 gb:nc06c05.s1 NCL_CGAP_Pr1 Homo sapi	SS TM	3.3 3.3
45	429609	AF002246	Hs.210863	cell adhesion molecule with homology to L	TM,fn3,ig	3.3
	413289	AA128061	Hs.114992	ESTs	TM	3.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	3.3
	401435	#(NOCAT)-	Hs.207725	0 ESTs	TM	3.3 3.3
50	420072 421426	AW961196 AA291101	Hs.33020	Homo saplens cDNA FLJ20434 fis, clone K	TM TM	3.3
•	425851	NM_001490	Hs.159642	glucosaminyl (N-acelyl) transferase 1, core	SS	3.3
	443295	AI049783	Hs.241284	ESTs	TM	3.2
	453116	A1276680	Hs.146086	ESTs	Ribosomal_L5_C	3.2
55	456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-related acid	TM	3.2
55	430016 418281	NM_004736 U09550	Hs.227656 Hs.1154	xenotropic and polytropic retrovirus recepto oviductal glycoprotein 1, 120kD (much 9,	TM con Glynn, hydro, 18	3.2 3.2
	433800	AI034361	Hs.135150	tung type-I cell membrane-associated glyco	asp,Glyco_hydro_18 TM	3.2
	425159	NM_004341	Hs.154868	carbamoyl-phosphale synthetase 2, aspartat	TM	3.2
60	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMA	carb_anhydrase	3.2
60	409533	AW969543	Hs.21291	miltogen-activated protein kinase kinase kin	TM	3.2
	411248 421379	AA551538 Y15221	Hs.69321 Hs.103982	KIAA1359 protein small inducible cytokine subfamily 8 (Cys-	TM SS,IL8	3.2 3.2
	430259	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog	TM	3.2
	414945	BE076358	Hs.77667	lymphocyte anligen 6 complex, locus E	SS	3.2
65	444471	AB020684	Hs.11217	KIAA0877 protein	TM	3.2 3.2
	421674	T10707	Hs.298355	neuronal PAS domain protein 2	Ribosomal_L31e	3.2
	434163 421991	AW974720 NM_014918	Hs.25206 Hs.110488	ESTs KIAA0990 protein	TM SS	3.2 3.2
	409589	AW439900	Hs.256914	ESTs .	TM	3.2
70	414147	BE091834	110.200011	gb:lL2-BT0731-240400-069-C03 BT0731	TM	3.2
	414661	T97401	Hs.21929	ESTs	TM	3.2
	437537	AA758974	Hs.121417	ESTs, Weakly similar to unnamed protein p	TM	3.2
	439702	AW085525	Hs.134182	ESTs	A2M	3.1
75	420552 441028	AK000492 Al333560	Hs.98806 Hs.17558	hypothetical protein ESTs	TM ICE_020,CARD	3.1 3.1
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin indu	TM	3.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	SS,Bombesin	3.1
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG	TM	3.1
80	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMA	SS,Ephrin	3.1
υV	447866 419978	AW444754 NM_001454	Hs.211517 Hs.93974	ESTs forkhead box J1	homeobox Fork_head	3.1 3.1
	446219	Al287344	Hs.149827	ESTs	MIP	3.1
	448428	AF282874	Hs.21201	nectin 3; DKFZP566B0846 protein	TM,ig	3.1
	407615	AW753085		gb:PM1-CT0247-151299-005-e03 CT0247	TM	3.1
				200		

```
410518
                      AW976443
                                                                                                           RasGEF,PH,RhoGEF
                                        Hs.285655
           418396
                      AJ765805
                                        Hs.26691
                                                       ESTs
                                                                                                                                          3.1
                      R61253
                                                                                                           ТМ
           427855
                                        Hs 98265
                                                       ESTs
                                                                                                                                          3.1
           429272
                      W25140
                                                                                                           TM
                                                                                                                                          3.1
                                        Hs.110667
                                                       ESTs
  5
           450171
                       AL133661
                                                       hypothetical protein DKFZp434C0328
                                        Hs.24583
                                                       plasminogen activator, uroldnase
replication factor C (activator 1) 3 (38kD)
hypothetical protein LOC57163
                      X02419
T55979
           414774
                                        Hs.77274
                                                                                                           SS, kringle, trypsin
                                                                                                                                          3.1
           422363
                                        Hs 115474
                                                                                                           TM
                                                                                                                                          3.1
                                                                                                           TM
                                                                                                                                          3.1
           420062
                       AW411096
                                        Hs.94785
                       AA852773
                                        Hs.297939
                                                       ESTs; Wealdy similar to neogenin [H.saple
                                                                                                           TM
10
           427051
                       BE178110
                                        Hs.173374
                                                       ESTs
                                                                                                           TM
                                                                                                                                          3.1
                                                                                                           SS
                                                       leukemia Inhibitory factor (cholinergic diffe
                                                                                                                                          3.1
           428242
                       H55709
                                        Hs.2250
                       BE207039
                                                       serine (or cysteine) proteinase inhibitor, cla
                                                                                                           TM
                                                                                                                                          3.1
           452906
                                        Hs.75621
           429419
                       AB023226
                                        Hs.202276
                                                        KIAA1009 protein
                                                                                                           TM
                                                                                                                                          3.1
                      AF001176
#(NOCAT)
                                                                                                           TM
           417517
                                        Hs.82238
                                                       POP4 (processing of precursor, S. cerevisia
                                                                                                                                          3.1
15
                                                                                                           TM
                                                                                                                                          3.1
           406137
           424800
                       AL035588
                                        Hs.153203
                                                       MyoD family inhibitor
                                                                                                           TM
                                                                                                                                          3.1
                                        Hs.61418
                                                       microfibrillar-associated protein 1
           410252
                       AW821182
           420392
                       Al242930
                                        Hs.97393
                                                        KIAA0328 protein
                                                                                                           SS
                                                                                                                                          3.1
                                                       Homo sapiens cDNA: FLJ21909 fis, clone
Homo sapiens cDNA: FLJ23038 fis, clone
                                                                                                           voltage_CLC,CBS
           423629
                       AW021173
                                        Hs.18612
                                                                                                                                          31
20
                                        Hs 186180
           429334
                       D63078
                                                                                                           Glyco_hydro_2
                                                                                                                                          3.1
                                                       hypothetical protein FLJ20147
fibroblast activation protein; alpha
                       AW901804
                                                                                                                                          3.1
           449802
                                        Hs.23984
                                                                                                           TM
           450506
                       NM_004460
                                        Hs.418
                                                                                                           SS,Peptidase_S9
           433849
                       BE465884
                                        Hs.280728
                                                                                                           TМ
                                                                                                                                          3.0
                                                        signal transducer and activator of transcript
                                                                                                           SH2,STAT
                      NM_005419
AW972300
           411984
                                        Hs.72988
                                                                                                                                          3.0
25
           422530
                                        Hs.118110
                                                       bone marrow stromal cell antigen 2
                                                                                                           TM
                                                                                                                                          30
           422128
                       AW881145
                                                       gb:QV0-OT0033-010400-182-e07 OT0033
                                                                                                           TM
                                                                                                                                          3.0
           409757
                       NM_001898
                                        Hs.123114
                                                       cystatin SN
                                                                                                           SS,cystatin
                                                                                                                                          3.0
           418727
                       AA227609
                                        Hs 94834
                                                        ESTs
                                                                                                           TM
                                                                                                                                          3.0
                                                       karyopherin (importin) beta 3
CDP-diacyfglycerol synthase (phosphatidat
                                        Hs. 113503
                                                                                                           TM
                                                                                                                                          3.0
           422244
                       Y08890
30
                                                                                                                                          3.0
           456844
                       AI264155
                                        Hs.152981
                                                                                                           TM
           432358
                       AJ093491
                                        Hs.72830
                                                        ESTs
                                                                                                           SS
                                                                                                                                          3.0
           416896
                       Al752862
                                        Hs.5638
                                                        KIAA1572 protein
                                                                                                           BTB
                                                                                                                                          3.0
                                                       activating transcription factor 1
Homo septens cDNA FLJ11163 fis, clone P
fucosyltransferase 8 (alpha (1,6) fucosyltran
myo-inositol 1-phosphate synthase A1
           447312
                       A1434345
                                        Hs.36908
                                                                                                           TM
                                                                                                                                          3.0
           445021
                      AK002025
AA158177
                                        Hs.12251
                                                                                                           TM
                                                                                                                                          3.0
35
                                                                                                                                          3.0
                                                                                                           SS
                                        Hs.118722
           422611
                                                                                                                                          3.0
           453597
                       BE281130
                                        Hs.33713
                                                                                                           TM
                       #(NOCAT)
                                                                                                                                          3.0
           401197
                                                                                                           arf,Ets
           403000
                       BE247275
                                        Hs.151787
                                                        U5 snRNP-specific protein, 116 kD
                                                                                                                                          3.0
                                                        gb:zm20h12.s1 Stratagene pancress (93720 regulator of G-protein signalling 1
           410008
413268
                       AA079552
AL039079
                                                                                                           TM FG-GAP
                                                                                                                                          3.0
40
                                        Hs.75256
                                                                                                                                          3.0
                                                                                                           RGS
                                                        ESTs, Weakly similar to T12540 hypotheti
                                                                                                                                          3.0
           414080
                       AA135257
                                        Hs.47783
                                                                                                           TM
                       AA393108
                                        Hs.97365
                                                                                                           TM
                                                                                                                                          3.0
           426882
                                                                                                                                          3.0
3.0
3.0
           427651
                       AW405731
                                        Hs.18498
                                                        Home saplens cDNA FLJ12277 fis, clone M
                                                                                                           TM
                       A1277652
                                        Hs.5457B
                                                                                                           TM
           439444
                                                        FST<sub>8</sub>
45
                                        Hs.279905
                                                        clone HQ0310 PR00310p1
           433001
                       AF217513
                                                                                                           TM
           444895
                                        Hs.301192
                                                        EST cluster (not in UniGene)
                                                                                                                                           3.0
                       A1674383
                                                                                                            TMLASC
                                                        Homo seplens cDNA: FLJ21814 fis, clone
Homo seplens cDNA: FLJ3148 fis, clone N
hypothetical protein PRO3077
TRAM-like protein
                                                                                                                                          3.0
           441962
                       AW972542
                                        Hs.289008
                                                                                                           TM
                                        Hs.120355
           414725
                       AA769791
                                                                                                           TM.7tm_1
                                                                                                                                          3.0
                                                                                                                                           3.0
                       AF119913
                                        Hs 283607
           434241
                                                                                                           SS
50
                                                                                                                                           3.0
           424962
                       NM_012288
                                        Hs.153954
                                                                                                           TM
                                        Hs.183380
                                                        ESTs, Moderately similar to ALU7_HUMA
                                                                                                                                           3.0
           411987
                       AA375975
                                                                                                           TM
                       W94197
                                        Hs.110165
                                                        ribosomal protein L26 homolog
                                                                                                           TM
                                                                                                                                           3.0
           421977
           436481
                       AA379597
                                        Hs.5199
                                                        HSPC150 protein similar to ubiquitin-conju
                                                                                                           TM
                                                                                                                                           3.0
                       AB039723
                                        Hs.40735
                                                        frizzled (Drosophila) homolog 3
                                                                                                           TM,7tm_2,Fz,Frizzled
           407872
                                                                                                                                           3.0
55
                                        Hs.163900
                                                                                                                                           3.0
                       AA292998
           442577
                                                        ESTs
                                                                                                           TM
                                                        gb:yo14h02.s1 Soares adult brain N2b5HB5
           416120
                       H46739
                                        Hs.204732
                                                                                                            TM,Peptidase_M10,7tm_1
           443775
                       AF291664
                                                        matrix metalloproteinase 26
                                                                                                                                           3.0
                                                        Homo saplens HSPC311 mRNA, partial cd
           414664
                       AA587775
                                        Hs.66295
                                                                                                           TM
                                                                                                                                           30
                                                        spondin 1, (f-spondin) extracellular matrix
                       Al612809
                                        Hs.5378
                                                                                                           SS
           457590
                                                                                                                                           3.0
60
           418946
                       AI798841
                                        Hs.132103
                                                                                                            TM
                                                                                                                                           3.0
                                                        EST8
           457940
                       AL360159
                                        Hs.30445
                                                        Homo sapiens mRNA full length insert cON
                                                                                                           TM,SPRY,7tm_1
                                                                                                                                           3.0
           TABLE 15B:
           Pkey: Unique Eos probeset identifier number
65
           CAT number: Gene cluster number
           Accession: Genbank accession numbers
                         CAT Number
                                          AW753085 AW753082 AW054744 AW753107 AW753087
           407615
                         1005404_1
70
                                          AA063458 AA063018 A1444822
                         109851_1
           409073
                                          AA077391 AJ347618 AJ361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
            409745
                         115237_1
                                          AA079552 BE142525 BE142527
            410008
                          116812_1
            414147
                          142127_-1
                                           BE091634
                                          Z24878 AA494098 F13854 AA494040 AA143127 · H46739 H51513 H19779
            414315
                          143512_1
 75
                          1571266_1
            416120
                                           AA689591 AW974261 AA236240 Al077451 AA631399 AW974262
            419311
                          183793_1
                          185766_1
                                           AA244199 AA244272 H57440
            419546
                                           AW881145 AA490718 M85637 AA304575 T05067 AA331991
H38046 W69645 AA397968 H38047
            422128
                         211994_1
                         274884 1
            427072
 80
                                           AA431765 AA432015
                          294049_1
            428679
                                           AA828995 AA834879 AI926361
            438993
                          467651_1
                          711623_1
                                           R36075 Al366546 R36167
            447197
```

TABLE 15C:

Page: Unique mumber corresponding to an Ecs probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402489-495

Strand: Indicates DNA strand from which excus were predicted

NI_position: Indicates nucleotide positions of predicted excus

	Pkey	Ref	Strand	Nt_position
	400881	2842777	Minus	91446-91603,92123-92265
10	401197	9719705	Pius	176341-176452
	401435	8217934	Minus '	54508-55233
	404440	7528051	Plus	80430-81581
	404939	6862697	Plus	175318-175476
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
15	405547	1054740	Plus	124361-124520,124914-125050
	406137	9166422	Minus	30487-31058
	406367	9256126	Minus	58313-58489
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

20

Table 16A lists about 92 genes up-regulated in mucinous-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile emongst various mucinous-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 16A: ABOUT 92 UP-REGULATED GENES, MUCINOUS OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID

25 .

Title: UniGene title Prot. Dom.: Predicted protein domain structure

30 ratio: ratio tumor vs. normal tissues

	Pkey	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
	430691	C14187	Hs.103538 Hs.3132	ESTs	START	34.9 28.0
35	432938	T27013		steroidogenic acute regulatory protein		
"	418007 451181	M13509 Al796330	Hs.83169 Hs.207461	Matrix metalioprotease 1 (interstitial collag ESTs	SS,Peptidase_M10	22.3 10.8
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		10.0
	407638	AJ404672	Hs.288693	EST		9.3
	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN		9.2
40	426890	AA393167	Hs.41294	ESTS, Weakly Similar to CANZ_ROWAN		9.1
70	421155	H87879	Hs.102267	lysyl oxidase	SS,Lysyl_oxidase	8.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	taminin_EGF	7.6
	453866	AW291498	Hs.250557	ESTs	and the contract of the contra	7.6
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-rel		7.4
45	418738	AW388633	Hs.6682	solute carrier family 7, member 11		7.2
-15	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone P	RA	7.0
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	141	6.7
	424586	NM_003401		X-ray repair complementing defective repa		6.7
	445891	AW391342	Hs.199460	ESTs		6.2
50	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	6.1
50	452705	H49805	Hs.246005	ESTs	With	6.1
	421285	NM_000102		cytochrome P450, subfamily XVII (steroid	TM,p450	5.5
	408562	Al436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote	· inqp too	5.3
	420159	AI572490	Hs.99785	ESTs		5.3
55	451105	Al761324	12.551.55	gb:wi60b11.x1 NCI_CGAP_Co16 Homo s		5.2
	409049	AJ423132	Hs.146343	ESTs		5.0
	448674	W31178	Hs.154140	ESTs	TM	5.0
	423811	AW299598	Hs.50895	homeo box C4	***	4.9
	427469	AA403084	Hs.269347	ESTs		4.9
60	447033	AL357412	Hs.157601	EST - not in UniGene	PH	4.9
	424433	H04607	Hs.9218	ESTs		4.9
	448811	AI590371	Hs.174759	ESTs	TM	4.8
	444330	AI597655	Hs.49265	ESTs		4.8
	409041	AB033025	Hs.50081	KIAA1199 protein		4.7
65	418735	N48769	Hs.44609	ESTs		4.5
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	4.5
	430073	U86136	Hs.232070	telomerase-associated protein 1	WD40	4.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	4.4
70	422260	AA315993	Hs.105484	ESTs; Weakly similar to LITHOSTATHIN		4.4
70	421110	AJ250717	Hs.1355	cathepsin E	SS,asp	4.3
	445676	A1247763	Hs.16928	ESTs		4.2
	430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186	Epimerase	3.8
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	3.8
~~	438078	AI016377	Hs.131693	ESTs		3.7
75	434032	AW009951	Hs.206892	ESTs	. 0	3.7
	445657	AW612141	Hs.279575	ESTs	7tm_1	3.6
	439759	AL359055	Hs.67709	Homo septens mRNA full tength insert cDN		3.5
	455666	BE065813		gb:RC2-8T0318-110100-012-a08 BT0318		3.5
90	448844	AI581519	Hs.177164	EST8		3.5
80	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	3.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM •	3.4
	458123	AW892676	11- 0200	gb:CM3-NN0004-280300-131-c12 NN0004		3.4
	407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMA	00.100	3.4
	424894	H83520	Hs.153678	reproduction 8	SS,UBX	3.3

	424639	A1017404	D- 121200	ESTs		3.3
	414083	A1917494 AL121282	Hs.131329 Hs.257786	ESTs		3.2
	426471	M22440	Hs.170009	transforming growth factor, alpha	SS.EGF	3.2
	428927	AA441837	Hs.90250	ESTs		3.1
5	406129	#(NOCAT)		0	TM,cNMP_binding	3.1
_	452699	AW295390	Hs.213062	ESTs		3.1
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	homeobax	3.1
	428976	AL037824	Hs.194695	ras homolog gene family, member I	ras	3.1
• •	435396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fls, clone H	wnt	3.0
10	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	SS,insulin,pkinase	3.0
	404253	#(NOCAT)		0	histone	29
	452461	N78223	Hs.108106	transcription factor	G9a,PHD	2.9
	429597	NM_003816		a disintegrin and metalloproteinase domain	TM	29
15	413289	AA128061	Hs.114992	ESTs		29
15	429703	T93154	Hs.28705	ESTs		2.9 2.8
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 ffs, clone N		2.8
•	424796	AW298244	Hs.293507	ESTs	Lucid auditors	2.8
	424086	AI351010	Hs.102267	lysyl oxidase · ESTs	Lysyl_oxidase	2.7
20	408427	AW194270	Hs.177236	a disintegrin and metalloproteinase domain		2.7
20	450375 446999	AA009647 AA151520	Hs.8850 Hs.279525	hypothetical protein PRO2605		2.7
	428819	AL135623	Hs.193914	KIAA0575 gene product		2.7
	422956	BE545072	Hs.122579	ESTs		2.7
	428949	AA442153	Hs.104744	ESTs, Wealdy similar to AF208855 1 BM-0		2.7
25	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	2.6
23	420380	AA640891	Hs.102406	ESTs	,,a	2.6
	428651	AF196478	Hs.188401	annexin A10	TM,annexin	2.6
	417849	AW291587	Hs.82733	Nidogen 2	EGF,ldl_recept_b	2.6
	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	TM	2.6
30	417975	AA641836	Hs.30085	Homo saplens cDNA: FLJ23186 ffs, clone		2.6
	448756	A1739241	Hs.171480	ESTs		2.6
	425087	R62424	Hs.126059	ESTs		2.5
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	Kelch	2.5
	443211	Al128388	Hs.143655	ESTs		2.5
35	415263	AA948033	Hs.130853	ESTs	histone	2.5
	432867	AW016936	Hs.233364	ESTs	GSHPx	2.5
	438639	A1278360	Hs.31409	ESTs		2.5
	455386	AW935875		gb:QV3-DT0019-120100-055-d06 DT0019		2.5
40	419092	J05581	Hs.89603	mucin 1, transmembrane	TM,SEA	2.5
40	452055	AJ377431	Hs.293772	ESTs		2.5
45	CAT numb	8: que Eos probesi er: Gene cluste : Genbank acce	r number			
	Pkey	CAT Numbe	r Accession			
	430704	322217_1		AW206655 AA484440		
	451105	859083_1	AJ761324 A	W880941 AW880937		
50	455386	1287756_1		BE069116 BE160251		
	455666	1349545_1	BE065813	BE065788 BE065889 BE065832		
	458123	479942_1	AW892676	AA853877 D44747		
	T101 F 40			•		
55	TABLE 16			as Cas ambasal		
22	Prey: Uni	que number cor	ho 7 deit eur	an Eos probeset nbers in this column are Genbank Identifier (GI) numbers.	"Dunham Let al " refers t	o the publication entitled "The DNA sequence of
				n, et al. (1999) <u>Nature</u> 402:489-495	, Community of the Toloro	a dio pediadaeni dinadae into di I rodi anno di
				ch exons were predicted		
	All nocitio	a. Indicates are	dentida nocili	ons of predicted exons		
60	порожи	ii. Holbates not	aconne bosin	ors or produces exerts		
50	Pkey	Ref	Strand	Nt_position		
	404253	9367202	Minus	55675-56055		
	406129	9160131	Plus	2567-3056		
						•
65						
	Table 17A	lists about 183	genes up-rea	ulated in endometrioid-type ovarian cancer compared to	normal adult tissues. Thes	e were selected as for Table 14A, except that the
	"average"	ovarian cancer	level was set	to the 75th percentile amongst various endometriold-type	ovarian cancers, and the t	tumor/normal tissue ratio was greater than or equa
	2.5.					

ne Jual to 25.

TABLE 17A: ABOUT 183 UP-REGULATED GENES, ENDOMETRIOID OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primakey Ex Acon: Exemplar Accession UG ID: UniGene ID Title: UniGene title Prot. Dom.: Predicted protein domains ratio: ratio tumor vs. normal tissue 70

75

	Pkey	Ex. Acon	UGID	Title	Prot. Corn.	ratio
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		38.9
80	435094	AI560129	Hs.277523	EST		28.8
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SR		24.1
	428187	AI687303	Hs.285529	ESTs		23.9
	449034	AI624049		ab:ts41a09.x1 NCI_CGAP_Ut1 Homo sapi		19.9
	453102	NM_007197	Hs.31664	frizzted (Drosophila) homolog 10	TM,Fz,Frtzzled	15.7

	412925	AI089319	Us 4702/2	Ecto		15.7
	438817	AI023799	Hs.179243 Hs.163242	ESTs ESTs		13.6
	447033	Al357412	Hs.157601	EST - not in UniGene	PH	13.5
5	433222		Hs.238415	ESTs, Moderately similar to ALU8_HUMA		13.1
J	422956 450451	8E545072 AW591528	Hs.122579 Hs.202072	ESTs ESTs		12.9 11.9
	453964	AI961486	Hs.12744	ESTS	homeobox	11.5
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sa		11.4
10	431989 413623	AW972870 AA825721	Hs.291069 Hs.246973	ESTs ESTs	SS	10.3 9.7
10	440901	AA909358	Hs.128612	ESTs		9.6
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	9.6
	421478	A1683243	Hs.97258	ESTs .	CC Tierus foe	9.3 9.2
15	448706 410566	AW291095 AA373210	Hs.21814 Hs.43047	class II cytokine receptor ZCYTOR7 Homo saptens cDNA FLJ13585 fis, clone P	SS,Tissue_fac	9.2 8.7
	438993	AA828995		Integrin; beta 8	SS,integrin_B	8.7
	427121	Al272815	Hs.173656	KIAA0941 protein	C2,	8.4
	420610 427356	AI683183 AW023482	Hs.99348 Hs.97849	distal-less homeo box 5 ESTs	homeobox	8.1 8.0
20	446577	AB040933	Hs.15420	KIAA1500 protein		8.0
	431118	BE264901	Hs.250502	carbonic anhydrase VIII	carb_anhydrase	7.5
	448112	AW245919	Hs.301018	ESTs, Weakly similar to ALUB_HUMAN	Indiah. Il h	6.9
	451106 449433	BE382701 AI672096	Hs.25960 Hs.9012	N-myc ESTs	HLH,Myc_N_term	6.6 6.3
25	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (y		6.3
	434636	AA083764	Hs.241334	ESTs		6.1
	453688 422805	AW381270 AA436989	Hs.194110 Hs.121017	Homo sapiens mRNA; cDNA DKFZp434C	histone	5.9 5.8
	400292	AA250737	Hs.72472	H2A histone family; member A BMPR-lb; bone morphogenetic protein rec	nsule	5.7
30	443179	AI928402	Hs.6933	Homo saplens cDNA FLJ12684 fis, clone N		5.6
	418134	AA397769	Hs.86617	ESTs	to an about	5.5
	452249 409269	BE394412 AA576953	Hs.61252 Hs.22972	ESTs Homo sapiens cDNA FLJ13352 fis, clone O	homeobox TM,UPF0016	5.5 5.5
	413335	AI613318	Hs.48442	ESTs .	Titique i do to	5.4
35	441081	A1584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	5.4
	428029	H05840	Hs.293071	ESTs	-150	5.3 5.3
	419183 409094	U60669 AW337237	Hs.89663	cylochrome P450, subfamily XXIV (vitami gb:xw82f01.x1 NCI_CGAP_Pan1 Homo sa	p450	5.3 5.2
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	START	5.1
40	410102	AW248508	Hs.279727	ESTs;	SS	5.1
	447835 438202	AW591623 AW169287	Hs.164129 Hs.22588	ESTs ESTs		5.1 5.0
	423992	AW898292	Hs.137206	Homo saplens mRNA; cDNA DKFZp564H		5.0
	425905	AB032959	Hs.161700	KIAA1133 protein	TM	5.0
45	452461	N78223	Hs.108106	transcription factor	G9a,PHD	4.9 4.8
	430691 441675	C14187 A1914329	Hs.103538 Hs.5461	ESTs ESTs		4.0
	425695	NM_005401		protein tyrosine phosphatase, non-receptor	Band_41,Y_phosphatase	4.6
50	440340	AW895503	Hs.125276	ESTB		4.5
50	428579 444783	NM_005756 AK001468	Hs.184942 Hs.62180	G protein-coupled receptor 64 ESTs	TM PH	4.5 4.4
	451459	Al797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMA	***	4.4
	413395	AI266507	Hs.145689	ESTs		4.3
55	415263	AA948033	Hs.130853	ESTS	histone	4.2 4.2
55	413988 452030	M81883 AL137578	Hs.75668 Hs.27607	glutamate decarboxylase 1 (brain, 67kD) Homo sapiens mRNA; cDNA DKFZp564N	pyridoxal_deC	4.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069		4.1
	446431	R45652	Hs.153486	ESTs		4.1
60	434891 415139	AA814309 AW975942	Hs.123583 Hs.48524	ESTs ESTs	G-patch	4.0 4.0
00	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN A	Ороши	4.0
	447112	H17800	Hs.7154	ESTs		3.9
	420633	NM_014581		odorant-binding protein 28 Homo sapiens cDNA FLJ14232 fis, clone N	TM, lipocalin	3.9 3.9
65	459574 415138	Al741122 C18356	Hs.101810 Hs.78045	tissue factor pathway Inhibitor 2 TFP12	Kunitz_BPTI,G-gamma	3.9
	414083	AL121282	Hs.257786	ESTs		3.7
	442006	AW975183	Hs.292663	ESTs	Thomash	3.7
	409731 424906	AA125985 Al566086	Hs.56145 Hs.153716	thymosin, beta, identified in neuroblastoma Homo sapiens mRNA for Hmob33 protein,	Thymosin	3.7 3.7
70	456662	NM_002448		msh (Drosophila) homeo box homolog 1 (fo	homeobox	3.7
-	429125	AA446854	Hs.271004	ESTs	7.37	3.6
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related pro	oun	3.6 3.5
	458861 418506	A1630223 AA084248	Hs.85339	gb:ad06g08.r1 Proliferating Erythrold Cells G protein-coupled receptor 39	PHD	3.5 3.5
75	423123		Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS,AIRS	3.4
	437960	A1669586	Hs.222194	ESTs		3.4
	400298	AA032279	Hs.61635	STEAP1	TM	3.4 3.4
	407162 408621	N63855 A1970872	Hs.142634 Hs.46638	zinc finger protein chromosome 11 open reading frame 8; feta		3.3
80	445829	A1452457	Hs.145526	ESTs		3.3
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA	TH	3.3 3.3
	457979 402606	#(NOCAT)	Hs.270942	ESTs	TM	3.3 3.2
	426471	M22440	Hs.170009 .	transforming growth factor, alpha	SS,EGF	3.2

	400004			505		
	430294	AI538226	Hs.135184	EST8	polyprenyt_synt	3.2
	448027 432619	AV458437 AW291722	Hs.177224	ESTs	TRC	3.2 3.2
	432019	BE182082	Hs.278526	related to the N terminus of tre	TBC	
5	441377	BE218239	Hs.246973 Hs.202656	ESTs ESTs		3.2 3.2
,	441085	AW136551	Hs.181245	Homo sapiens cONA FLJ12532 ffs, clone N		3.2
	433527	AW235613	Hs.133020	ESTs		3.2
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.2
	419807	R77402		gb:yl75f11.s1 Soares placenta Nb2HP Hom		3.1
10	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	homeobox	3.1
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N		3.1
	450480	X82125	Hs.25040	zinc finger protein 239	zf-C2H2	3.1
	420149	AA255920	Hs.88095	ESTs		3.1
1.5	413415	AA829282	Hs.34969	ESTs	•	3.1
15	438966	AW979074		gb:EST391184 MAGE resequences, MAGP		3.1
	431041	AA490967	Hs.105276	ESTs	Oxysterol_8P	3.1
	415245	N59650 '	Hs.27252	ESTs		3.0
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6	kinesin	3.0
20	431707	R21326 AB033052	Hs.267905	hypothetical protein FLJ10422		3.0
20	448816 447866	AW444754	Hs.22151 Hs.211517	KIAA1226 protein ESTs	homeobox	3.0 3.0
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	IDITIOUUX	3.0
	406997	U07807	Hs.194762	Human metallothionein IV (MTIV) gene, c		3.0
	433426	H69125	Hs.133525	EST8	TM	3.0
25	420440	NM_002407		mammaglobin 2	Uteroglobin ·	3.0
	420181	Al380089	Hs.158951	ESTs		3.0
	458627	AW088642	Hs.97984	ESTs; Wealty similar to WASP-family pro		2.9
	452055	Al377431	Hs.293772	ESTs		2.9
20	429663	M68874	Hs.211587	Human phosphalidylcholine 2-acylhydrolas	C2,PLA2_B	2.9
30	415125	AF061198	Hs.301941	Homo saplens mRNA for noreplnephrine tr	TM,SNF	2.9
	412708	R26830	Hs.106137	ESTs	TM,7tm_2,Rho_GDI	2.9
	451389	N73222	Hs.21738	KIAA1008 protein		2.9
	423337	NM_004655		exin 2 (conductin, exil)	DIX,RGS	29
35	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrotase		2.9
22	428054	A1948688	Hs.266619	ESTs		2.9
	448243	AW369771	Hs.77496	ESTs	00	2.9
	425723 432415	NM_014420 T16971	Hs.159311 Hs.289014	dickkopf (Xenopus laevis) homolog 4 ESTs	SS	2.9
	432413	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)		2.9 2.9
40	400195	030072	113.77204	0		2.9
	449874	AA135688	Hs.10083	ESTs		2.8
	452367	U71207	Hs.29279	eyes absent (Orosophila) homolog 2	Hydrolase	2.8
	428093	AW594506	Hs.104830	ESTs	1,4.5.55	2.8
	409640	U78722	Hs.55481	zinc finger protein 165	TM,zf-C2H2,SCAN	2.8
45	424169	AA336399	Hs.153797	ESTs	mito_carr	2.8
	409638	AW450420	Hs.21335	ESTs	\ \ \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	2.8
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [2.8
	426890	AA393167	Hs.41294	ESTs		2.8
50	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93		2.8
50	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce		2.8
	416624	H69044	40.00	gb:yr77h05.s1 Soares fetal liver spleen 1NF	zf-C3HC4	2.8
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.7
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone		2.7
55	447342	Al199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAM		2.7
55	421247 419752	BE391727 AA249573	Hs.102910 Hs.152618	general transcription factor IIH, polypeptid ESTs		2.7 2.7
	410658	AW105231	Hs.192035	ESTs		2.7
	437698	R61837	Hs.7990	ESTs		2.7
	458027	L49054	Hs.85195	ESTs, Highly similar to 1(3;5)(q25.1;p34) f		2.7
60	438689	AW129261	Hs.250565	ESTs	•	2.7
	439876	AI376278	Hs.100921	ESTs, Weakly similar to ALU7_HUMAN A	SCAN	2.7
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	pkinase	2.7
	436406	AW105723	Hs.125346	ESTs		2.7
c =	437938	A1950087		ESTs; Weakly similar to Gag-Pol polyprote		2.7
65	419917	AA320068	Hs.93701 .	Homo sapiens mRNA; cDNA DKFZp434E		2.7
	434836	AA651629	Hs.118088	ESTs		2.7
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709		2.7
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	WD40	2.7
70	409757		Hs.123114	cystatin SN	SS,cystalin	2.6
70	443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	2.6
	427961 426668	AW293165	Hs.143134 Hs.97162	ESTs ESTs		2.6 2.6
	426668 424717	AW136934 H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	2.6
	434669	AF151534	Hs.92023	core histone macroH2A2.2	histona,A1pp,DUF27	26
75	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM,PTN_MK	2.6
, 5	451009	AA013140	Hs.115707	ESTs	Colluct in an	2.6
	429774	AJ522215	Hs.50883	ESTs	pkinase	2.6
	439951	AI347067	Hs.124636	ESTs	TM	2.6
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfera	AIRS,formyl_transf	2.5
80	416806	NM_000288		peroxisomal biogenesis factor 7	WD40	2.5
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C	2.5
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	Dihydroorolase	2.5
	459583	A1907673		gb:IL-BT152-080399-004 BT152 Homo sa		2.5
	440870	A1687284	Hs.150539 .	Homo saplens cDNA FLJ13793 fis, clone T	PAX,	2.5

	446693 407289 400882	AW750373 AA135159	Hs.42315 Hs.203349	Homo sapiens cDNA FLJ13036 fis, clone N Homo sapiens cDNA FLJ12149 fis, clone M 0	ТМ	25 25 25						
5	431322 424081 451996 403381	AW970622 NM_006413 AW514021 #(NOCAT)	Hs.139120 Hs.245510	gb:EST382704 MAGE resequences, MAGK ribonuclease P (30XD) ESTs 0		25 25 25 25 25						
10	419488 418882	AA316241 NM_004996	Hs.90691 Hs.89433	nucleophosmin/nucleoplasmin 3 ATP-binding cassette, sub-family C (CFTR	SS TM_ABC_membrane	2.5 2.5 2.5						
	TABLE 17B: Piey: Unique Eos probeset identifier number CAT number: Gene duster number Accession: Genbank accession numbers											
15												
20	Pkey 409094 416624 419807 431322 437938	1099611_1 1604694_1 188252_1 331543_1 44573_2	AW337237 AW861642 AW661655 AW858008 AW657990 AW858007 H69044 T47567 H75691 T50292 R77402 AA262462 AA250988 R05794 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 Al251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493									
25			AA927794 AL560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 Al890387 Al950344 Al741346 Al689062 AA282915 AW102898 AI872193 AJ763273 AW173386 AW175329 Al653832 AJ762688 AA988777 AA48882 Al356394 AW103813 Al539642 AA642789 AA856975 AW505512 Al961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 Al819225 AW205662 Al683338 Al858509 AW276905 Al6533006 AA972584 AA908741 AW072629 AW513995 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 Al022058 AA780419 AA551005 W80701 AW613456 Al373032 Al564269 F00531									
30	438966 438993 442438 448404 449034	467436_1 ⁻¹ 487651_1 542469_1 761515_1 794817_1	H83488 W37181 W78802 R66056 A1002839 R67840 AA300207 AW959581 T63226 F04005 AW979074 AA834841 AA828650 AA828995 AA834879 A1926361 AA995998 A1916584 R61781 T777332 F07756 F08149 F07647 BEG089373 A1498612 AW805032 A1624049 AW117770 A1858360									
35	452771 458861	930983_1 798085_1	T05477 T07855 Al917711 Al630223 Al630470									
40	TABLE 17C: Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (Gi) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Natura 402:489-495 Strand: Indicates DNA strand from which exons were predicted NL_position: Indicates nucleotide positions of predicted exons											
45	Pkey 400882 402606 403381	Ref 2842777 9909429 9438267	Minus Minus	Nt_position 110431-110708 81747-82094 26009-26178								
50	Table 18 lists lists 178 genes up-regulated in ovarian cancer compared to normal edult tissues that are likely to encode proteins that are secreted into blood, tymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal edult tissues was greater than or equal to 2.4,											
55	and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various 149 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.											
60	TABLE 18: ABOUT 178 UP-REGULATED GENES ENCODING SECRETED PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey EX. ADOI: Exemplar Accession UG ID: UniGene ID Title: UniGene IID Title: UniGene IID Title: Title: Title: UniGene IID											
65	Pkey 428579 436982	Ex. Accn NM_005756 AB018305		Title G protein-coupled receptor 64 spondin 1, (f-spondin) extracellular mat	ratio 30.5 29.4							
70	427585 423739 418007 438993 428664 439820	D31152 AA398155 M13509 M73780 AK001666 AL360204		collagen; type X; atpha 1 (Schmid mataph ESTs Mathit matalloprotease 1 (Interstitial c Integrit; bata 8 similar to SALL1 (sal (Drosophila)-like Homo saotens mRNA full length insert cDN	27.0 22.7 20.6 16.7 16.5 16.5							
75	400289 421155 431989 426635	X07820 H87879 AW972870 BE395109 M62062	Hs.2258 Hs.102267	Matrix Metalloproteinese 10 (Stromolysin lysyl oxidase ESTs ESTs caterun (cadherin-associated protein), a	16.2 16.1 15.9 15.9 15.7							
80	424581 428976 416209 439706 452055 410102 428392	AL037824 AA236776 AW872527 AI377431 AW248508 H10233	Hs.194695 Hs.79078 Hs.59761 Hs.293772	casam (carinam ressociation protein), a ras homolog gene family, member I MAD2 (milotic arrest deficient, yeast, h ESTs ESTs ESTs, secretory gramule, neuroendocrine protei	15.1 15.0 14.7 13.2 12.5 12.4							
	720332			215								

	402606	AA434329	Hs.36563	hypothetical protein FLJ22418	11.5
	443715		Hs.9700	cyclin E1	10.7
	433496 418601	AF064254 AA279490	Hs.49765 Hs.86368	VLCS-H1 protein calmegin	10.6 10.3
5	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis,	10.1
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	9.9
	427344 428479	NM_000869 Y00272	Hs.2142 Hs.184572	5-hydroxytryptamine (serotonin) receptor cell division cycle 2, G1 to S and G2 to	9.7 9.7
	429782	NM_005754		Ras-GTPase-activating protein SH3-domain	9.5
10	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.4
	407881	AW072003 AI458679	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot ESTs	9.4 9.3
	435509 408908	BE296227	Hs.181915 Hs.48915	serine/threonine kinase 15	9.0
1.5	433764	AW753676	Hs.39982	ESTs .	9.0
15	445413 438078	AA151342	Hs.12677	CGI-147 protein ESTs	8.7 8.6
	447342	AI016377 AI199268	Hs.131693 Hs.19322	ESTs; Weakly similar to IIII ALU SUBFA	8.1
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	7.7
20	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	7.5
20	426320 424001	W47595 W67883	Hs.169300 Hs.137476	transforming growth factor, beta 2 KIAA1051 protein	7.5 7.4
	458861	NM_007358	Hs.31016	DNA-BINDING PROTEIN M96	7.3
	425465	L18964	Hs.1904	protein kinase C; lota	7.2
25	425776 424620	U25128 AA101043	Hs.159499 Hs.151254	parathyroid hormone receptor 2 kallikrein 7 (chymotryptic; stratum com	7.1 7.0
25	409178	BE393948	Hs.50915	kallikrein 5	6.8
	433159	AB035898	Hs.150587	kinesin-like protein 2	6.6
	410530 449048	M25809	Hs.64173 Hs.22920	ESTs, Highly similar to VAB)	6.5 6.5
30	422095	Z45051 Al868872	Hs.288966	similar to \$68401 (cattle) glucose induc ceruloplasmin (ferroxidase)	6.4
	425371	D49441	Hs.155981	mesothelin	6.4
	448706 .	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	441081 447207	A1584019 AA442233	Hs.169006 Hs.17731	ESTs, Moderately similar to plakophilin hypothetical protein FLJ12892	6.4 6.3
35	420440	NM_002407	Hs.97644	mammaglobin 2	6.2
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	6.2
	415139 440870	AW975942 AI687284	Hs.48524 Hs.150539	ESTs Homo sapiens cDNA FtJ13793 ffs, clone TH	6.1 6.0
	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	6.0
40	437960	AI669586	Hs.222194	ESTs	6.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.9 5.9
	433447 437099	U29195 N77793	Hs.3281 Hs.48659	neuronal pentraxin II ESTs, Highly similar to LMA1	5.9
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.9
45	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	5.8 5.7
	444478 445640	W07318 AW969626	Hs.240 Hs.31704	M-phase phosphoprolein 1 ESTs, Weakly similar to KIAA0227 [H.sapi	5.7 5.7
	453775	NM_002916		replication factor C (activator 1) 4 (37	5.6
50	419917	AA320068	Hs.93701	Homo saplens mRNA; cDNA DKFZp434E232	5.6
50	424539 441645	L02911 A1222279 ·	Hs.150402 Hs.201555	activin A receptor, type I ESTs	5.5 5.5
	424345	AK001380	Hs.145479	Horno saptens cDNA FLJ10518 fis, clone NT	5.4
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	5.4
55	425154 416530	NM_001851 U62801	Hs.154850 Hs.79361	collagen, type IX, alpha 1 kallikrein 6 (neurosin, zyme)	5.4 5.3
55	445236	AK001676	Hs.12457	hypothetical protein FLJ 10814	5.2
	452930	AW195285	Hs.194097	ESTs	5.2
	431130	NM_006103		epididymls-specific; whey-acidic protein hypothetical protein FLJ20516	5.1 5.1
60	411571 432158	AA122393 W33165	Hs.70811 Hs.55548	ESTs, Weakly similar to unknown protein	5.0
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.0
	443268 448133	AI800271	Hs.129445	hypothetical protein FLJ12496	4.9 4.9
	418882	AA723157 NM_004996	Hs.73769 Hs.89433	folate receptor 1 (adult) ATP-binding cassette, sub-family C (CFTR	4.8
65	428555	NM_002214		integrin, beta 8	4.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.7
	406400 439024	AA343629 R96696	Hs.104570 Hs.35598	kaliikrein 8 (neuropsin/ovasin) ESTs	4.7 4.6
~~	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.6
70	448027	A1458437	Hs.177224	ESTs	4.6
	404996 443933	NM_001333 AI091631	Hs.87417 Hs.135501	Cathepsin L2 ESTs	4.6 4.5
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	4.4
75	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	4.3
75	423123	NM_012247 BE514434	Hs.124027 Hs.20830	SELENOPHOSPHATE SYNTHETASE synaptic Res GTPase activating protein 1	4.3 4.2
	448275 419926	AW900992	Hs.20830 Hs.93796	DKFZP586D2223 protein	4.1
	420736	A1263022	Hs.82204	ESTs	4.1
80	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.1 4.0
οV	414343 450654	AL036168 AJ245587	Hs.75914 Hs.25275	coated vesicle membrane protein Kruppel-type zinc finger protein	4.0
	445808	AV655234	Hs.298083	ESTs	3.9
	417389	BE260964	Hs.82045	Midkina (neurita growth-promoting factor	3.9
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	3.8

	420524	Alócacra	No occor	rm.	••
	430634 431846	Al860651 BE019924	Hs.26685 Hs.271580	ESTs Uroplakin 1B	3.8 3.7
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.7
_	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.7
5	420585	AW505139	Hs.279844	hypothetical protein FLJ10033	3.7
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
	411773	NM_006799		protease, serine, 21 (testisin)	3.6
	421928 431958	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.5
10	431336	X63629 AF102546	Hs.2877 Hs.63931	Cadherin 3, P-cadherin (placental) dachshund (Drosophila) homolog	3.5 3.5
10	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.5
	422278	AF072873	Hs.114218	ESTs	3.5
	431B40	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.4
15	408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.4
15	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	3.3
	421841 439864	AA908197 Al720078	Hs.108850	KIAA0936 protein	3.3
	456546	AI690321	Hs.291997 Hs.203845	ESTs Weakly similar to TWIK-related act	3.3 3.2
	410687	U24389	Hs.65436	lysyl oxidase-like 1	3.2
20	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.2
	420552	AK000492	Hs.98806	hypothetical protein	3.1
	421991	NM_014918		KIAA0990 protein	3.1
	418140	BE613836	Hs.83551	microfibrillar-essociated protein 2	3.1
25	458924	BE242158	Hs.24427	DKFZP56601646 protein	3.1
23	411789 434241	AF245505 AF119913	Hs.72157 Hs.283607	Homo saplens-mRNA; cDNA DKFZp564119 hypothetical protein PRO3077	3.1 3.1
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.1
	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase	3.1
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.1
30	412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.1
	425851	NM_001490		glucosaminyl (N-acetyl) transferase 1, c	3.0
	431259	NM_006580		claudin 16	3.0
	418557 428242	BE140602 H55709	Hs.246645 Hs.2250	ESTs leukemia inhibitory factor (cholinergic	3.0 3.0
35	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.0
-	457590	AI612809	Hs.5378	spondin 1, (f-spondin) extracellular mat	2.9
	419741	NM_007019		ubiquitin carrier protein E2-C	2.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.9
40	417315	A1080042	Hs.180450	ribosomal protein S24	2.9
40	438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 (M.musculus	2.9
	442295	A1827248	Hs.224398	ESTs	2.9
	428248 403019	A1126772 AA834626	Hs.40479 Hs.66718	ESTS	2.9 2.8
	435252	AI539519	Hs.120969	RAD54 (S.cerevisiae)-like Homo sepiens cDNA FLJ11562 fis	2.8
45	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.8
	434288	AW189075	Hs.116265	ESTs	2.7
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	2.7
	431611	U58766	Hs.264428	tissue specific transplantation antigen	2.7
50	443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT	2.7
30	453779 433000	N35187	Hs.43388	ESTs	2.7 2.7
	433068 426841	NM_006456 AI052358	Hs.193726	sialyltransferase ESTs	2.7
	428778	AK000530	Hs.193326	fibroblast growth factor receptor-like 1	2.7
	451346	NM_006338		glioma amplified on chromosome 1 protein	2.6
55	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.6
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.6
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	2.6
	433656	AW974941	Hs.292385	ESTs	2.6
60	408210 430651	N81189 AA961694	Hs.43104 Hs.105187	ESTS	2.6 2.5
00	422599	BE387202	Hs.118638	kinesin protein 9 gene non-metastatic cells 1, protein (NM23A)	2.5
	421802	BE261458	Hs.108408	CGI-78 protein	2.5
	446211	Al021993	Hs.14331	S100 calcium-binding protein A13	2.5
~	404029	W72881	Hs.266470	protocadherin beta 2	2.5
65	453012	T95804	Hs.31334	putative mitochondrial outer membrane pr	2.5
	419981	AA897581	Hs.128773	ESTs	2.5
	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	419220 432180	AA811938 Y18418	Hs.291759 Hs.272822	ESTs RuvB (E coli homolog)-like 1	2.5 2.4
70	406850	AI624300	Hs.172928	collagen, type I, aipha 1	2.4
. •	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.4
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.4
	409956	AW103364	Hs.727	H.sapiens activin beta-A subunit (exon 2	2.4
75	407584	W25945	Hs.18745	ESTs	2.4
75	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.4

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Table 19 lists about 17 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or atone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affyrmetrix/Eos Hu03 GeneChip array such that the ratio of "everage" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-mailgnant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-mailgnant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 19: ABOUT 17 GENES, AND COMBINATIONS THEREOF, USEFUL FOR DIAGNOSIS OF OVARIAN CANCER UG ID: UniGene ID Title: UniGene Title

5 % tumors: percent of tumors detected expressing gene

	Single gener	S:	
	UGID	Title	% tumors
	Hs.5378	spondin 1, (f-spondin) extracellular matrix protein	77
10	Hs.12844	EGF-like-domain 6	88
	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	66
	Hs.97644	mammaglobin 2	73
	Hs.155981	mesothelin (cytokine)	57
	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	21
15	Hs.50915	kalikrein 5	27
	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)	54
	Hs.79361	kallikrein 6 (neurosin, zyme)	38
	Hs.83169	MMP 1 (Interstifial collagenase)	23
	Hs.72026	protease, serine, 21 (testisin)	16
20	Hs.39384	putative secreted ligand homologous to fix1	46
	Hs.2719	epididymis-specific; whey-ecidic protein type; four-disulfide core	91
	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	11
	Hs.1584	cartilage oligomeric matrix protein	25
	Hs.169300	TGF beta 2	21
25	Hs.2250	leukemia Inhibitory factor (cholinergic differentiation factor)	23
	Exemplary C	Combinations:	
		EGF-like-domain 6 + mammaglobin 2	93
		kallikrein 7 + mesothelin	71
30		mammaglobin 2 + bone morphogenic protein 7	88
		EGF-like-domain 6 + bone morphogenic protein 7	91
		kallikrein 7 + bone morphogenic protein 7 + testisin	75
		kallikrein 7 + mammaglobin 2 + mesothelin	84
		mammaglobin 2 + bone morphogenic protein 7 + TGF beta 2	91
35		EGF-like-domain 6 + bone morphogenic protein 7 + MMP 1	95
		, - ,	

Table 20A lists about 1025 genes up-regulated in ovarian cancer compared to normal adult lissues. Genes associated with ovarian cancer were selected from the 53462 probesels such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens; the "average" normal adult tissue level was set to the 95th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Tables 208-24B list accession numbers for Pkey's lacking UnigenelD's for tables 20A-24A. For each probeset is listed a gene cluster number from which oligonuclaotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 20C-24C list genomic positioning for Pikey's lacking Unigene ID's and accession numbers in tables 20A-24A. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 20A:
Pkey: Unique Eos probesel Identifier number
ExAcon: Exemplar Accession number, Genbank accession number
UnigenelD: Unitgene number
Unigenel Title: UniGene fitle
Pred. Protein Dom.: Predicted protein domain
R1: Relio of turnor to normal body tissue

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60	Pkey 421296 453028 422310	ExAcon NM_002666 AB006532 AA316622	Hs.31442 Hs.98370	Unigene Tifle perilipin RecQ protein-like 4 cytochrome P450, subfamily IIS	Pred. Protein Dom. perilipin,SS DEAD,helicase_C,Fork_head SS,TM,pkinase,fn3.ig	R1 32.5 27.6 26.5
65	437897 446374 441021 409518	AA770561 AA329256 AW578716 BE384836	Hs.146170 Hs.24756 Hs.7644 Hs.3454	hypothetical protein FLJ22969 ESTs, Moderately similar to al H1 histone family, member 2 KIAA1821 protein	SS,TM,zFDHHC	26.3 22.6 22.3 21.3
70	413436 424420 422645 422098 429556	AF238083 BE614743 L40027 H03117 AW139399	Hs.68061 Hs.146688 Hs.118890 Hs.111497 Hs.98988	sphingosine kinase 1 prostaglandin E synthase glycogen synthase kinase 3 alp similar to mouse neuronal prot ESTs	DAGKc MAPEG,SS,TM,MAPEG pkinase,SS,Ets TM SS,pkinase,PMP22_Claudin	21.2 20.7 20.7 20.2 20.1
75	436485 423652 431773 422179	X59135 AF052122 BE409442 AF091619	Hs.156110 Hs.130712 Hs.268557 Hs.112667	immunoglobulin keppa constant Homo sapians clone 23929 mRNA pleckstrin homology-like domai dynein, exonermal, intermediate	SS.jg.SS ABC1,SS.PID,PID PH,SS,UM,Troponin WD40,SS SS.DS.UBED130 Chara hadro	19.9 19.8 19.4 19.3 18.5
80	420839 441356 424659 439924 458814 451643 439108 432945	A1792682 BE384361 AW891298 A1985897 A1498957 M64437 AW163034 AL043683	Hs.282950 Hs.182885 Hs.331601 Hs.125293 Hs.170861 Hs.234799 Hs.6467	hypothetical protein MGC10870 ESTs, Waddy similar to JC5024 Homo sepiens, Similar to cyste ESTs ESTs, Wealdy similar to Z195_H breakpoint duster region synaptogyrin 3 hypothetical protein FLJ10803	SS,DS,UPF0139,Glyco_hydro SS,TM,ank SS,Fork_head SS SS,TM,IdI_recept_a,kil_re RhoGEF,RhoGAP,PH,C2 Synaptogyrin,SS,TM,PDZ,WD SS	18.5 18.4 18.1 17.5 17.2 16.9

	440440				007117	40.0
	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldL_recept_a,trypsi	16.8
	438424	AI912498	Hs.25895	hypothetical protein FLJ14998	SS,TM	16.7
	409435	AJ810721	Hs.95424	ESTs	SS ·	16.4
5	418969 421612	W33191 AF161254	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	16.2 16.0
J	456177	NM_012391	Hs.106196	8D6 antigen prostate epithelium-specific E	kit_recept_e,SS,TM Els,SAM_PNT	. 15.7
	414837	U24266	Hs.77448	eldehyde dehydrogenase 4 famil	akdedh	15.6
	432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArfGap,homeob	15.5
	454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	15.5
10	401278			Target Exon	Band_41	15.4
	444804	Al084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
	410259	AK000337	Hs.61485	hypothetical protein	GFO_IDH_MocA,GFO_IDH_MocA	15.4
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	15.1
1.5	423081	AF262992	Hs.123159	sperm associated antigen 4	TM	14.9
15	421495	AI583067	Hs.149152	ESTs, Weakly similar to RHOP M	00 00	14.7
	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	14.7
	413244 406901	AW955951 M14624	Hs.159265	kruppel-related zinc finger pr gb:Human 4-beta-galactosyltran	SS,TM,BTB,Pep_M12B_propep	14.6 14.6
	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
20	436186	BE390717	Hs.5074	similar to S. pombe dim1	DIM1,SS	14.5
	455557	AW995839	(101001 1	gb:QV4-BN0044-110200-108-h07 B	Metallophos	14.4
	434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	14.2
	421489	Al922821	Hs.32433	ESTs	SS,PI-PLC-X,PI-PLC-Y,C2	14.1
~ ~	444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
25	435017	AA336522	Hs.12854	angiotensin II, Jype I recepto		14.0
	446572	AV659151	Hs.282961	ESTs		13.9
	434068	AA977935	Hs.127274	ESTs	SS CONTRACTOR TOTAL	13.7
	432481	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis	SS,Collagen,COLFI,TSPN	13.7
30	447304	Z98883	Hs.18079 Hs.104480	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6 13.3
30	421182 407767	AA284855 W15398	Hs.38628	ESTs hypothetical protein	SS,Topoisomerase_1,Topois SS,zf-CCCH	13.3
	456642	AW451623	Hs.109752	putative c-Myc-responsive	00,2700011	13.3
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657	SQS_PSY	13.2
	430178	AW449612	Hs.152475	ESTs	SS	13.1
35	430399	Al916284	Hs.199671	ESTs	Sec7,PH	12.9
	436725	BE045223	Hs.136912	hypothetical protein MGC10798		12.9
	410219	T98226 .	Hs.171952	occludin -	SS,TM,Occludin,BIR	12.7
	442620	C00138	Hs.8535	Homo saplens mRNA for KIAA1668	SS,RNA_pol_K	12.7
40	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
40	425018	BE245277	Hs.154196	E4F transcription factor 1	zf-C2H2,LIM,SS,Exo_endo_p	12.6
	423801 417826	T85105	Hs.132942 Hs.15471	GTPase regulator associated wi ESTs	RhoGAP,SH3,PH SS,cadherin,Cadherin_C_te	12.6 12.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	odioanicinioanicini_o_to	12.6
	420568	F09247	Hs.247735	protocadherin alpha 10	cadherin,SS,TM,cadherin	12.6
45	411570	BE144584	Hs.314341	ESTs		12.5
	430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.5
	423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	12,4
	441805	AA285136	Hs.301914	neuronal specific transcriptio	UM,SS,UM	12.3
50	402365 414371	AI905865		Target Exon	SS,SS,TM,lg	12.2 12.2
50	446780	R31107		thymosin, beta 4, X chromosome gb:yh61g01.s1 Soares placenta	Thymosin	12.1
	428782	X12830	Hs.193400	Interleukin 6 receptor	SS,TM,fn3,lg,SS,TM	12.1
	427695	R88483	Hs.172862	intron of Bicaudal D homolog 1	and trust all and trust	12.1
	400460			C11002253*:gi 129091 sp P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
55	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_H	SS,TM	12.0
	424049	AB014524	Hs.138380	KIAA0624 protein	SS	11.9
	422872	BE326788	Hs.187646	ESTs	TM	11.9
	450800	BE395161	Hs.1390	proteasome (prosome, macropain	SS	11.8
60	428648	AF052728	Hs.188021	potassium voltage-gated channe	cNMP_binding	11.7
60	432329	NM_002962		S100 calcium-binding protein A	S_100,efhand,SS,efhand,S_	11.7
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis	CIF_NFI	11.5
	451195	U10492 AA424317	Hs.438 Hs.6259	mesenchyme homeo box 1 KIAA1698 protein	homeobox,SS SS TM Chro. hwdm 31 Chro.	11.5 11.5
	417595 426500		Hs.170156	KIAA0450 gene product	SS,TM,Glyco_hydro_31,Glyc SS	11.4
65	433124	U51712	Hs.13775	hypothetical protein SMAP31	•	11.4
•••	444001	AI095087	Hs.152299	ESTs, Moderately similar to S6		11.4
	419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	11.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (hom	88	11.3
=-	411408	U76666	Hs.69949	caldum channel, voltage-depen	ion_trans,SS,TM	11.2
70	404438			Target Exon		11.2
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
	406230	41107000-	11. (00000	Target Exon	Deed 44 ED14	11.2 11.2
	432125	AW972667	Hs.183006	Homo saplens cDNA FLJ12300 fis	Band_41,ERM	11.2
75	408832	AW085690	Hs.63428	ESTs, Wealdy similar to Z195_H Eos Control	SS SS Glyco tranf 43 COLE	11.1
, ,	400206 450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS,SS,Glyco_tranf_43,COLF SS	11.0
	407605	W03512	Hs.6479	hypothetical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	11.0
	432143	AL040183	Hs.123484	Homo saplens, clone IMAGE:4178	SS.TM.cvs_rich_FGFR	10.9
	446839	BE091926	Hs.16244	mitolic spindle colled-coll re	Troponin SS glycolytic_en	10.8
80	443559	Al076765	Hs.269899	ESTs, Moderately similar to AL	SS,TM,BIR,UQ_con	10.8
	411298	AW835858		gb:PM0-LT0017-031299-001-h07 L	·	10.8
	409557	BE182896	Hs.211193	ESTs		10.8
	435158	AW663317		OAZ associated protein 1 ESTs, Moderately similar to S6	rm,88,rm 88	10.8 10.6
	444410	BE387360	Hs.33719	Ed 15, MCADI diciy billingi to do	0.10	10.0

						10.0
	428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	10.6 10.6
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 lis	SS,SS,TM,Sema pkinase,SS,TM,OTU,K_tetra	10.5
	416819 419341	U77735 N71463	Hs.80205 Hs.118888	pim-2 oncogene ESTs, Weakly similar to ALU1_H	SS,TM,UPF0016	10.5
5	444359	AI697160	Hs.143594	ESTs, Weakly similar to HS4L_H	opposition to the	10.5
•	404333	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		C7001735*gi[7768636]dbj[BAA95	vwd	10.5
	401210			C12000519:pi7710046 ref NP_05		10.5
	457941	AI004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	10.4 10.3
10	401594 441790	AW294909	Hs.132208	NM_024817:Homo saplens hypothe ESTs		10.3
10	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.3
	438185	Y19188	Hs.320461	ESTs	SS	10.2
	432031	AF039196	Hs.272367	hairtess protein (putative sin	jmjC	10.2
	410471	T88872		gb:yd31a12.s1 Soares fetal liv	0071171 0505	10.1 10.1
15	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	10.0
	417371	N74613 AA770021	Hs.269149 Hs.16332	ESTs .	SS.lg.fn3	10.0
	428167 419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis	COABINIO	10.0
	412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	10.0
20	425863	U43604	Hs.159901	Human unidentified mRNA, parti		9.9
	442739	NM_007274		cytosofic acyl coenzyma A thio	Acyl-CoA_hydro,SS,TM	9.9 9.9
	429469	M64590	Hs.27	glycine dehydrogenase (decarbo -	GDC-P,GDC-P aldo_ket_red,SS,TM,gla	9.8
	420029 445625	8E258876 8E246743	Hs.94446	polyamine-modulated factor 1 hypothetical protein FLJ22635	SS,TM .	9.8
25	435339	Al358300		ESTs -	SS,ras	9.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin muta	SS,TM,Ribosomal_S13,Galac	·9.8
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	9.8 9.7
	401349		11. 000040	Inositol polyphosphale-1-phosp		9.7
30	437915	A1637993	Hs.202312 Hs.193557	Homo sapiens clone N11 NTere2D ESTs, Moderately similar to AL		9.7
30	424511 423366	BE300512 Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.7
	405143	200010	1101141414	NM_013432*:Homo saplens nucles	ank,SS,TM,CPSF_A	9.6
	427497	AW139476	Hs.31240	ESTs		9.6
25	420423	AA827718	Hs.88218	ESTs	SS Handa Coolda	9.6 9.6
35	431512	BE270734	Hs.2795	lactate dehydrogenase A	kdh,kdh_C,SS,ldh zf-C3HC4,zf-B_box	9.5
	450052 412738	A1681298 N34731	Hs.236524 Hs.74562	ESTs slah binding protein 1; FBP in	homeobox	9.5
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	9.5
	451165	AI340575	Hs.286084	MRIP-1 protein		9.5
40	411450	H49619	Hs.127301	ESTs	\$S,pkinase pkinase,UM,PDZ	9.5 9.5
	405371	N49433	Hs.285737	NM_005569":Homo sapiens LIM do Homo sapiens cDNA: FLJ20895 fi	SS,G6PD,Glucosamine_iso,G	9.5
	435782 416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos, Metallophos	9.4
	405474	70 20,000		NM_001093°:Homo sapiens acetyl	CPSase_L_chain,blotin_lip	9.4
45	412837	AI922293	Hs.58389	hypothetical protein MGC4090		9.3 9.3
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.3 9.3
	431081	AA491594	Hs.75813 Hs.180015	polycystic kidney disease 1 (a D-dopachrome tautomerase	SS,TM MIF,late_protein_L2,SS,GS	9.2
	427640 427435	AF058293 AW938739		hypothetical protein FLJ13881	SS	9.2
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA		9.2
	407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.2
	400833			C11000890:gi[3746443[gb]AAC639	SS,TM,7tm_1	9.2 9.2
	422064	AW452589	Hs.335742 Hs.29549	ESTs C-type lectin-like receptor-1	TM lectin_c,SS,TM	9.2
55	452434 451752	D30934 AB032997	N3.23343	KIAA1171 protein	TBC,SS,TM,pkinase,taminin	9.2
33	432931	AF174487	Hs.293753	Bcl-2-related ovarian killer p		9.1
	407893	BE408359	Hs.43621	Homo saplens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.1
	427397	A1929685	Hs.177656		efhand,RmaAD,SS,efhand	9.1 9.1
60	405159	AW411307	Hs.114311	ENSP00000243337*:CDNA FLJ13984 CDC45 (cell division cycle 45,	CDC45	9.1
00	422283 407058	X94563	13.114311	gb:H.saplens dbl/acbp gene exo	SS	9.0
	448045	AJ297436	Hs.20166	prostate stem cell antigen	SS,TM,UPAR_LY6,toxin,SS,T	9.0
	400772			NM_003105":Homo sapiens sortil	ldi_recept_a,fn3,ldi_rece	9.0 9.0
65	427315	AA179949			spectrin,SH3,PH,CH	9.0
65	414391	BE409872 ·AI525268	Hs.164303	gb:601299655F1 NIH_MGC_21 Homo ESTs	TM	9.0
	447867 422639	AI929377	Hs.173724		ATP-gua_Ptrans,ATP-gua_Pt	9.0
	454319	AW247736			SS	8.9
=-	428781	AF164799			2071	8.9 8.9
70	408645	AW245738			SS,TM	8.9
	429527 406651	AA454184 Al559224	Hs.289014	gb:tq32c02.x1 NCI_CGAP_Ut1 Hom		8.9
	430893	BE502068	Hs.282067			8.8
	414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
75	413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	8.8 8.8
	432211	BE274530				. 8.8
	421694	BE387430 AL079854			SS	8.8
	453683 456741	W37608	Hs.18449		SS,pktnase	8.7
80	442995	AA532511		Homo saplens cONA: FLJ23270 fi		8.7
	415898	Z43379	Hs.17719	3 gb:HSC1AE111 normalized infant		8.7 8.7
	456977	AK000252			SS,TM,transmembrane4	8.7
	439632 431462	AW41071 AW58367			SS	8.7
	701702			•	220	

	400128			Eas Control	TM,E1-E2_ATPase,HMA,Hydro	8.7
	438582	AJ521310	Hs.283365	ESTs, Wealdy similar to ALU5_H	SS	8.7
	450958	AL137669	Hs.348012	Homo saplens mRNA; cDNA DXFZp4		8.7
5	410855 415126	X97795 D60945	Hs.66718	RAD54 (S.cerevisiae)-like gb:HUM141D04B Clontech human f	SNF2_N,helicase_C,SS SS,TM	8.7 8.7
,	418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.6
	431157	AIB23969	Hs.132678	ESTs	SS,MAPEG,SS,MAPEG	8.6
	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
10	419167 432343	AI589535 NM_002960	Hs.94875 Hs. 2961	ESTs, Weakly similar to A35363 S100 calcium-binding protein A	SS S_100,SS,efhand,S_100,efh	8.6 8.6
10	458440	A1095468	Hs.135254	Homo sapiens clone 1 thrombosp	0_100 00 01a.io_100 01.	8.6
	407065	Y10141		gb:H.saplens DAT1 gene, partia	SNF,SS,TM	8.6
	452851 422418	AW173191 AK001383	Hs.213117 Hs.116385	ESTs hypothetical protein FLJ10521	SS,Sema RhoGEF	8.6 8.6
15	420836	AW958453	Hs.204959	hypothetical protein FLJ14886	SS,ras	8.6
	455588	Al129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.5
	431974	AW972689	Hs.200934	ESTs	DCC C commo DCD CC DCC D	8.5 8.5
	410720 449751	AF035154 AW207115	Hs.65756 Hs.25555	regulator of G-protein signali ESTs	RGS,G-gamma,DEP,SS,RGS,DI	8.5
20	434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	8.5
	405557			Target Exon	Els,SAM_PNT	8.5
	443780	NM_012068		activating transcription facto	bZIP,NTP_transf_2,SS,TBC	8.5
	428860 421901	U38291 AB014554	Hs.194301 Hs.109299	microtubule-associated protein protein tyrosine phosphalase.	M SAM,SS,TM,rm,PDZ	8.5 8.4
25	401885	יינירוטמא	113.103233	Target Exon ->	kinesin,SS,TM	8.4
	449382	AI650407	Hs.197875	ESTs .	SS,rm,zf-RanBP	8.4
	432862	AW004958	Hs.236720	amnionless protein	SS,MATH,zf-TRAF,zf-C3HC4	8.4 8.4
	441363 407363	AW450211 AF035032	Hs.126825 Hs.181125	ESTs, Weakly similar to A46302 gb:Homo sapiens done MCA1L my	SS,TM,HSP20,7tm_1 SS,ig,SS,G_glu_transpept	8.4
30	425380	AA356389	Hs.32148	AD-015 protein	SS,TM,LRR,P,Peptidase_SB	8.4
•	424893	AW295112	Hs.153648	Homo saptens cDNA FLJ13303 fis	SS,SAM,SS,TM,7im_1	8.4
	424080	AW189983	Hs.139119	Homo sepiens cDNA FLJ10967 fis		8.3 8.3
	439772 431765	AL365406 AF124249	Hs.10268 Hs.268541	Homo saplens mRNA full length novel SH2-containing protein 1	SH2,SS,TM	8.3
35	404365	10 12-12-10	110.200011	Target Exon	SS	8.3
	424310	AA338648	Hs.50334	testes development-related NYD	SS,TM	8.3
	401935	A 4.0450.40		Target Exon	PH CC mate DNA binding mate DN	8.3 8.3
	434796 423098	AA812046 AA321980	Hs.204682	ESTs ESTs	SS,myb_DNA-binding,myb_DN	8.3
40	434552	AA639618	Hs.325116	Homo saplens, clone MGC:2962,	SS	8.2
	457082	AA470687	Hs.104772	ESTs	SS	8.2
	432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.2 8.2
	402445 422078	AW872378	Hs.120170	Target Exon hypothetical protein FLJ21415	fn3,SS,TM,BNR SS	8.2
45	418361	AW505368	Hs.12460	gb:UI-HF-BN0-alu-d-03-0-ULr1		8.2
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS,PWWP,PHD	8.2
	403885	446772200	LI- nemoca	Target Exon	TM, Sulfate_transp, STAS, HM	8.2 8.2
	450029 452512	AW073380 AW363486	Hs.267963 Hs.337635	hypothetical protein FLI 10535 ESTs	SS,Pyridox_oxidase,zf-C2H SS	8.2
50	420138	BE268854	Hs.177729	ESTs	ŞS	8.2
	439788	N71241	Hs.119275	ESTs	UQ_con	8.2
	423662	AK001035	Hs.130881	8-ceil CLL/lymphoma 11A (zinc ESTs	SS PIP5K	8.2 8.1
	449656 452295	AA002008 BE379936	Hs.188633 Hs.28866	programmed cell death 10	SS,serpin	8.1
55	448650	AW769385	Hs.204891	ESTs	SS,IL8	8.1
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine pro .	KH-domain	8.1
	444406	AI147237		immunoglobulin heavy constant Human clone 23564 mRNA sequenc	SS SS	8.1 8.1
	437215 408891	AL117488 NM 006577	Hs.284284	ESTs, Highly similar to beta-1	SS,TM,DIX,PDZ,DEP,Disheve	8.1
60	400409	AF153341	1100001001	Homo sapiens winged hellxfork	SS	8.0
	443801	AW206942	Hs.253594	Intron of: trichorhinophalang	GATA	8.0
	425281	AA444390	Hs.155482 Hs.104938	hydroxyacyl glutathlone hydrol hypothetical protein MGC15906	lactamase_B,SS	8.0 8.0
	458216 401507	ATTUZAZOZ	NS. 104330	C15000810*:gil 11131272[spiP793		8.0
65	401180			eukaryotic translation elongat	SS,TM,lon_trens,IQ	8.0
	454291	AW384847	Hs.213534	ESTs, Wealthy similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0 8.0
	444014 412128	AI095718 AW894709	Hs.135015	ESTs gb:CM1-NN0032-020500-212-d05 N	SCAN,zI-C2H2,KRAB	0.U 7.9
	408363	NM 003389	Hs.44396	coronin, actin-binding protein	WD40	7.9
70	425694	U51333	Hs.159237	hexoldnase 3 (white cell)	hexoldnase,hexoldnase2,he	7.9
	425263		Hs.155419	BCL2-interacting killer (apopt	SS,TM,TspO_MBR	7.9
	447045	AW392394 AA598869	He 173770	sorting nexin 17 ESTs	SS,IF-2B,PP2C	7.9 7.9
	457613 410338	W03445	Hs.173770 Hs.38205	gb:ze05g11.r1 Soares melanocyt	pkinasa	7.9
75	402545			Target Exon	•	7.9
	454246	AW245185	Hs.6996	ESTs	Ohan hand O	7.9
	410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8 SS	7.9 7.9
	443678 404676	AW009605	Hs.231923	ESTs Target Exon	w	7.9
80	406849	Al569392		gb:tn86a02.x1 NCI_CGAP_Ut2 Hom		7.9
-	420230	AL034344	Hs.284186	forkhead box C1	Fork_head,SS,Fork_head	7.9
	413534	BE146961	He 242	gb:QV4-HT0222-011199-019-b12 H glucose-6-phosphalase, catalyt	ss,TM Pap2,SS,TM	7.8 7.8
	444628 410839	U01120 NM 00684	Hs.242 9 Hs.66581	grucose-o-phosphatase, catalyt protein disulfide isomerase	thiored,Rho_GDi,gntR,SS,T	7.8
					221	

	444046	AI360834	Hs.135094	ESTs	SS,GTP_EFTU,EFG_C,GTP_EFT	7.8
	439501	AF086321	Hs.287452	Homo sapiens cDNA FLJ 11760 fis ESTs	ТМ	7.8 7.8
	415441 450461	R13977 BE408081	Hs.9634 Hs.46736	hypothetical protein FLJ23476	SS	7.8 7.8
5	448993	A1471630	1 10.10100	KIAA0144 gene product		7.8
	400923			Target Exon	SS,TM,DUF289	7.8
	440546	AJ491994	11- 02070	gb:tp07g09.x1 NCI_CGAP_Ui2 Hom	SS,HATPase_c	7.8 7.8
	419757 451721	AA773820 NM_006946	Hs.63970 Hs.26915	ESTs spectrin, beta, non-erythrocyt	SS,TM spectrin,PH,CH,SS,Peptida	7.8 7.8
10	458834	Al566883	Hs.196446	ESTs	operand internet operan	7.8
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	enolase, SS, TM, kinesin, FHA	7.7
	438452	Al220911	Hs.288959	hypothetical protein FLJ20920	SS SS THE STATE IN SALE	7.7
	421445 434743	AA913059 AI363410	Hs.104433	Homo sapiens, clone IMAGE:4054 ribosomal protein S18	esp,SS,TM,ion_trans,K_tet SS,TM	7.7 7.7
15	450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.7
	442394	R62926	Hs.285193	ESTs		7.7
	434333	AA186733	Hs.292154	stromal cell protein	\nn ~	7.7
	427221 429099	L15409 BE439952	Hs.174007 Hs.196177	von Hippel-Lindau syndrome phosphorylase kinase, gamma 2	VHL,TM pkinase,SS,SNF2_N,helicas	7.7 7.7
20	444670	H58373	Hs.332938	hypothetical prolein MGC5370	SS_zi-RanBP,MDM2	7.7
	449495	AI652833		gb:wb22c11.x1 NCI_CGAP_GC6 Hom	SS	7.7
	444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	. 7.7
	449125 447151	A1671439 A1022813	Hs.196029 Hs.92679	Homo sapiens mRNA for KIAA1557 Homo sapiens clone CDABP0014 m	TIMP SS,TM,LRR,aminotran_1_2	7.7 7.6
25	448626	W27670	Hs.55613	hypothetical protein FLJ22531	35,111,L14 (animod an_1_2	7.6
	430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
	401822			C17001422:gi 2695866 emb CAA75		7.6
	428909	Al190714	Hs.98945	ESTS	SS harmona ma of CA	7.6 7.6
30	414534 421620	BE257293 AA446183	Hs.76366 Hs.91885	BCL2-antagonist of cell death ESTs, Wealdy similar to 155214	SS,hormone_rec,zf-C4	7.6 7.6
50	441650	Al261960	Hs.132545	ESTs	SS,TM,KOW	7.6
	442232	AJ357813	Hs.337460	ESTs, Wealty similar to A47582	SS,TM,TGFb_propeptide,TGF	7.6
	439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
35	400286 452833	BE559681	Hs.30736	C16000922:gi[7499103[pir[[T209 KIAA0124 protetn	TM,ABC_tran,ABC_membrane WD40	7.5 7.5
55	417390	AA196552	Hs.85852	hypothetical protein MGC3169	115-10	7.5
	427721	AI582843	Hs.180455	RAD23 (S. cerevislae) homolog	ubiquitin,UBA,Integrin_B,	7.5
	450716	T57758	Hs.10255	ESTs		7.5
40	407435 413956	AF211976 AI821351	Hs.193133	gb:Homo sapiens LENG9 mRNA, pa ESTs, Weakly similar to ALU7_H		7.5 7.5
40	427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	7.5
	406495			Target Exon	SRCR,TM,Acetyltransf	7.5
	430387	AW372884	Hs.240770	nuclear cap binding protein su	mm,SS,TM,mm	7.5
45	408601	U47928	Hs.86122	protein A	SS,7tm_1,SS,ig,WD40,zf-UB	7.5 7.4
43	424364 409832	AW383226 AW963293	Hs.163834	ESTs, Wealdy similar to G01763 gb:EST375366 MAGE resequences,	SS,ras SS	7.4 7.4
	448043	A1458653	Hs.201881	ESTs	PHD	7.4
	421148	AF008936	Hs.102178	syntaxin 16	Syntaxin,SS,Peplidase_M17	7.4
50	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.4
50	419295 448330	BE397712 AL036449	Hs.144027	ESTs ESTs	myb_DNA-binding,myb_DNA-b	7.4 7.4
	419639	AK001502	Hs.91753	hypothetical protein		7.4
	431488	AB037785	Hs.257594	KIAA1364 protein	ss,ch,lim,ss	7.4
55	456487	AF064804 Al910868	U- 0100E7	suppressor of Ty (S.cerevisiae	SS	7.4 7.4
22	448615 427433	D82070	Hs.212957 Hs.177972	ESTs chromosome 4 open reading fram	SS,pkinase	7.4
	441076	N49809	Hs.11197	Homo saplens, clone IMAGE:3343		7.4
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	7.4
60	411448	AA178955	Hs.271439	ESTs, Weakly similar to 138022	rm,PDZ	7.4 7.4
00	442318 425055	Al792199 AW961959	Hs.96940	ESTs ESTs	SS,zf-C2H2	7.4
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	SS,TM,transmembrane4	7.4
	403748			Target Exon	TM	7.4
65	447282	Al989963	Hs.197505	ESTS	TM	7.3 7.3
05	422305 416472	A1928242 AA180756	Hs.293438 Hs.340316	ESTs, Highly similar to AF1984 ESTs, Moderately similar to AL	SS z1-C2H2	7.3 7.3
	427273	AW139032		hypothetical protein DKFZp434N	SS,SS,TM	7.3
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
70	447859	AK002194	Hs.19851	peroxisomal biogenesis factor	DLIDAG (01-11-00 TH DLIDAG	7.3
70	432747 406727	NM_014404 Al219282	Hs.278907 Hs.2186	calcium channel, voltage-depen eukaryotic translation elongat	PMP22_Claudin,SS,TM,PMP22 SS,G-gamma	7.3 7.3
	404199	71213202	110.2100	ENSP00000211797*:Helicase SKI2	SS,RasGAP,PH,SS,PHD	7.3
	445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	7.2
75	428550	AW297880		ESTs	SS,homeobox,homeobox	7.2
75	454718	AW815144		gb:QV4-ST0212-120100-075-d10 S	SS,ATP-synt_ab,ATP-synt_a SS,TM,ISK_Channel	7.2 7.2
	407686 418304	AW901268 AA215702	Hs.126043	chromosome 21 open reading fra ab:zr97g10.r1 NCL_CGAP_GC81 Ho	serpin	7.2
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,lg,lRK,SS,TM,fn3,ig,R	7.2
00	407581	R48402	Hs.173508	P3ECSL	SS,TM,7tm_1	7.2
80	430746	AW977370	Hs.222012		SS ion trace	7.2 7.2
	402651 407323	AA181183	Hs.143504	NM_000721°:Homo sapiens calciu gb:zp57c02.s1 Stratagene endot	ion_trans SS,Ribosomal_S4e,ubiquiti	7.2 7.2
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.2
	434035	A1762074	Hs.204769		SS,TM	7.2
					222	

	400419	AF084545		Target	EGF,ig,lectin_c,sushi,XII	7.2
	424241		Hs.182339	Homo saplens pyruvate dehydrog	SAM_PNT	7.2 7.2
	445837	AI261700	Un 100522	ESTS	pkinase	7.2 7.1
5	427725 421879	U66839 AW959607	Hs.180533	mitogen-activated protein kina gb:EST371677 MAGE resequences,	hunge	7.1
,	418285		Hs.293756	ESTs	SS,EMP24_GP25L	7.1
	442893	H78133		gb:vu86c11.s1 Soares fetal liv		7.1
	437829		Hs.103834	ESTS		7.1
10	450873		Hs.238956	ESTs	SS,zf-C2H2,mm	7.1
10	433396		Hs.133205	ESTs .	SS,TM	7.1
	415595		Hs.278707	chromosome 21 open reading fra	SS TM	7.1 7.1
	436629 414593	AA861011 BE386764	Hs.249795	ESTs gb:601273249F1 NIH_MGC_20 Homo	LM	7.1
	422765		Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	7.1
15	419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	7.1
10	405247			Target Exon	SS	7.1
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 B		. 7.1
	431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
20	435717	AF227905	Hs.105794	UDP-glucose:glycoprotein gluco	Glyco_transf_8	7.1
20	405113	T00040	11- 400043	Target Exon	SS Executio Executio M/D40	7.1 7.1
	428070	T63918	Hs.182313	retinol-binding protein 2, cel for muscle specific ring finge	lipocatin, lipocatin, WD40 SS	7.1
	429029 430354	AA443443 AA954810	Hs.85524 Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	7.0
	412970	AB026436	Hs.177534	dual specificity phosphalase 1	Rhodanese, DSPc, SS, DSPc	7.0
25	438701	AA937112	Hs.207788	ESTs	TM,sushi	7.0
	454756	AW819273		gb:CM2-ST0284-061299-046-a12 S		7.0
	401264			C18000090°:gi 6878656 ref NP_0	SS,laminin_Nterm,laminin_	7.0
	408080	AW149754	Hs.248652	ESTs, Weakly similar to T00273	SS	7.0
20	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	7.0
30	431402	AA743534	Hs.250861	ESTS	SS	7.0 7.0
	423790 450688	BE152393 AW272352	Hs.60450	gb:CM2-HT0323-171199-033-a08 H ESTs	TM	7.0
	405928	ATTECHE	115.00430	Target Exon	SS,cystatin,Coprogen_oxid	7.0
	454438	AA224053		cell division cycle 27	SS,TM,SPRY,7tm_3,ANF_rece	7.0
35	407281	AJ307226	Hs.164421	ESTs	SS	6.9
	423386	AW136098	Hs.314081	ESTs	SS,WD40,EPO_TPO	6.9
	459360	BE384526	Hs.25734	gb:601277913F1 NIH_MGC_20 Homo		6.9
	420187	AK001714	Hs.95744	hypothetical protein similar t	ank,TM	6.9
40	431549	AA507036	Hs.170673	ESTS		6.9 6.9
40	423384	AL133632	Hs.127808	Homo saplens mRNA; cDNA DKFZp4		6.9
	454577 438118	AW809272 AW753311		gb:MR4-ST0118-040100-034-c08_1 ESTs	SS,lipocalin	6.9
	416233	AA176633		gb:zp13g01.s1 Stratagene fetal	oc, i pocali i	6.9
	417012	N38970	Hs.194214	ESTs		6.9
45	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	6.9
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_lb,Lipase_GDSL,SS,	6.9
	418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	6.9
	404956			C1003210*:gi[6912582]ref[NP_03	PI3_PI4_kinase,PI3K_C2,PI	6.9
50	451606	AA018791	Hs.7945	AIE-75 binding protein protein	SS	6.9 6.9
50	438525	AW368528	Hs.100855	ESTS C18000224 will 12220028 cnlODPTW	SS	6.9
	400906 411411	AA345241	Hs.55950	C18000324:gi 12229928 sp Q9PTW ESTs, Weakly similar to KIAA13	SS	6.8
	406834	Al318680	113.33330	gb:ta49g09.x1 NCI_CGAP_Lu25 Ho	•••	6.8
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	SS,COesterase,SS,COestera	6.8
55	424198	AB029010	Hs.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Calx-beta,	6.8
	445873	AA250970	Hs.251948	poly(A)-binding protein, cytop	SS,PABP,rm,pkinase,14-3-	6.8
	439605	AF086431	Hs.22380	ESTs	SS,TM	6.8
	432284	AA532807	Hs.105822	ESTs	SS,TM,pkinase	6.8
60	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	5	6.8 6.8
60	443136	NM_001440		exostoses (multiple)-like 3 Gardner-Rasheed feline sarcoma	Exostosin,SS,TM SH2,SH3,pkinase	6.8
	421758	8E397336 NM_016578	Hs.1422	HBV pX associated protein-8	PHD, Virus_HS, SS, I Cin_chan	6.8
	448148 400205	MW_010310	113.20303	NM_006265*:Homo sapiens RAD21	SS	6.8
	434315	AW196608		ESTs	• • •	6.8
65	418184	AA367375		Homo sapiens cDNA FLJ14015 fis		6.8
	431898	AK000020	Hs.272018	hypothetical protein FLJ20013		6.7
	438627	AJ087335	Hs.123473	ESTs	TM,Reticulon	6.7
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	6.7
70	429712	AW245825		ENSP00000233627*:NADH-ubiquino	oxtdored_q6,SS,TM,rrm	6.7 6.7
70	456886	AW089093		ESTs, Weakly similar to 138022	SS,TM,ACAT,LRR	6.7
	427461	AA531527 BE002846	Hs.332040 Hs.112964	hypothetical protein MGC13010 ESTs	30, HANGKI, LAK	6.7
	434000 432530	AF131786	Hs.278303		SS_proteasome	6.7
	435141	AA970001	Hs.150319	Homo sapiens, clone IMAGE:3610	SS,TM	6.7
75	441794	AW197794		ESTs	•	6.7
. •	450287	AW291483		ESTs		6.7
	441523	AW514263		ESTs, Wealdy similar to ALUF_H	SS	6.7
	452798	AI918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
00	451937	AF119564	Hs.27299	transcriptional regulator prot	SS,integrin_B,fn3,Calx-be	6.7 6.7
80	421417	AA291004	Hs.326088			6.7 6.7
	440317	BE561888	ก มัก เกาะกา	gb:601346093F1 NIH_MGC_8 Homo	aminotran_1_2,SS,TM,LRR	6.7
	421321 444904	AW452054	9 Hs.103502 Hs.161139		ammont 1400, may	6.7
	449730	R72290	Hs.117557		RasGAP,thyroglobulin_1,Ri	6.7
	+10100					
					223	

	450000			FOT- In-bb. al-nest- mild II	CC Tid your	6.7
	450622 425424	AI660285 NM_004954	Hs.58210	ESTs, Highly similar to ITH4_H ELKL motif kinase	SS,TM,vwa pkinase,KA1,UBA,SS	6.7
	435864	AL036499	Hs.188491	ESTs	parastra to	. 6.7
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS.homeobox,UPF0160,DUF23	6.7
5	454262	AW612232	Hs.254835	ESTS	SS,TM,voltage_CLC,CBS	6.7
	453023	AW028733	Hs.31439	serine protease Inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	6.6
	419157	AA234540	Hs.23871	ESTs	pkinase	6.6
	412464	T78141	Hs.22826	ESTs. Weakly similar to 155214	SS,cadherin,crystali	6.6 6.6
10	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis	SS,adh_short,Transglutami	6.6
10	456643	AW751497	Hs.98370	cytochroma P450, subfamily IIS	SS	6.6
	411490 455885	R39474 BE153524		gb:yh95b09.r1 Soares placenta gb:PM0-HT0339-241199-002-C03 H	SS,pkinase	6.6
	4338657	Al627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.6
	420307	AW502869	Hs.66219	ESTs	SS.TM	6.6
15	453496	AA442103	Hs.33084	solute carrier family 2 (facil	sugar_tr,SS,TM	6.6
	419182	AA234822	Hs.66147	ESTs	SS,TM,ion_trans,ion_trans	6.6
	406301			Target Exon	TM	6.6
	433938	AF161538	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.6
	448980	AL137527	Hs.289038	hypothetical protein MGC4126		6.6
20	454095	AW178110	Hs.191705	gb:lL3-HT0061-010999-013-H04 H	SS,TM,homeobox,trypsin,PD	6.6 6.6
	459702	Al204995		gb:an03c03.x1 Stratagene schiz	7tm 4 CC TM	6.6
	422201	NM_001505		G protein-coupled receptor 30	7tm_1,SS,TM	6.6
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg C6002509*:gij5031885[ref]NP_00	SS,SS SS,TM,kringle	6.6
25	404149	AW968159	Hs.302740	Epithelial calcium channel 2,	SS,TM	6.6
23	418576 421363		Hs.103854	docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	6.6
	458919	Al681567	Hs.13349	KIAA0756 protein	TM	6.6
	427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	6.5
	412289	AW935967	Hs.170162	KIAA1357 protein	SS	6.5
30	447105	AW377610	Hs.11123	DKFZP564G092 protein	SS,TM	6.5
50	444672	Z95636	Hs.11669	laminin, alpha 5	taminin_EGF,taminin_G,EGF	6.5
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	6.5
	420003	AA256906	Hs.111364	ESTs, Weakly similar to ubiqui	SS,TM	6.5
	431849	Al670823	Hs.85573	hypothetical protein MGC10911	SS,TM	6.5
35	430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF,SS	6.5
	437662	AA765387		ESTs	WD40,RCC1,SPRY	6.5
	436543	NM_002212	Hs.5215	integrin beta 4 binding protei	elF6	6.5
	405375			CX000741*:gi[4885461]ref[NP_00	SS,TM	6.5
40	430116	AA465350	Hs.119400	ESTs	SS,TM,adh_short	6.5 6.5
40	406109			Target Exon		6.5
	414871 -	BE549179	Hs.29008	gb:601078714F1 NIH_MGC_12 Homo		6.5
	440656	AI979248	Hs.148221	ESTS	SS,oxidored_nitro,SS	6.5
	438951	U51336	Hs.6453	Inositol 1,3,4-triphosphale 5/	SS,TM	6.5
45	405376	NM 001106	U- 215680	Target Exon Homo sapiens cDNA: FLJ22373 fi	SS	6.5
45	426925 400500	NW_001190	Hs.315689	Target Exon	00	6.5
	408294	BE141732		gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	6.5
	447904	AW206303		ESTs		6.4
	439211	A1890347	Hs.271923	Homo saplens cDNA: FLJ22785 fi	SS	6.4
50	426828		Hs.172670	activin A receptor type II-lik	pkinase,Activin_recp,SS,T	6.4
50	446100	AW967109		hypothetical protein d.1462O23.	SS,TM	6.4
	442146	R52599		gb:yg81g01.r1 Soares infant br	TM .	6.4
	425041	Al377150	Hs.150914	ESTs	SS	6.4
	457584	AA147979	Hs.285005	mitochondrial Import receptor	Josephin	6.4
55	435449	AA682379	Hs.303460	EST		6.4 6.4
	406284			Homo sapiens mRNA full length		6.4
	425944	AK000664	Hs.164256	hypothetical protein FLJ20657	00.774	6.4
	453387	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM	6.4
60	419725	U66048	Hs.92683	Homo saplens clone 161455 brea suppression of tumorigenticity	SS	6.4
OU	412452	AA215731	11- 402100		Sm,SS,IRNA-synt_1,GST_C,G	6.4
	421273 432746	AJ245416 AA564512	Hs.103106 Hs.24301	UE snRNA-associated Sm-like pr polymerase (RNA) II (DNA direc	SS,TM,EF1BD	6.4
	429398	AA452239	N5.24001	KIAA0970 protein	00/11/421 120	6.4
	404430	MAJZZZJJ		C8000066*:gi[10432395]emb[CAC1	SS	6.4
65	427339	A1734109	Hs.97984	SRY (sex determining region Y)		6.4
03	436389	AI811706	10.01001	CHMP1.5 protein		6.4
	428890	AA525226	Hs.303293			6.4
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
	414756	AW451101			hexckinase2,hexokinase	6.4
70	423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4,SS,TM,h	6.4
	408493	BE206854		phosphoglycerate mutase 2 (mus	PGAM,BRCT,RNA_pol_L	6.4
	439569	AW602168			CUB,EGF,SS	6.4 6.4
	457274	AW674193			SS,TM,SS,TM,Clathrin_lg_c	6.4
75	444550	BE250716	Hs.87614	ESTs	SS ·	6.4
75	407198	H91679		gb:yv04a07.s1 Soares fetal liv	BIR CC TM cuchi	6.4
	423228	AL137491		Homo sapiens mRNA; cDNA DXFZp4	SS,TM,sushi	6.3
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	. 6.3
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	6.3
OΛ	400137	*******	N- 62200	Eos Control	SS	6.3
80	408784	AW971350		ESTs D ESTs		6.3
	435028	AW193035 AJ467908	5 Hs.18737(Hs.8882	ESTs	SS,TM,7tm_1	6.3
	438113 417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_desm	6.3
	436050	A1057205	Hs.14584	ESTs		6.3
				•		

				0.400.404.4	A.AII.a Tha	6.3
	403672 448269	BE622358		C4001244:gij539933[pirj]A61275 hypothetical protein FLJ13164	tubulin, TM	6.3
	430217	N47863		ribosomai protein S24	Ribosomal_S24e	6.3
_	426675	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.3 6.3
5	423510 428573	AB000824 AA430651		trehalase (brush-border membra ESTs	Trehalase	6.3
	457052	BE167242	Hs.47099	hypothetical protein FLJ21212	SS	6.3
	445099	BE163341		gb:QV3-HT0458-230200-099-b01 H	242260	6.3 6.3
10	450334	AF035959	Hs.24879	phosphatidic acid phosphatase ESTs, Wealdy similar to S65657	PAP2,SS SS,TM,sugar_tr	6.3
10	416000 427880	R82342 AA436011	Hs.79856 Hs.98187	ESTs '	201111100877	6.3
	426722	U53823	Hs.171952	occludin	Occludin, SS, TM, BIR	6.3
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,art,SS,PDEase SS	6.2 6.2
15	431161 413055	AA493591 AV655701	Hs.75183	gb:nh01a12s1 NCI_CGAP_Thy1 Ho cytochrome P450, subfamily IIE	p450	6,2
13	431250	BE264649	Hs.251377	taxol resistance associated ge		6.2
	406373			Target Exon	SS,TM,vwa,FG-GAP,integrin TM	6.2 6.2
	403003 437834	AA769294		NM_024944*:Homo saplens hypoth gb:nz36g03.s1 NCI_CGAP_GCB1 Ho	SS	6.2
20	406299	TVIIODEOT		Target Exon		6.2
	439327	AF086141	Hs.50760	ESTs, Highly similar to BimL (SS	6.2 6.2
	414246	BE391090 AA770424	Hs.280278 Hs.98162	ESTs	SS	6.2
	427812 420926	AA830402	Hs.221216	ESTs ·	UQ_con	6.2
25	443766	N91071	Hs.109650	ESTs		6.2 6.2
	431082	AA491600		gb:ne80a11.s1 NCI_CGAP_Ew1 Hom coagulation factor VIII-essoci		6.2
	420530 407360	AI218431 X13075		gb:Human 2a12 mRNA for kappa-i		6.2
	449008	AW578003	Hs.22826	tropomodulin 3 (ublquitous)		6.2
30	409948	AW162263	Hs.312468	ESTs, Wealdy similar to ALUC_H	Rasgap,C2,PH,BTK SS	6.2 6.2
	413272	AA127923 AW205483	Hs.147260	ESTs ESTs	SS,trypsin,kringle,fn2,EG	6.2
	445050 458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,erf	6.2
	449940	AW291126	Hs.187520	Homo sapiens, clone IMAGE:3834	SS,zf-C2H2	6.2 6.2
35	440390	AW207385	Hs.36475	KIAA0493 protein	•	6.2
	423106 402501	N52572	Hs.13702	ESTs, Moderately similar to AL sperm specific antigen 2	ig,MHC_I,SS	6.1
	431470	AA832417	Hs.139650	ESTs	SS,ig,pkinase,LRR,LRRCT	6.1
40	416597	H66891		gb:yr71c03.r1 Soares fetal IIv	SS,WD40	6.1 6.1
40	412122	AW852707 AB004662	Hs.77867	G-rich RNA sequence binding fa adenosine A1 receptor	55,₩D40 7tm_1,SS,TM	6.1
	415056 400358	AF181286	H3.77007	Homo saplens mutant dystrophin	raicile aloni	6.1
	405473			NM_001093*:Homo saplens acetyl	CPSase_L_chain,blotin_lip	6.1 6.1
A.E	422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin Gal-bind_lectin	6.1
45	422262 401121	AL022315	Hs.113987	lectin, galactoside-binding, s C12001638*:gij7291960 gb AAF47	Garono_com	6.1
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	TM	6.1
	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796	bzip_maf,ss,p5CR,EF1BD	6.1 6.1
50	456021	BE246628 AW406289	Hs.250726 Hs.96593	gb:TCBAP1D5030 Pediatric pre-8 hypothetical protein	SS,TM,SS ras,arf	6.1
50	420319 410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	SS,HECT,phoslip	6.1
	450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhombold,lactam	6.1 6.1
	437050	AA766420	Un 70272	ESTs ESTs	SS SS	6.1
55	458835 412777	A1868753 A1335773	Hs.76372	ESTs	55	6.1
33	454364	BE263928	Hs.323806	gb:601191272F1 NIH_MGC_7 Homo	SS,TM	6.1 6.1
	448877	A1583696	Hs.253313	ESTS	Metallophos, TPR	6.1
	413045 408054	X92121 AW816490	Hs.75180 Hs.8102	protein phosphatase 5, catalyt ESTs	matanoprios(1777	6.1
60	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.1
	410445	AA199830		gb:zq75h01.r1 Stratagene hNT n		6.1 6.1
	415870	H15578 M34429	Hs.21017	ESTs gb:Human PVT-IGLC fusion prote		6.1
	438723 441307	AW071696	Hs.209065		SS,TM	6.0
65	406575	***************************************		Target Exon	SS.pkinase_pkinase_C,RFX_	6.0 6.0
	401488		11- 00000	Target Exon	Glyco_hydro_1	6.0
	437650 439827	AA814338 AA846538			ckinase,DAG_PE-bind,PH	6.0
	456373	BE247706		membrane-spanning 4-domains, s	SS,TM	6.0
70	454513	BE159271	Hs.109731	gb:MR0-HT0407-180100-004-h05 H	SS,TM	6.0 6.0
•	414944	C15044 AK001123	Hs.26176	gb:C15044 Clontech human aorta hypothetical protein FLJ10261	TM,SS,TM,death,DED	6.0
	451277 421190	U95031	Hs.102482		Cys_knot,vwc	6.0
	401215	•		C12000457*:gi]7512178 pir [T30	trypsin,SS,TM	6.0
75	408117	AL138255		ESTs, Weakly similar to 138022	SS,zf-C3HC4,BIR	6.0 6.0
	426357	AW75375		gb:RC3-CT0283-271099-021-a08 C poly(A)-binding protein, cytop	SS_pkinase .	6.0
	418630 400389	AJ351311 AL135841		olfactory receptor, family 2,	7tm_1,SS,TM,CSD	6.0
	447128	Al271898		cyclin K		6.0
80	431297	AA65177		ESTS ADD showdimesferose (NAD: n	PARP,PARP_reg,SS,TM,Pepti	6.0 6.0
	431857 430023	W19144 AA15824	Hs.27174 3 Hs.22772		SS,FKBP,SS,PDGF,C2,PI-PLC	6.0
	450023	AW95277		FSTs	TM	6.0
	407383	AA53257		ESTs, Moderately similar to AL	SS,Patatin,ank	6.0
					225	

					00 00 THE	6.0
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	SS,SS,TM,ig EMP70	6.0
	459111 405770	AU077013	Hs.28757	transmembrane 9 superfamily me NM_002362-Homo saplans malanom	MAGE	6.0
	415811	T26376		gb:AB123C11R Infant brain, LLN	SS,TM,mm,sushi	6.0
5	453413	AJ003294		gb:AJ003294 Selected chromosom	SS,Folate_carrier	6.0
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase, SS, Atrophin-1, Atr	5.9 6.9
	426048	AI768853	Hs.134478	EST8	TM SS,TM	5.9
	435750 439469	AB029012 W69836	Hs.4990	kIAA1089 protein gb:zd48a02r1 Soares_fetal_hea	SS,pkinase,C2,pkinase_C,D	5.9
10	445664	AW968638	Hs.237691	ESTs, Weakly similar to KIAA06		5.9
10	418830	BE513731	Hs.88959	hypothetical protein MGC4816	TM,COP-OH_P_transf	5.9
	452113	A1859393		gb:wm11a02.x1 NCI_CGAP_Ut4 Hom	actin	5.9
	449101	AA205847	Hs.23016	G protein-coupled receptor	7tm_1,SS,TM	5.9 5.9
15	437640	AA764893	Hs.272155	ESTs, Wealdy similar to 138022	SS.Peptidase_M10,hemopexi	5.9
13	400748 442370	AI143593	Hs.129419	NM_022122:Homo saplens mairtx ESTs	oo, chooso_in opionspore	5,9
	442419	AI749893	Hs.270532	ESTs, Weakly similar to 138022	Adaptin_N,Alpha_adaptinC2	5.9
	439986	AW750272	Hs.128608	ESTs	SS,TM,ISK_Channel	5.9
	407553	Z11168		gb:H.saplens 5HT1A receptor re	SS,TM	5.9
20	431424	Al222969		ESTs	SS	5.9 5.9
	442297	NM_006202		phosphodiesterase 4A, cAMP-spe	PDEase SS,TM,WD40	5.9
	457845	H93040	Hs.297729 Hs.128521	ESTs, Moderately similar to AL	SS	5.9
	446912 451381	Al347650 BE241831	Hs.172330	hypothetical protein MGC2705	SS,Ribosomal_L28e	5.9
25	416024	AW886484	Hs.343522	ATPase, Ca transporting, plasm	E1-E2_ATPase,Hydrolase,Ca	5.9
	446329	NM_013272		solute carrier family 21 (orga	kaza!,OATP_N,OATP_C	5.9
	431321	AW136372	Hs.1852	acid phosphatase, prostate	SS,TM,ackl_phosphat	5.9
	420039	NM_004605		sulfotransferase family, cylos	Sulfotransfer, SS, DAGKc	5.9
20	428223	AA424313	Hs.98402	ESTs	HECT	5.9 5.9
30	433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina SS	5.9
	450251	BE080483	Un 27268	gb:QV1-BT0630-280200-086-a05 B ESTs	33	5.9
	408511 414348	AW206404 AF041430	Hs.27268 Hs.75922	brain protein 13	SS,SH3	5.9
	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
35	412173	T71071		gb:yc50b05.r1 Stratagene liver	CPSase_L_chain	5.8
	404001			Target Exon		5.8
	445263	H57646	Hs.42586	KIAA1560 protein	SS	5.8 5.8
	441583	AI791499	Hs.205742	ESTs, Weakly similar to ALUA_H	SS.TM.efhand,efhand	5.8
40	430168	AW968343		DKFZP43411735 protein gb:MR3-ST0220-151299-027-b10 S	filament	5.8
40	454682 453829	AW816029 AL138200		gb:DKFZp547N052_r1 547 (synony	SS,TM,ATP-synt_C,Galactos	5.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G	SS	5.8
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	5.8
	451045	AA215672		gb:zr96e09.s1 NCI_CGAP_GCB1 Ho	SS,Peptidase_C1,zf-C2H2	5.8
45	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis	SS,TM	5.8 5.8
	455679	BE066529		gb:RC3-BT0333-300300-017-a12 B	UBX	5.8 5.8
	457125	AW444451	Hs.134812	ESTs	SS ubiquitin,SS,TM,G-patch,a	5.8
	430600	AW950967		HLA-B associated transcript-3 lectomedin-2	Latrophilin, OLF, 7tm_2, Gal	5.8
50	421707 436127	NM_014921 W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	5.8
50	414347	BE275835	113.11000	gb:601121639F1 NIH_MGC_20 Homo	SS	5.8
	439910	H66765	Hs.339397	ESTs	SS	5.8
	410382	AW664971		ESTs	LIM	5.8 5.8
<i></i>	426391	AW161050		second mitochondria-derived ac	SS SS	5.8 5.8
55	423358	AI815474	Hs.343866	gb:au47f10.y1 Schneider fetal Homo sapiens cDNA: FLJ22930 fi	Pepiidase_M1	5.8
	440146 402189	AW014231	Hs.90790	ENSP00000247423*:D-siglec prec	, chagaso	5.8
	439949	AW979197	Hs.292073	ESTs, Weakly similar to ALU7_H		5.8
	457978	AA776638		gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	5.8
60	436685	W28661	Hs.5288	Homo sapiens mRNA; cONA DKFZp4	SS,TM,pkinase,Activin_rec	5.8
	411602	L01406	Hs.767	growth hormone releasing hormo	7tm_2,HRM	5.8 5.8
	433357	T05639		gb:EST03528 Fetal brain, Strat	SS TM	5.8
	404311	A140704.44		Target Exon ESTs	SS,TM	5.8
65	428092 452620	AW879141 AA436504			SS	5.8
OJ.	401938	74430304	113.113200	Target Exon	SS,PHD,proteasome	5.7
	407202	N58172	Hs.109370		SS,F5_F8_type_C,pkinase,E	5.7
	458882	R34993	Hs.226666		SS,CRAL_TRIO,PKI	5.7 5.7
20	452357	AI638176	Hs.283865		SS,TM,SS,TM	5.7
70	452625	AA724771		ESTs	mito_carr,SS,TM	5.7
	430281	AI878842	Hs.237924		TM	5.7
	430490 450122	AW902951 BE313765			SS,TM,Y_phosphalase,LON,A	5.7
	450801	AI739013	Hs.203348		SS,TM,Hint,HH_signal	5.7
75	413413	D82520	Hs.13239		SS,mm,DUF185	5.7
, •	445631	AK001822		Homo sapiens cDNA FLJ10980 fis		5.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	5.7 5.7
	423139	AW40272		hypothetical protein FLJ21106	DI2 DIA Monte CATO CC TIA	5.7 5.7
00	426221	AB007881		KIAAD421 protein	PI3_PI4_kinasa,FATC,SS,TM	5.7
80	443785	AW44995			WD40,SS,TM,fn3,EGF,fn3,ig	5.7
	417900 446596	BE250127 AW20451				5.7
	432353		58 Hs.27441		SCAN	5.7
	427625	AF008216				5.7
	-					

	421543	AK000519		hypothetical protein FLJ20512	ТМ	5.7 5.7
	418087	AA961613		ESTs Interleukin 17C	SS	5.7
	432751 433943	AF152099 AA992805		lymphoid enhancer-binding fact	•	5.7
5	414274	AW300961		Homo sapiens, clone IMAGE:4127	SS,Vps26,Acyl-CoA_dh	5.7
-	431328	AA502999	Hs.291591	ESTs		5.7 5.7
	451481	AA300228		hypothetical protein DKFZp434N	HLH	5.6
	430344 419516	AA476827 H82550	Hs.171012	hypothetical protein FLJ22349 ATP-binding cassette, sub-fami	SS,TM,ABC_tran,ABC_membra	5.6
10	413564	BE260120		gb:601146990F1 NIH_MGC_19 Homo		5.6
	415958	H10942		gb:ym06c11_r1 Soares infant br	SS,TM	5.6
	401402			Target Exon	OO DIV DOZ DED Dishamila	5.6 5.6
	456145	BE299427	Hs.21446	KIAA1716 protein	SS,DIX,POZ,DEP,Dishevelle TM,SAM_decarbox,SS,pkinas	5.6
15	431536	AL133066 L29073	Hs.341908 Hs.198726	ESTs cold shock domain protein A	CSD,homeobox,SS,TM,7tm_2,	5.6
13	456266 435800	AI248285	Hs.118348	ESTs	TM,ECH,chromo	5.6
	449285	AI912702	Hs.139135	ESTs		5.6
	418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.6 5.6
20	417442	AA199940	Hs.124039	ESTs		5.6
20	405931	DE444204		Terget Exon gb:MRO-HT0166-191199-004-c11 H	SS	5.6
	455286 446931	BE144384 Al348856	Hs.21627	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho	66	5.6
	446548	AI769392	Hs.200215	ESTs	SS,TM,Ribosomal_S25,sugar	5.6
	401984	,		C17000146*:gij2143629 pir jA57	pkinase,SS,TM,P2X_recepto	5.6
25	404066			Target Exon	SS,tRNA-synt_2b,HGTP_anti	5.6 5.6
	418363	AA218628	Hs.202977	ESTs .		5.6
	458198 432278	Al286100 AL137506	Hs.274256	hypothetical protein FLJ23563	SS,TM,GNS1_SUR4,SS,TM,Rho	5.6
	432328	AL1373739	Hs.195471	6-phosphofructo-2-kinase/fruct	PGAM,6PF2K	5.6
30	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Sterold_dh,SS	5.6
	415514	F11301 .	Hs.138329	ESTs	SS,TM	5.6 5.6
	426208	A1370379	Hs.132216	ESTs	SS,TM Sema,PSI,TIG,SS,TM,TIG,Se	5.6
	429367	AB007867	Hs.278311	plexin B1 Target Exon	38/18/13/13/33/18/13/33	5.6
35	405939 457331	AV647405	Hs.18443	aldehyde dehydrogenase 8 famil	GTP_EFTU	5.6
33	438705	AI049624	Hs.283390	ESTs, Wealty similar to 210926	SS,E2F_TDP,E2F_TDP	5.6
	428624	Al125222	Hs.98712	hypothetical protein DKFZp434H	SS,TM,ras,MSP_domain	5.6
	419389	A1074951	Hs.319095	ESTs	SS,DPPIV_N_term	5.6 5.6
40	447595	AW379130		phosphodiesterase 9A	PDEase	5.6
40	408015		-Hs.244349 Hs.61622	epidermal differentiation comp gb:MR0-BT0249-091299-201-c07 B	SS	5.5
	413041 452849	BE061580 AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	5.5
	434357	AW732284		mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.5
	455274	BE151622		gb:PMO-HT0302-271099-001-a08 H	SS,TM,RNA_pol_L	5.5 5.5
45	453904	AW003821		ESTs	Fork_head	5.5
	424624	AB032947	Hs.151301	Ca2+dependent activator proteingb:EST94853 Activated T-cells	walnlegdn_A,FG-GAP	5.5
	426576 440682	AA381720 AW362152	Hs.27181	nuclear receptor binding facto	And modified 4.	5.5
	419125	AA642452		B-cell CLL/lymphoma 11A (zinc	SS	5.5
50	450207	T87615	Hs.14716	ESTs		5.5 5.5
	405211			C7000900:gi 4508027 ref NP_003	SS	5.5 5.5
	413937	H65775	Hs.207915	ESTS	WD40, Clathrin, Clathrin_pr	5.5
	426793	X89887 R06185	Hs.172350	HIR (histone cell cycle regula gb:ye94d03.r1 Soares fetal liv	SS,TMIBRIBR	5.5
55	412091 446538	W74413	Hs.15251	hypothetical protein	SS	5.5
55	451117	AA015752		ESTS		5.5
	409547	AW409885		Homo saplens, clone MGC:4558,	TM	5.5 5.5
	412673	AL042957		ESTS	sugar_tr,SS,TM,sugar_tr	5.5
60	426440 449225	BE382756 R39108	Hs.169902 Hs.6777	solute carrier family 2 (facil ESTs	SS,TM,Na_sulph_symp	5.5
UU	403938	FW3100	ris.urr	Target Exon	Ephrin	5.5
	441197	BE244638	Hs.166	sterol regulatory element bind	HLH	5.5
	455604	BE011183	3	gb:PM3-BN0218-100500-003-d09 B		5.5 5.5
~	457468	AW97134			SS,zI-C2H2,SCAN,SCAN,zI-C	5.5
65	447677	Al419235			TM.ion_trans	5.5
	415473	R39986 AW97703	Hs.12778 Hs.143554	ESTs ESTs, Highly similar to 845036	1 (c)	5.5
	408422 442780	AI017521		ESTs	SS,TM,7tm_1	5.5
	451558		89 Hs.26630	ATP-binding cassette, sub-famil	ABC_tran,SRP54,SS,TM,ECH	5.5
70	439422	AW45279			SS,TM	5.5 5.5
	423479		26 Hs.129208		pkinase SS	5.5
	459558	AI539821 AW19523		ESTs, Wealdy similar to 210926 hypothetical protein FLJ22174	SS,TM,tubulin	5.5
	441187 420894	AA74459		ESTs	SS,ank	5.5
75	404710	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		C9001584:gi[7499208[plr][T2099		5.5
	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	5.5 5.5
	448387	AI874402				5.5 5.5
	419541	AW7496				5.5
80	449686 426315	AW07281 AA85421			SS,crystaff	5.5
60	426315 451312	Al769831		4 ESTs	SS	5.5
	432538	BE25833	12 Hs.27836	2 male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5 5.5
	446790	AW4521	05	ESTs	SS,zf-C2H2	5.5 5.5
	448682	T09471	Hs.25082	0 hypothetical protein FLJ14827		J.,

	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022	SS	5.5 5.5
	411219 439742	AW832917 AJ827721	Hs.284298	gb:QV2-TT0003-161199-013-h06 T Homo saplens mRNA full length	SS	5.5
	432004	BE018302	Hs.2894	placental growth factor, vascu	PDGF,SS	5.5
5	402916			ENSP00000202587*:Bicarbonate (HCO3_cotransp,SS	5.5 5.5
	405348 415976	R43144	Hs.21919	Rag C protein ESTs	RCC1 TM	5.4
	435064	170740	Hs.31433	ESTs	SS,MDM2	5.4
	440024	AA969333	Hs.160098	ESTs		5.4 5.4
10	431525	AA506656	Hs.6185	KIAA1557 protein		5.4 5.4
	458644 410895	AW270149 AW809679		ESTs, Moderately similar to GG gb:MR4-ST0124-261099-015-705 S		5.4
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2		5.4
1.5	413034	BE392896	Hs.129126	Homo saplens, clone MGC:10992,	SS DSDs Bhadasana SS TM	5.4 5.4
15	444664	N26362 NM_004729	Hs.11615 Hs.9933	map kinase phosphatase-like pr Ac-like transposable element	DSPc,Rhodanese,SS,TM zf-BED	5.4
	443887 445871	AI702901	Hs.145582	ESTs, Wealty similar to FOR4 M	SS,TM,efhand,efhand	5.4
	411992	AW816214	Hs.143055	ESTs	SS,TM	5.4
20.	458341	AW373583	Hs.221994	gb:QV4-BT0534-281299-053-e08 B		5.4 5.4
20	451677 432658	AA059222 NM_000246	Hs.33538	ESTs, Weakly similar to oxygen MHC class II transactivator	LRR	5.4
	417739	Z43995	112.0010	gb:HSC1QB121 normalized infant	SS,ArfGap,vwa,TSPN,fn3,Co	5.4
	424618	L29472	Hs.1802	major histocompatibility compl	TM,Ig,MHC_II_beta,SS,TM,A	5.4 5.4
25 ·	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fi ESTs	SS,TM,BNR,fn3,ldl_recept_	5.4
23	436094 433168	A1798701 A1085436		gb:ow84g06.s1 Soares_fetal_liv	SS,TM,PID	5.4
	417359	T99264	Hs.191117	ESTs		5.4
	436014	AF281134	Hs.283741	exosome component Rrp48	RNase_PH,RNase_PH_C,SS,TG	5.4 5.4
30	435154	AA668764 NM_002204	Hs.301637 Hs.265829	ESTs Integrin, alpha 3 (antigen CD4	SS,TM Integrin_A,FG-GAP,Rhabd_g	5.4
20	431630 444064	W85970	Hs.16292	ESTs	SS,TM,Dihydroorotase	5.4
	415970	H23333	Hs.29002	KIAA1706 protein		5.4
	445303	AW362198	Hs.12503	Interleukin 15 receptor, alpha	SS,sushi,SS SS,SS	5.4 5.4
35	421542 459704	AA411607 AA719572	Hs.118964 Hs.274441	ESTs, Weakly similar to KIAA11 Homo sapiens mRNA; cDNA DKFZp4	33,33	5.4
33	402285	A4115512	113.21441	sclerostin	SS,TM	5.4
	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.4 5.4
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4 ESTs	SS,TM,ras TM	5.4 5.4
40	417516 423233	AA203473 BE048021	Hs.81529 Hs.11067	ESTs, Highly similar to T46395	i mi	5.4
40	420733	AW291446	Hs.88651	ESTs	SS	5.4
	404807			Target Exon	UPF0027	5.4 5.4
	436483	AJ272063	Hs.283010	vanilloid receptor subtype 1 ESTs, Moderately similar to T1	SS,TM,ank,lon_trans,SS,TM SS,pkinase,ig	5.4
45	425316 425565	AA354977 AA359485	Hs.99010 Hs.173084	gb:EST68511 Fetal lung II Homo	o o i prancao, i g	5.4
-1.5	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967	_	5.4
	401203			Target Exon	filament .	5.4 5.4
	422452	AL110255	Hs.116808 Hs.289053	Homo saptens mRNA; cDNA DKFZp5 hypothetical protein FLJ14733	SS,asp,PGAM SS,TM	5.4
50	436718 428501	AW015227 AL041162	Hs.98587	ESTs	TM	5.4
	439695	W28548	Hs.285050	ESTs	TM,ion_trans,K_tetra,Kv2c	5.3
	417514	AA203445	Hs.325819	ESTs		5.3 5.3
	441358 401722	AW173212		ESTs Target Exon	TM.PLAT,SS	5.3
55	408905	AV655783	Hs.661	Target CAT		5.3
	454453	AW752781		hypothetical protein FLJ12614	Mary de	5.3 5.3
	410312	AW850953		gb:IL3-CT0220-150200-068-A11 C small GTP-binding protein	Vinculin SS,TM,TPR	5.3
	437926 458682	BE383605 AV659151	Hs.300816 Hs.282961	ESTs	00,111,111	5.3
60	411605	AW006831		ESTs	TM,synaptobrevin	5.3
	409164	AA706639		gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hint,HH_signal,tubu	5.3 5.3
	438868 439034	AW246243 AF075083		hypothetical protein FLJ20974 gb:Homo sapiens full length in	filament.filament	5.3
	411426	BE141714		gb:QV0-HT0101-061099-032-c04 H	SS	5.3
65	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A,	Gtyco_hydro_38,SS,TM,Pept	5.3 5.3
	438470	AW936329			SS,TM	5.3
	427789 430230	AA412428 BE257724		hypothetical protein FLJ23093 seb4D	rm,SS,2-Hacid_DH,WD40	5.3
	434314	BE392921		RAB26, member RAS oncogene fam	ras,arf,SS	5.3
70	428539	AW410063	3 Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.3 5.3
	414927	T83587	Hs.186476		SS,Sulfatese SS	5.3
	404596 454151	AA047169	Hs,154088	Target Exon hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.3
	431627	AW60972		HSPC042 protein		5.3
75	422379	AA932860	Hs.133864	ESTs	1444799	5.3 5.3
	426765	AA743603			MAM33 SS	5.3 5.3
	433325 403128	AW20698	6 Hs.143906	5 ESTs KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_t	5.3
	447730	AI421251	Hs.11408		SS,Transglutamin_C,Transg	5.3
80	405085			Target Exon	SS,SS,SNF2_N,helicase_C	5.3 5.3
	438080	AA777381			KH-domain	5.3 5.3
	439091 427326	AAB3014 AI287878		3 ESTs, Moderately similar to 13 gb:gv23f06.x1 NCI_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	5.3
	427859	AA41685			SS,TM,DUF60,trypsin,CUB,u	5.3
					228	

	421770	Alozoteo	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.3
	421779 408270	AW177805		gb:IL3-HT0059-180899-007-B06 H	John Commercial Commer	5.3 5.3
	418437 409879		Hs.348000 Hs.56851	ESTs, Moderately similar to AL hypothetical protein MGC2668	SS,TM	5.3
5	428304	AI743177	113.30031	ESTs	SS,TM	5.3
•	418678	NM_001327		cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.3 5.2
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM SS,TM	5.2
	437161 400171	AA054477	Hs.25391	ESTs ENSP00000211797:Helicase SKIZW	SS,proteasome	5.2
10	431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.2
	402197			Target Exon	SS,TM,ATP1G1_PLM_MAT8,lg,	5.2 5.2
	449514	AW970440	Hs.23642	protein predicted by clone 236	SS,PX,arf,lipocalin,PHD,z SS,TM,lnos-1-P_synth,Occl	5.2
	442472 409679	AW806859 BE250521		gb:MR0-ST0020-081199-004-c03 S ras homolog gene family, membe	SS,homeobox,CUT	5.2
15	439150	AF086006		gb:Homo sapiens full length in	SS	5.2
	412934	BE011437		gb:CM4-BN0220-080500-170-f03 B	00	5.2 5.2
	435186	AL1 19470		ESTs	SS CARD,ICE_p20,SS,ICE_p20,I	5.2
	400668 409125	R17268	Hs.343567	Target Exon exonal transport of synaptic v	SS.kinesin,PH,FHA,kinesin	5.2
20	445904	AW449920	Hs.248855	ESTs	SS,homeobox	5.2
	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	SS,TM,ank,Adap_comp_sub	5.2 5.2
	414551	AI815639	Hs.76394	encyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM DUF25,SS,Ribosomal_L3,PDZ	5.2 5.2
	432872 419492	A1908984 AA243547	Hs.279623 Hs.19447	selenoprotein X, 1 PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	5.2
25	407478	L77559	163.15777	gb:Homo sapiens DGS-B partial		5.2
	457892	AA744389		gb:ny51e10.s1 NCL_CGAP_Pr18 Ho	CDCTV DCAM	5.2 5.2
	457228	U15177	Hs.206984	Human cosmid CRI-JC2015 at D10	6PF2K,PGAM SS,TM,Na_Ca_Ex	5.2
	437536 420285	X91221 AA258124	Hs.144465 Hs.293878	ESTs . ESTs, Moderately similar to ZN	00,1111102002=x	5.2
30	431275	T56571	Hs.10041	ESTs	SS,HLH	5.2
-	428021	A1022287	Hs.111991	ESTs, Wealty similar to T33900	SS	5.2 5.2
	422400	AA974434	Hs.128353	ESTs		5.2
	446442 415585	BE221533 R59946	Hs.257858 Hs.184852	ESTs KIAA1553 protein	SS	5.2
35	438429	D16918	Hs.12547	Homo saptens cDNA: FLJ23388 fi	TM	5.2
55	401677	510015		BAI1-associated protein 3	SS,TM,zf-C2H2,kinesin,Vau	5.2
	405637			Target Exon	ce	5.2 5.2
	450437	X13956	Hs.24998	hypothetical protein MGC10471 syntaxin 10	SS SS,SS,TM,HLH,TRM,zf-CCCH	5.2
40	408215 452666	BE614290 AW194601	Hs.13219	ESTs	PI-PLC-X,PI-PLC-Y,C2,PH	5.2
10	401553	,		Target Exon		5.2 5.2
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	zf-CCHC	5.2 5.2
	453434 450351	AJ271378 BE547267	Hs.333243 Hs.59791	ESTs hypothetical protein MGC13183	SS,TM	5.2
45	411456	AW847588	113.33131	gb:IL3-CT0213-161299-038-G09 C	SS,TM	5.2
	445634	AI624849	Hs.344612	ESTs, Weakly similar to NEL1_H	bwv	5.2 5.2
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC	SS,TM,EPH_lbd,pkinase,fn3	5.1
	426318 416470	AA375125 N90464	Hs.147112 Hs.303023	Homo saptens cDNA: FLJ22322 fi beta tubulin 1, class VI	SS,tubulin,SS	5.1
50	432022	AL162042	Hs.272348	Homo saptens mRNA; cDNA DKFZp7		5.1
•	457579	AB030816	Hs.36761	HRAS-like suppressor	TM	5.1 5.1
	438484	AW021671	Hs.293330	ESTs, Weakly similar to p40 [H	DUF158,ank	5.1
	422802 401724	NM_00427	Hs.27008	phosphatidylinositol glycan, c C16001374:gij6755086 refjNP_03	TM,PLAT,SS	5.1
55	438670	A1275803	Hs.123428			5.1
-	414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.1 5.1
	425098	AW295349		ESTs ESTs	SS,TM SS	5.1
	431896 416732	AW297844 H81066	Hs.101428 Hs.285017		SS	5.1
60	404571	710 1000	110.200011	NM_015902*:Homo saplens proges	HECT,zf-UBR1,PABP	5.1
	433675	AW977653	Hs.75319	ribonucleolide reductase M2 po	SS	5.1 5.1
	426358	AA376438	Hs.129064	gb:EST88856 HSC172 cells II Ho Homo saptens chromosome 19, co	TM SS,TM,trypsin,kringle,UPA	5.1
	456767 412915	AJ086412 AW087727		NM_004541:Homo saplens NADH de		5.1
65	443553	AL040535		ATP-binding cassette, sub-fami	ABC_tran,SS	5.1 5.1
	415886	Z42737		gb:HSC0SE081 normalized Infant	SS FAD-oxidase_C,FAD_binding	5.1
	401674	A A 227040	U= 14015	C16001417*:gi[7500345]pirl[T21 2 ESTs, Weakly similar to RHOP M	LWD-ovingso_oft vp_origing	5.1
	424266 455035	AA337810 AW851734		gb:MR2-CT0222-011199-007-e10 C		5.1
70	408567	S72921	•	ciliary neurotrophic factor	CNTF	5.1
	436616	AW799109			14-3-3	5.1 5.1
	409078	AW32751		ESTs 1 ESTs, Highly similar to CR2_HU		5.1
	447976 457720	AW97265 AA992835				5.1
75	400528	. 1 100000		NM_020975*:Homo saplens ret pr	cadherin,pkinase,SS	5.1 5.1
	407757	BE048414			SS,EF1G_domain,GST_C,GST_	5.1 5.1
	452446	AA086123		6 EST8 gb:w117b08.x1 NCI_CGAP_Co16 Ho	mm,NTF2	5.1
	450807 432540	AI739262 AI821517			SS,TM	5.1
80	449324	A1638706		ESTs, Weatily similar to A47582		5.1 5.1
	426434	M17755	Hs.2041	thyroid peroxidase	EGF,sushi,An_peroxidase,p	5.1 5.1
	407652	W27953	. Hs.29291	1 ESTs, Highly similar to \$60712 ESTs	Troponin SS.pidnase	5.1
	443952 448869	AI149108 AI792798			SS,TM	5.1
	71,0003	. 3. 02. 00			229	
					447	

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					T- 400 THT- 1	5.1
	422837	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	51
	407143	C14076	Hs.332329	EST	SS,TM SS,TM,Glyco_hydro_56,Glyc	5.1
	442295	NM_007275		tung cancer candidate pyridoxal (pyridoxine, vitamin	ptk8,SS	5.1
5	407722	BE252241	Hs.38041	TNF receptor-associated factor	MATH SS. MATH A2M_N,A2M,NT	5.1
)	427336	NM_005658	Hs.26412	ring finger protein 26	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.1
	447960 400863	AW954377	N3.20412	C11002296:gi]11692557[gb]AAG39	SS.TM	5.1
	409034	Al684149	Hs.172035	hypothetical protein similar t	SS	5.1
	421696	AF035306	Hs.106890	Homo saplens clone 23771 mRNA		5.1
10	427587	BE348244	Hs.284239	ESTs, Weakly similar to 178885	SS,UDPGT	5.1
10	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	5.1
	454219	X75042	Hs.44313	v-rel avian reticuloendothelio	RHD,TIG	5.1
	434213	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	5.1
	435902	AA701867	Hs.297726	ESTs	•	5.1
15	442743	AI801351	Hs.302110	ESTs, Wealthy similar to MUC2_H	SS,fibrinogen_C,Rhodanese	5.1
13	454923	AW897236	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:CM0-NN0057-150400-335-c06 N	SS,Caldesmon	5.1
	440518	AAB88046	Hs.233235	ESTs	SS,TM	5.1
	448237	AI471790	Hs.309386	ESTs	TM_Ribosomal_S7	5.1
	428924	AI016405	Hs.98959	ESTs, Wealthy similar to JC5314	SS,TM,lectin_c	5.1
20	412081	Z24895	Hs.293818	gb:HSB67F122 STRATAGENE Human	SS,TM,SQS_PSY,GATA	5.1
20	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.1
	421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	5.1
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	SS,TM,GDPD,SS,TM,SH3,PDZ,	5.0
	417151	AA194055	Hs.293858	ESTs	PH	5.0
25	408307	AI761786	Hs.204874	ESTs	Armadillo_seg	5.0
20	404752	,		NM_024778:Homo saplens hypothe		5.0
	453126	AA032155	Hs.61622	ESTs		5.0
	413983	BE348384	Hs.279194	ESTs		5.0
	405366	000.000.	(10.0)	NM_003371*:Homo saplens vav 2	SS	5.0
30	412425	AW949156		gb:QV4-FT0005-110500-205-b06 F		5.0
50	437036	AI571514	Hs.133022	ESTs	SS,TM,Glycos_transf_2	5.0
	448455	AI252625	Hs.269860	ESTs, Moderately similar to S6	SS,TM	5.0
	411413	BE379438	Hs.211573	heparan sulfate proteoglycan 2	ig,laminin_B,laminin_EGF,	5.0
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD, SS, HSF_DNA-bind, E2F_	5.0
35	424874	AA347951	•	Homo saplens cDNA FLJ20812 fis	\$S .	5.0
55	408023	BE018269	Hs.279688	ESTs		5.0
	411758	AW860667	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:QV0-CT0383-210400-204-d03 C	homeobox,homeobox	5.0
	410660	AI061118	Hs.65328	Fanconi anemia, complementatio		5.0
	427411	AA402242		ESTs	•	5.0
40	437018	AA889078		ESTs	SS,TM,ERG4_ERG24	5.0
-10	427029	AA397596		ESTs	SS,ras	5.0
	452047	N35953	Hs.43510	ESTs, Wealty similar to BOX B	SS	5.0
	432093	H28383	,	gb:yl52c03.r1 Soares breast 3N	Band_41,ERM	5.0
	453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	5.0
45	441456	AI458911	Hs.127765	ESTs		5.0
73	414356	AW505085		gb:UI-HF-BN0-als-a-10-0-Ul.r1	SS,TM	5.0
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 ffs		5.0
	436393	AW022213		ESTs	Galactosyl_T_2	5.0
	409227	AA806165		Homo sapiens, clone IMAGE:3960	•	5.0
50	448680	AW245890		JM5 protein	WD40,SS,TM,KOW,HLH	5.0
50	439343	AF086161	Hs.114611	hypothetical protein FLJ11808		5.0
	428079	AA421020		ESTs	SS,TM,trypsin	5.0
	421951	BE327432		H1 histone family, member X		5.0
	427204	AA405404		ESTs	SS,SS	5.0
55	409690	W45393	Hs.55888	activating transcription facto		5.0
55	436574	AW293527				5.0
	457761	AW401809		KIAA1150 protein	ss,lim,ss	5.0
	435294	T84084	Hs.196008		HMG_box	5.0
	445372	N36417	Hs.144928		SS,PID,PDZ	5.0
60	440511	AF132959		eNOS Interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.0
00	424437	BE244700			CUT,homeobox,beta-lactama	5.0
	401539	DC211100		NM_002675:Homo sapiens promyel	zf-B_box,zf-C3HC4,SS	5.0
	417903	NM 00234	42 Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.0
	442451	A1498080			SS	5.0
65	450536	Al699529		gb:tt17e02.x1 NCL_CGAP_GC6 Hom	SS,G-alpha,arf	5.0
05	425169	AW29250	0 Hs.128514		SS	5.0
	435262	AA677088		ESTs		5.0
	444855	BE409261		Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.0
	433507	Al817336			pkinase	5.0
70	432396	AW29595		hypothetical protein FLJ14972	SS	5.0
, 0	438395	AA017514		methyl-CpG binding domain prot	MBD,zf-CXXC,SS,zf-CXXC	5.0
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	400762	1110110		Target Exon	- -	5.0
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75	445903	AI347487			SS,TM,EF1BD	5.0
, ,	412940	BE29570		homeo box B7	homeobox,SS,homeobox,home	5.0
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80

TABLE 208: Picey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

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70	454453	1205627_1	AMBROOTTO AMBROOTEG AMBROOTTO AMBROOTTO AMBROOTTO AMBROOTTO AWBROOTTO AMBROOTTO AMBROOTTO AMBROOTTO AMBROOTTO
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Prey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled The DNA sequence of
10
                  human chromosoma 22° Dunham, et al. (1999) Nature 402:489-495
           Strand: Indicates DNA strand from which exons were predicted
           Nt_position: Indicates nucleotide positions of predicted exons
15
                                                       Nt_position
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                                        Plus
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	405637	6289229	Plus	189852-189978
	405770	2735037	Plus	61057-62075
	405928	7717155	Minus	2923-3209
15	405931	6758795	Minus	148233-148705
	405939	6758795	Plus	170500-170654
	406109	9127147	Minus	58328-58485
	406230	4760409	Plus	71716-72515
	406284	7549620	Plus	74002-74199
20	406299	5686278	Minus	35655-36119
	406301	8575868	Plus	57291-57494
	406373	9256130	Plus	188922-189152
	406495	7711328	Minus	174661-17497B
	406575	7711679	Plus	142034-142473
25				

Table 21A lists about 933 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "everage" ovarian cancer to "everage" normal adult tissues was greater than or equal to 3.0, the "everage" ovarian cancer level was set to the 95th percentile value amongst various ovarian cancer specimens, the "everage" normal adult tissue level was set to the 75th percentile value amongst variou non-malignant tissues, the "everage" ovarian cancer value was greater than or equal to 400 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., ig, fn3, efg, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted. 30

TABLE 21A: 35 Pkey: Unique Eos probeset identifier number ExAcon: Exemplar Accession number, Genbank accession number UG ID: Unigene number
Title: UniGene gene title
Pred. Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal body tissue

	Pkey	ExAcon	UGID	Title	Pred. Protein Dom.	R1
	407223	H96850		gb:yw03b12.s1 Soares melanocyt	SS,TM,SS,TM,DDOST_48kD	58.9
	421296	NM_002666	Hs.103253	perilipin	perilipin,SS	47.6
45	430281	A1878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	46.7
	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,kdl_recept_a,trypsi	41.0
	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	37.1
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	35.6
	438424	A)912498	Hs.25895	hypothetical protein FLJ14996	SS.TM	35.3
50	450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS	34.4
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	33.9
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	32.5
	422310	AA316622	Hs.98370	cytochreme P450, subfamily IIS	SS,TM,pkinase,fn3,ig	30.5
	452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	29.6
55	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	28.2
	416819	U77735	Hs.80205	pim-2 oncogene	pkinase,SS,TM,OTU,K_tetra	27.9
	430397	Al924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	27.7
	427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	27.5
	454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	27.2
60	445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	26.8
•	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	26.5
	419451	Al907117	Hs.90535	syntaxin binding protein 2	Sec1,SS,TM	25.1
	424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	25.1
	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	25.0
65	412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand, SS, CAP_GLY	24.4
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS.FKBP.SS.PDGF,C2.PI-PLC	24.3
	444672	Z95636	Hs.11669	taminin, alpha 5	laminin_EGF.laminin_G.EGF	24.0
	413726	AJ278465	Hs.75510	annexin A11	annexin, SS, annexin	23.1
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	23.0
70	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	23.0
	422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase, SS, Ets	22.4
	427899	AA829286	Hs.332053	serum armyloid A1	SS,SAA_proteins,SS,SAA_pr	22.2
	407117	AA146625	110.002000	gb:zo71c07.s1 Stratagene panor	SS	21.3
	402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp,SS	20.8
75	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase,SS,TM	20.7
, 5	422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.6
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	20.1
	453157	AF077036	Hs.31989	DKFZP586G1722 protein	SS,Tropomyosin	20.0
	422179	AF091619	Hs.112667	dynein, exonemal, intermediate	WD40,SS	20.0
80	419444	NM_002496	Hs.90443	Target CAT	fer4,SS,TM,V_ATPase_sub_a	19.5
OU	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	19.2
	434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS SS	19.1
	411813	NM_014931	Hs.72172	KIAA1115 protein	SS,TM,Y_phosphatase	18.9
	422305	A1928242	Hs.293438	ESTs, Highly similar to AF1984	SS SS	18.8
	422300	M360646	uarasino	CO 191 LIMITA PITTING ID ML 1204	00	10.0

	440467	AIFROFAF	11-0/075	FOT- 14114 -1 1 1 4 25252	00	18.6
	419167 406663	AI589535 U24683	Hs.94875	ESTs, Weakly similar to A35383 immunoglobulin heavy constant	SS SS	18.5
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxddored_q6,SS,TM,rrm	18.5 -
_	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	GST_C,GST_N,Tropomyosin,S	18.4
5	447151	AJ022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	18.4
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	18.2
	450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	17.7
	427721 443780	AI582843 NM_012068	Hs.180455 Hs.9754	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B, bZiP,NTP_transf_2,SS,TBC	17.6 17.2
10	421612	AF161254	Hs.106196	activating transcription facto 8D6 antigen	kd_recept_a,SS,TM	17.1
~ ~	444507	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C	16.7
	406621	X57809	Hs.181125	Immunoglobulin (ambda locus	SS	16.6
	443496	AJ006973	Hs.9482	target of myb1 (chicken) homol	VHS,GAT,TM,Heme_oxygenase	16.6
1.5	440104	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	16.3
15	427640	AF058293	Hs.180015	D-dopacturome tautomerase	MIF, late_protein_L2, SS, GS	16.2
	445625 427461	BE246743 AA531527	Hs.332040	hypothelical protein FLJ22635 hypothelical protein MGC13010	SS,TM SS,TM,ACAT,LRR	16.1 15.9
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
	409017	T86957	Hs.272299	hypothetical protein RP4-622L5	SS,TM	15.6
20	428167	AA770021	Hs.16332	ESTs	SS,lg,fn3	15.5
	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	15.5
	400460			C11002253*:gij129091 spjP23267	SS,TM,SCAN,zf-C2H2,KRAB	15.4
	407787	W15398	Hs.38628	hypothetical protein	SS,zi-CCCH	15.4
25	406918	M88357	11- 00000	gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	15.4
25	435158 407619	AW663317 AL050341	Hs.65588 Hs.37165	DAZ associated protein 1 collagen, type IX, alpha 2	rm,SS,mm SS,Collagen,SS,Collagen	15.3 15.3
	421273	AJ245416	Hs.103106	U6 snRNA-essociated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	15.1
	402365	70210110	113.100100	Target Exon	SS,SS,TM,ig	14.9
	450503	R35917	Hs.301338	hypothetical protein FLJ 12587	SS	14.8
30	427502	AI811865	Hs.7133	Homo saplens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	14.6
	432872	A1908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	14.5
	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Suffale_trans	14.5
	416897	M78146	Hs.324700	hypothetical protein MGC2663	SS SS Bootidoon C3	14.3
35	447304 431543	Z98883 AW969619	Hs.18079 Hs.259768	phosphatidylinositol glycan, c adenylata cyclase 1 (brain)	SS,Peptidase_C2 TM	14.2 14.0
55	447544	AA401573	Hs.288284	hypothelical protein FLJ22378	SS,TM	14.0
	417595	AA424317	Hs.6259	KIAA 1698 protein	SS,TM,Glyco_hydro_31,Glyc	13.8
	436127	W94824	Hs.11565	RIKEN cDNA 2010100O12 gene	Corona_7,SS,TM	13.8
40	412623	R28898	Hs.74170	metallothionein 1E (functional	SS,TM,metalthio,DEAD,meta	13.7
40	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec.SS	13.5
	453367	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM . SS	13.5
	431462 408724	AW583672 A1685842	Hs.256311 Hs.294143	granin-like neuroendocrine pep ESTs, Weakly similar to T22914	SS,pkinase,tubulin	13.2 13.2
	423464	NM_016240	Hs.128856	CSR1 protein	Collagen,SS	13.1
45	428539	AW410083	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	13.0
	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	12.9
	438857	AI627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	12.8
	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	12.8
50	427527	AI809057	Hs.153261	immunoglobulin heavy constant	SS,TM,lg	12.6
30	430168	AW968343	Da 7447	DKFZP434I1735 protein	SS,TM,efhand,efhand	12.5 12.4
	437543 413711	H16443 AW291765	Hs.7117 Hs.75486	glutamate receptor, ionotropic heat shock transcription facto	SS,TM,lig_chan,ANF_recept NA,SS,E2F_TDP	12.3
	422625	AW504698	Hs.155976	culin 48	SS,SS,Cutlin,Cullin	12.2
	443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosin, SS, TM	12.1
55	407143	C14076	Hs.332329	EST	SS,TM	12.1
	424707	BE061914	Hs.10844	Homo saplens cDNA FLJ14476 fis	SS,SS,TM,Sema	12.1
	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
	427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	12.0 12.0
60	421572 447946	· AA531607 Al566164	Hs.165827	hypothetical protein FLJ22678 ESTs	SS,TM,TGF-beta,ASC SS,PTN_MK,7tm_1,DAGKc,DAG	11.9
UU	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	11.7
	427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	11.7
	427397	AJ929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD,SS,efhand	11.7
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase, SS, Alrophin-1, Atr	11.7
65	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	11.6
	447451	Al379925	Hs.207525	ESTS	SS,pkinase,PH,pkinase_C	11.5
	410397 430354	AF217517	Hs.63042 Hs.239784	DKFZp564J157 protein human homolog of Drosophila Sc	SS,homeobox,UPF0160,DUF23 SS,TM,lg	11.4 11.3
	419390	AA954810 AI701162	Hs.90207	hypothetical protein MGC11138	SS.TM.PMP22_Claudin.PMP22	11.3
70	422682	W05238	Hs.94316	ESTs, Weakly stmilar to T31613	SS,TM,DEAD,helicase_C,Lam	11.3
	422178	AL122083	Hs.112645	Homo septens mRNA; cDNA DKFZp4	SS,TM	11.2
	450122	BE313765	Hs.343443	ESTs, Wealdy similar to I38022	SS,TM,Y_phosphatase,LON,A	11.1
	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	11.1
75	444744	BE394732	Hs.147562	ESTs	SS	10.9
75	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	10.9 10.9
	417116	Z43916	Hs.7634 Hs.279574	hypothetical protein FLJ12287 CGI-39 protein; cell death-reg	SS,TM,filament,IF_tall SS,SS	10.8
	406779 450593	AA412048 AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	10.7
	406837	R70292	Hs.156110	immunoglobulin kappa constant	SS	10.7
80	452434	D30934	Hs.29549	C-type lectin-like receptor-1	tectin_c,SS,TM	10.7
	440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	10.6
	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	10.6
	414313	NM_004371	Hs.75887	coatomer protein complex, subu	WD40,SS,WD40,Ribosomal_S2	10.6 10.6
	420307	AW502869	Hs.66219	ESTs	SS,TM	10.0

			•			
	414918	AJ219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	10.6
	446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	10.5
	419846	NM_015977	Hs.285681	Williams-Beuren syndrome chrom	SS,HLH,SS,TM,WD40	10.4 ·
_	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	10.4
5	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	10.3
_	431275	T56571	Hs.10041	ESTs	SS.HLH	10.3
	407241	M34516		gb:Human omega light chain pro	SS,ig,PH,ig,PH	10.3
	441238	Al372555	Hs.322456	hypothetical protein DKFZp761D	homeobox, SS, TM, Rho_GDI, th	10.3
	436325	AL390088	Hs.7393	hypothetical protein from EURO	SS, Synapsin_C, SS	10.3
10	435605	AF151815	Hs.4973		SS,TM,SS,TM,ABC_tran,ABC_	10.3
10				hypothetical protein		
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	10.3
	425597	U28694	Hs.158324	chemotine (C-C motif) receptor	7tm_1	10.3
	415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicese_C,bromodo	10.2
1.5	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	Nol1_Nop2_Sun,SS,SNF2_N,h	10.2
15	414874	D26351	Hs.77515	inositol 1,4,5-triphosphate re	TM,RYDR_ITPR,ion_trans,MI	10.2
	423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thaumat	10.2
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	10.2
	406836	AW514501	Hs.156110	Immunoglobulin kappa constant	SS	10.1
	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	10.1
20	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	10.1
	427672	AA356615	Hs.336916	death-associated protein 6	SS,BTB,abhydrolase_2,RasG	10.0
	423218	NM_015896	Hs.167380	BLu protein	zf-MYND,SS,TM,Glyco_hydro	10.0
	403028	MM_012020	15.107500		SS,trefoil	10.0
		404 04222	11- 74500	Target Exon		10.0
25	412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	
23	419823	AW271708	Hs.118918	-ESTs, Weakly similar to M2OM_H	SS,TM	10.0
	433886	AA613598	Hs.28412	ESTs	SS	9.9
	428092	AW879141		ESTs	SS,TM	9.8
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
	420423	AA827718	Hs.88218	ESTs	SS	9.7
30	452302	AF173867	Hs.28906	glucocarticold modulatory elem	SAND,SS	9.7
	444681	AJ243937	Hs.28B316	chromosome 6 open reading fram	notch, EGF, ank, GoLoco, SS, T	9.7
	414249	Al797994	Hs.279929	gp25L2 protein	SS,TM,EMP24_GP25L,SS,TM,G	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	9.6
	438627	AI087335	Hs.123473	EST8	TM,Resculon	9.6
35			FI3.12.347.3		SNF,SS,TM	9.6
22	407065	Y10141	11- 000000	gb:H.saplens DAT1 gene, partia	SS.TM	
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225		9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	9.6
	424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	9.5
40	444633	AF111713	Hs.286218	junctional adhesion molecule 1	ig,SS,TM,HLH	9.4
40	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase,SS,TM,synaptobrev	9.4
	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	9.4
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	9.4
	400201			NM_006156*:Homo saplens neural	ubiquitin, SS, TM, Transglut	9.4
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	9.4
45	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rm,zf-RanBP,rm,GA	9.4
73					pkinase,SS	9.4
	445143	U29171	Hs.75852	casein kinase 1, delta		9.4
	407507	U73799	11. 05040	gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	
	450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase,GTP_EFTU,EFG_C,GT	9.4
50	411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	9.3
50	414625	AA335738	Hs.76688	glutathione peroxidase 1	GSHPx,SS,ræs,HLH	9.3
	456950	AF111170	Hs.306165	Homo saplens 14q32 Jagged2 gen	SS,TM,DSL	9.3
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	9.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	9.1
	412338	AA151527	Hs.69485	hypothetical protein FLJ12436	SS,TM,TIG,Sema,PSI	9.1
55	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_Ib,Lipase_GDSL,SS,	9.1
••	412104	AW205197	Hs.240951	Homo sepiens, Similar to RIKEN	SS,TM	9.1
	443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	9.1
	448984		Hs.22753	hypothetical protein FLJ22318	SS	9.0
		AW751955			SS,TNF,TNF	9.0
60	418776	AI401004	Hs.88411 Hs.89230	lymphocyte antigen 117	TM,CaMBD,SK_channel,TM	9.0
UU	418843	AJ251016		potassium intermediate/small c		
	419244	AI436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE,SS,mm,Ephrin	8.9
	451855	R54913	Hs.175804	ESTs	SS,TM,vwa	8.9
	424825	AF207069	Hs.153357	procellagen-lysine, 2-oxogluta	20G-Fell_Oxy,Glycos_trans	8.9
	447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tail,M	8.9
65	430167	Y08976	Hs.234759	FEV protein	Ets, SS, crystall	8.8
	409936	AK001691	Hs.57655	hypothetical protein FLJ 10829	SS,TM	8.7
	437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	8.7
	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	8.7
	424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	8.7
70				BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	8.7
, 0	414534	BE257293	Hs.76366		homeobox,pkinase,PH,pkina	8.7
	433333	AJ016521	Hs.71816	v-ekt mutne thymoma viral onc		8.7
	423228	AL137491	Hs.125511	Homo septens mRNA; cDNA DKFZp4	SS,TM,sushi	
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI,SS,CDK5_activator	8.7
75	420160	A1492840		ESTs	SS,TM	. 8.6
75	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM, Steroid_dh, SS	8.6
	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	8.6
	417193	A1922189	Hs.288390	hypothetical protein FLJ22795	SS	8.6
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS.TM.zf-C2H2	8.5
	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras,SS,Peptidase_M10,hemo	8.5
80			Hs.300697	immunoglobulin heavy constant	SS,TMJg	8.3
OU	406868	AA505445			TM,Rhombold,SS,TM	8.3
	434105	AW952124	Hs.13094	presentins associated rhombol		8.3
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	
	421707	NM_014921	Hs.107054	tectomedin-2	Latrophilin,OLF,7tm_2,Gal	8.2
	453898	AW003512	Hs.232770	arachidonate lipoxyganase 3	SS,TM,lipoxygenase,PLAT,s	6.2

	wo	02/102235			PCT/U	JS02/19
	456672 421592	AK002016 AF009801	Hs.114727 Hs.105941	Homo saplens, clone MGC:16327, bagpipe homeobox (Drosophila)	SS,PK,PK_C,myosin_head,Rh homeobox,SS	8.2 8.2
	409829 444341	M33552 AJ142027	Hs.56729 Hs.146650	lymphocyte-specific protein 1 ESTs	Caldesmon, SS, Ribosomal_S2 SS, TM, Reprolysin, Pep_M12B	8.1 · 8.0
5	413762	AW411479 •	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR,SS	8.0
•	435685	W28661	Hs.5288	Homo sapiens mRNA; cONA DXFZp4	SS,TM,pkinase,Activin_rec	8.0 8.0
	420932 431493	AW374605 AI791493	Hs.11607 Hs.129873	ESTs, Weakly similar to T21697 ESTs, novel cytochroms P450	SS,bZIP_Maf SS,p450,SS	7.9
	447598	A1799968	Hs.199630	ESTs	SS,TM	7.9
10	415758	BE270465	Hs.78793	protein kinase C, zeta	pkinase,DAG_PE-bind,pkina	7.8 7.8
	457022 426440	AW377258 BE382756	Hs.169902	gb:MR2-CT0222-261099-003-a10 C solute carrier family 2 (facil	SS,Ribosomal_L7Ae sugar_tr,SS,TM,sugar_tr	7.8
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.8
1.5	441084	W24563	Hs.9911	hypothetical protein FLJ11773	SS,TM,hormone_rec,zf-C4	7.8 7.7
15	424443 424198	AI751281 AB029010	Hs.284161 Hs,143026	hypothetical protein from EURO KIAA1087 protein	SS,TM,SS,TM SS,TM,Na_Ca_Ex,Calx-beta,	7.6
	430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	7.6
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, HSPC134 protein	WD40,SS,TM,fn3,EGF,fn3,ig SS,TM,ubiquitin,Transglut	7.6 7.5
20	432891 432234	AF161483 AA531128	Hs.279761 Hs.115803	ESTs	SS TAGUING TO THE STORE	7.5
	453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	7.5
	441327	AK001706	Hs.7778 Hs.14468	hypothetical protein FU10751 hypothetical protein MGC14226	SS,TM,7tm_1 SS,TM	7.5 7.5
	436540 418256	BE397032 AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	7.5
25	457274	AW674193	Hs.227152	-mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	7.5 7.5
	437141	BE304917 AL110261	Hs.31097 Hs.157211	hypothetical protein FLJ21478 DKFZP586B0621 protein	SS,TM,Glycos_transf_4 C1q,Collagen,SS	7.5 7.4
	425428 431934	AB031481	Hs.272214	STG protein	SS	7.4
20	418349	NM_001383	Hs.84183	diptheria toxin resistance pro	Diphthamide_syn,SS	7.4 7.3
30	430600 421758	AW950987 BE397336	Hs.274348 Hs.1422	HLA-B associated transcript-3 Gardner-Rasheed feline sarcoma	ubiquitin,SS,TM,G-patch,a SH2,SH3,pkinase	7.3 7.3
	412841	AI751157	Hs.101395	hypothetical protein MGC11352	SS,TM	7.3
	418313	BE244231	Hs.84038	. CGI-06 protein	SS,wap Sema,PSI,TIG,SS,TM,TIG,Se	7.3 7.3
35	429367 418837	AB007867 U48263	Hs.278311 Hs.89040	plexin B1 prepronociceptin	Oplods_neuropep,SS	7.2
33	423015	U18548	Hs.123034	G protein-coupled receptor 12	TM	7.2
	440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK,SS,TM SS,TM,ACAT	7.2 7.2
	421975 423858	AW961017 AL137326	Hs.6459 Hs.133483	hypothetical protein FLJ11856 Homo saplens mRNA; cDNA DKFZp4	SS,TM	7.2
40	446143	BE245342	Hs.306079	sec61 homolog	secY,SS,TM	7.2
	417704	NM_001747	Hs.82422	capping protein (actin filamen	Gelsolin,SS,Gelsolin lactamase_B,SS,XRCC1_N,BR	7.2 7.1
	440869 435099	NM_014297 AC004770	Hs.7486 Hs.4756	protein expressed in thyroid flap structure-specific endonu	XPG_N,XPG_I,5_3_exonuclea	7.1
4.5	438856	N40027	Hs.7473	ESTs	SS,TM,connexin	7.1 7.1
45	426268 418373	AF083420 AW750770	Hs.168913 Hs.84344	sertne/threonine kinase 24 (St CGI-135 protein	pkinase,pkinase SS,TM,PMP22_Claudin,20G-F	7.1 7.1
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
	421748	NM_014718	Hs.107809	KIAA0726 gene product	cadherin,TM,TPR	7.1 7.0
50	413837 426691	AW163525 NM_006201	Hs.171834	titin-cap (telethonin) PCTAIRE protein kinase 1	SS,Methyltransf_3 pkinase,SS,UCH-2,UCH-1,rr	7.0
50	409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	7.0
	424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,hellcase_C,brom integrin_A,FG-GAP,Rhabd_g	7.0 7.0
	431630 428156	NM_002204 BE269388	Hs.265829 Hs.182698	Integrin, alpha 3 (antigen CD4 mitochondrial ribosomal protei	SS	7.0
55	459255	Al493244	Hs.239500	hypothetical protein MGC13114	SS	7.0
	441323	AA928413	Hs.159089	ESTs, Weakly similar to ALU7_H gb:QV4-HT0538-040500-193-g02 H	SS,Peptidase_C1,zf-C2H2 SS	6.9 6.9
	455928 420856	BE170313 BE513294	Hs,205736	HLA class II region expressed	kazal,SS,TM,ig,pkinase	6.9
60	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM CC TM Chara haden EE Char	6.9 6.9
60	442296 445937	NM_007275 AI452943	Hs.8186 Hs.321231	tung cancer candidate UDP-Gat:beteGtcNAc beta 1,4- g	SS,TM,Glyco_hydro_56,Glyc Galactosyl_T_2,SS,TM,tsp_	6.9
	439732	AW629604	Hs.167641	hypothetical protein from EURO	ss,tm,ss,tm,a2m,a2m_n,ntr	6.8
	429542	AF038660	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,lg,SS,TM,A SS,dynamin_2,dynamin,PH,G	6.8 6.8
65	420190 408215	AI816209 BE614290	Hs.95867	hypothetical protein EST00098 syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	6.7
05	410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	6.7
	419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe SS,TM	6.7 6.7
	448677 425228	A1560769 NM_005253	Hs.301612	ESTs FOS-like anligen 2	bZIP,SS	6.6
70	432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	6.6
	421864	BE387198	Hs.108973	dolichyl-phosphate mannosyttra glutathlone S-transferase pi	SS,TM,SS,TM GST_C,GST_N,SS,efhand	6.6 6.6
	429962 406867	M69113 AA157857	Hs.226795 Hs.182265	keratin 19	filament,bZIP,SS,filament	6.6
~ ~	426068	AF029778	Hs.166154	jagged 2	DSL,EGF,vwc,granutin,SS,T	6.5 6.5
75	419344	U94905	Hs.277445	diacytgtycerol kinase, zeta (1	enk,DAGKa,DAGKc,DAG_PE-bl heilcase_C,PRK,SS,TM,7tm_	6.5 6.5
	424681 417903	AA054400 NM_002342	Hs.151706 Hs.1116	KIAA0134 gene product lymphotoxin beta receptor (TNF	TNFR_c6,SS	6.5
	423876	BE502835	Hs.15483	Homo sapiens, clone IMAGE:2959	SS,efhand	6.4
oΛ	433439	AA431176	Hs.133230	ribosomal protein S15	TM,SS,TM,TPR,res SS,RFX_DNA_binding	6.4 6.4
80	441379 432968	AW175787 BE614192	Hs.334841 Hs.279869	selenium binding protein 1 metanoma-associated antigen re	SS,TM,RGS,DIX	6.4
	456863	T16837	Hs.4241	ESTs	fusion_gly.homeobox.TM	6.4
	432269	NM_002447	Hs.2942	macrophage stimulating 1 recep Rho GDP dissociation inhibitor	pkinase, Sema, PSI, TIG, A4_E Rho_GDI, homeobox, SS, Cylld	6.4 6.4
	425676	AW410656	Hs.159161	NO OUT USSUCADOR HUMAN	1.500 Toltion is control of olive	3,4

	443420	R06846	Hs.191208	ESTs	SS	6.4
	435322	AL355092	Hs.120243	parvin, gamma	CH,SS,TM,CTF_NFI SS_xf-C3HC4,SPRY,xf-B_box	6.4 6.4
	440088	BE559877	Hs.183232	hypothetical protein FLJ22638 hypothetical protein MGC2963	SS,TM	6.3
5	447665 431785	BE044245 AA292385	Hs.30011 Hs.268763	Breakpoint cluster region prot	BAF,kazal,TM	6.3
,	422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221,SS,TM,TGFb_propept	6.3 6.3
	434916	AF161383	Hs.284207	Homo saplens, Similar to RIKEN	TM ECH,Peptidase_U7,SS,TM	6.3
	414551 413254	A1815639 U40272	Hs.76394 Hs.75253	encyl Coenzyme A hydratase, sh isocitrate dehydrogenase 3 (NA	isodh,SS	6.3
10	458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,tRNA-synt_2d	6.3
10	415010	NM_004203	Hs.77783	membrane-associated tyrosine-	ptdnase,SS,PMP22_Claudin SS	6.3 6.3
	410076	T05387	Hs.7991	ESTs homeo box 87	homeobox,SS,homeobox,home	6.2
	412940 440042	8E295701 Al073387	Hs.819 Hs.133898	ESTs	SS	6.2
15	414023	BE243628	12.70000	gb:TCBAP1D1053 Pediatric pre-B	SS 	6.2 6.2
	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS, PX.SS	6.2
	446662	NM_013323 AJ243191	Hs.15827 Hs.56874	sorting nexin 11 heat shock 27kD protein family	HSP20,SS,TM,zI-C2H2,BTB,E	6.2
	409882 414576	AK000405	Hs.76480	ubiquifin-like 4	ubiquitin,SS,TM,G6PD,G6PD	6.2
20	447507	H59696	Hs.18747	POP7 (processing of precursor,	SS,TM,WD40,vwd,MAM,EPO_TP	6.2 6.1
	453447	AW77131B	Hs.326586	hypothetical protein MGC11134	SS,TPR TM	6.1
	435968	AW161481	Hs.111577 Hs.147097	integral membrane protein 3 H2A histone family, member X	histone,CBFD_NFYB_HMF,SS,	6.1
	424441 434558	X14850 AW264102	Hs.39168	'ESTs	SS,TM,LRRCT,LRR	6.1
25	434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1 6.0
	432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS zf-C3HC4,SpoA,PHD,TM,syna	6.0
	444416	AW288085	Hs.11156 Hs.11006	hypothetical protein ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	6.0
	447205 407704	8E617015 BE315072	Hs.78768	malignant cell expression-enha	TM,MBOAT,SS,TM	6.0
30	453190	AB002354	Hs.32312	KIAA0356 gene product	PH,PHD,RUN,SS	6.0 6.0
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like,SS SS,PX,arf,lipocalin,PHD,z	6.0
	449514	AW970440	Hs.23642 Hs.3107	protein predicted by clone 236 CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	6.0
	432805 414362	X94630 A1347934	Hs.75932	N-ethylmalelmide-sensitive fac	NSF,SS,TM	6.0
35	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0 6.0
	427988	AA789333	Hs.181349	hypothetical protein 628	SS,SS zf-C2H2,SS,rm,ENTH	6.0
	423473	H49104	Hs.129888 Hs.76067	hypothetical protein FLJ 14768 heat shock 27kD protein 1	HSP20,SS	5.9
	406773 409938	AA812424 AW974648	rts./000/	gb:EST386752 MAGE resequences,	SS,Adap_comp_sub,GYF	5.9
40	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pkinase,SH3	5.9 5.9
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	SS,TM,ion_trens bZIP,5_3_exonuclease,M,SS	5.9
	452094	AF049105	Hs.27910 Hs.26516	centrosomal protein 2 hypothetical protein FLJ 10604	SS,SS,TM,pkinase,pkinase_	5.9
	451524 427438	AK001466 AW328515	Hs.178011	hypothetical protein FLJ20257	SS,TM	5.9
45	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	5.9 5.9
	440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17, SS,TM,ion_trans	5.9
	417334	AA337572 C75094	Hs.157240 Hs.334514	hypothetical protein MGC4737 NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	5.8
	425976 433173	Z35093	Hs.3196	surfeit 1	SURF1,SS,TM,SURF1,SURF4	5.8
50	437891	AW006969	Hs.6311	hypothetical protein FLJ20859	TM,SET	5.8 5.8
	410239	AI568350	Hs.61273	hypothetical protein MGC2650 hypothetical protein MGC3121	SS,ART,TM SS	5.8
	458060	R95860 AA532963	Hs.293629 Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,LIM,homeobox	5.8
	409591 409686	AK000002	Hs.55879	Homo saplens mRNA; cDNA DKFZp4	SS,ABC_tran,SS,TM	5.8
55	450778	U81375	Hs.25450	solute carrier family 29 (nucl	Nucleoside_tran,SS,TM,HSP G-atpha,arf,SS,G-atpha	5.8 5.8
	423612	NM_002067	Hs. 1688	guanine nucleolide binding pro	zt-C2H2,GST_C,PHD,SS,TM,H	5.8
	422701	NM_014699	Hs.119273 Hs.75087	KIAA0296 gene product Fas-activated serine/threonine	SS,pkinase	5.8
	412958 436957	BE391579 AA902488	Hs.122952	ESTs	SS,DAGKC,DAGKa,RA,DAG_PE-	5.8
60	423158	H97991	Hs.193313	Target CAT	MoaA_NifB_PqqE,SS,TM	5.8 5.8
	414788	X7B342	Hs.77313	cyclin-dependent kinase (CDC2- nuclear receptor subfamily 1,	pkinase hormone_rec,zf-C4,SS,DNA_	5.7
	420904	AL035964 BE261320	Hs.100221 Hs.158196	transcriptional adaptor 3 (ADA	pkinase	5.7
	410431 420508	AJ270993	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	5.7
65	435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	5.7 5.7
	433064	079991	Hs.30002	SH3-containing protein SH3GLB2	tm ss,tm,ss,tm	5.7
	451920	AA224483 A1878908	Hs.27239 Hs.31547	DKFZP586K0524 protein Target CAT	SS	5.7
	453054 415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosp	Viral_helicase1,SS,Amino_	5.7
70	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3.jg,Y_phosphatase,SS,T SRF-TF,flavodoxin,SS,TM,p	5.7 5.7
	425246	AI085561	Hs.155321	serum response factor (o-fos s	SS,TM	5.7
	433271	BE621697 BE613340	Hs.14317 Hs.334725	nucleolar protein family A, me Homo seplens, Similar to RIKEN	TM,SS,TM,Kunitz_BPTI	5.7
	448484 449139	8E268315	Hs.23111	phenylalanine-IRNA synthetase-	neur,SS,zf-C2H2,DNase_II	5.7
75	449181	X96783	Hs.23179	synaptotagmin V	C2,SS,TM,Y_phosphatase,Tr ATP-synt_C,SS,TM,pkinase	5.6 5.6
	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	actin.SS	5.6
	424964		Hs.153961 Hs.12185	ARP1 (actin-related protein 1, hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	5.6
	415193 407754		Hs.288987	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,tsp_3,SE	5.6
80	413049		Hs.823	hepsin (transmembrane protease	trypsin,SS,TM,ATP1G1_PLM_	5.6 5.6
	454252	H50256	Hs.63236	ribosomal protein S15a	SS SS,WD40,pkinase	5.6
	431787		Hs.343661 Hs.183669	ret finger protein KIAA1271 protein	SS,TM .	5.6
	431607 406782		113.100003	gb:zw20f11.s1 Soares overy turn	SS	5.6
	700104		•	238		

	444364	AL137294	Hs.10964	hypothetical protein FLJ22351	SS,TM,pktnase	5.6
	427834	AA506101	Hs.285813	hypothetical protein FLJ11807	SS,TM	5.5
	443759	BE390832	Hs.134729	FXYD domain-containing ion tra	SS,TM,ATP1G1_PLM_MAT8,ATP	5.5 · 5.5
_	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reduct	PSCR,Octopine_DH_N,SS,thi	5.5
5	406673	M34996	Hs.198253	major histocompatibility compl	SS,TM,MHC_JL_alpha,lg,SS, SS,TM,pkinase	5.5
	415351	U44755	Hs.78403	small nuclear RNA activating c 7-60 protein	SS,Collagen,Collagen	5.5
	411030 410653	BE387193 BE383768	Hs.67898 Hs.65238	95 kDa retinoblastoma protein	zf-C3HC4,SS,SNF2_N,helica	5.5
	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, y	HMA.SS.TM	5.5
10	437741	BE561610	Hs.5809	putative transmembrane protein	SS,TM,SS,TM,RA,VPS9,SH2	5.5
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil,Glyco_hydro_31,SS	5.4 5.4
	427361	AW732480	Hs.7678	cellular relinoic acid-binding	SS,TM,aminotran_1_2,LRR cofilin_ADF,SS,TM	5.4 5.4
	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	SS_mm_SS_Cytidytyttransf	5.4
16	457313	AF047002	Hs.241520 Hs.118282	transcriptional coactivator PAP-1 binding protein	SS,TM	5.4
15	428345 434845	AI242431 BE267057	Hs.325321	hypothetical protein R32184_1	SS,TM,CH,calponin,ARID	5.4
	427162	AB011133	Hs.173864	KIAA0561 protein	SS,pkinase,PDZ,SS,SH2,Rho	5.4
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	SS,TM	5.4
	433676	AW371389	Hs.250173	hypothetical protein FLJ13158	SS	5.4 5.4
20	424373	AJ133798	Hs.146219	copine VII	C2,SS SS	5.4
	423402	BE167615	Hs.141556	Homo septens cDNA FLJ12976 fis	BTB,Kelch,SS,TM	5.4
	409983	D50922	Hs.57729 Hs.237617	Kelch-like ECH-associated prot Homo saplens, clone IMAGE:3447	SS	5.3
	450184 431629	W31096 AU077025	Hs.265827	Interferon, alpha-inducible pr	pkinase,SH2,SH3	5.3
25	430413	AW842182	Hs.241392	small inducible cytokine A5 (R	ila,ss	5.3
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	5.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	5.3 5.3
	412276	BE262621	Hs.73798	macrophage migration inhibitor	MIF,SS,TM,MIF,sugar_tr SS,TM,GalP_UDP_transf,Gal	5.3
20	416181	AA174126	Hs.332163	ESTS	SS,Acyl-CoA_dh,Acyl-CoA_d	5.3
30	440609	Al287585	Hs.7301	G protein pathway suppressor 2 mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	5.2
	435327	BE301871	Hs.4867 Hs.301372	KIAA1552 protein	SS,TM	5.2
	421139 453449	AW953933 W16752	Hs.32981	sema domain, immunoglobulin do	SS,Sema,ig,PSI,SS,TM,G-al	5.2
	414411	X54079	Hs.76067	heat shock 27kD protein 1	HSP20,SS	5.2
35	440906	AW161556	Hs.240170	hypothetical protein MGC2731	SS,TM,Furin-like,pkinase,	5.2
	421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	5.2 5.2
	439473	Al215529	Hs.144787	ESTs	SS SS,Metallophos	5.2
	451585	AK001171	Hs.326422	hypothetical protein MGC4549 gb:ae56h07.s1 Stratagene lung	SS.Peptidase_C1	5.2
40	407191	AA608751 T79526	. Hs.179516	integral type I protein	EMP24_GP25L,SS	5.2
40	427515 405325	179320	. 113.113310	C14000786*:gij7023514 dbijBAA9	SS ·	5.2
	434119	AF193844	Hs.3758	COP9 complex subunit 7s	SS	5.1
	413052	BE249841		gb:600942857F2 NIH_MGC_15 Homo	TM,SS,TM	5.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate di	SS,TM,GDA1_CD39,SS,TM,pho	5.1 5.1
45	409323	H28855	Hs.53447	Homo saplens mRNA; cDNA DKFZp7	TPR,SS,TM,pkinase,ig SS,TM,ACAT,MBOAT,SS,TM,TB	5.1
	438707	L08239	11- 204054	amino acid system N transporte RelA-associated inhibitor	SH3,ank,SS,TM,HHH,lg	5.1
	442599	AF078037	Hs.324051 Hs.293660	Homo sapiens, clone IMAGE:3535	SS	5.1
	420372 436576	AW960049 AI458213	Hs.77542	ESTs	SS,TM,7tm_1,DnaJ	5.1
50	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	AAA,DnaB,UPF0079,SS,Cys_k	5.1
50	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	5.1
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase	5.1 5.1
	425743	BE396495	Hs.159428	BCL2-associated X protein	Bcl-2,SS,ferritin,Bcl-2,e TIM,SS,TM,zf-UBP,UCH-2,UB	5.0
55	418231	AA326895	Hs.83848	triosephosphate isomerase 1 hypothetical protein DKFZp564D	SS,TM,WH2	5.0
55	419238	AW959538 Al989925	Hs.321214 Hs.24891	ESTs, Highly similar to unknow	SS,TM,Ammonium_transp	5.0
	441917 437617	AI026701	Hs.5716	KIAA0310 gene product	SS,zf-C3HC4,Peptidase_M16	5.0
	412867	AU076861	Hs.74637	testis enhanced gene transcrip	UPF0005,SS,TM	5.0
	419579	W49529	Hs.296200	hypothetical protein AF053356_	MSP_domain,SS,TM,CUB,NTR, .	5.0 5.0
60	425824	A1939563	Hs.159589	ESTs, Moderately similar to RE	SS,PHD SS,SS,TM,GDI,Sema,TIG,PSI	5.0
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysoso cation-chloride cotransporter-	SS,TM,aa_permeases,SS,TM,	5.0
	436042	AF284422	Hs.119178 Hs.66196	nth (E.coil endonuclease III)-	HIH-GPD,SS,TM,REJ,PLAT,PK	5.0
	410775 453350	AB014460 Al917771	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	4.9
65	400300	X03363	15.01100	HER2 receptor tyrosine kinase	pkinase	4.9
05	426811	BE259228	Hs.172609	nucleobindin 1	efhand,SS,TM,GFO_IDH_MocA	4.9
	421179	U72664	Hs.148495	proteasome (prosome, macropain	UIM,SS,TM,PMP22_Claudin,P	4.9 4.9
	429762	AI346255	Hs.216354	ring finger protein 5	SS,zf-C3HC4,Palm_thioest SS,TM,7tm_1,BAH,zf-CXXC,D	4.9
70	419250	AW770185	11 490070	US snRNP-specific protein, 116	AdoHcyase,SS	4.9
70	426831	BE296216 AA333367	Hs.172673 Hs.8088	S-adenosylhomocysteine hydrola similar to S. cerevisiae Sec6p	SS	4.9
	442103	AA371931	Hs.77422	proteolipid protein 2 (colonic	SS	4.9
	414820 426347	AA454912	Hs.169407	SAC2 (suppressor of actin muta	SS,RasGEF,RA,RasGEFN,horm	4.9
_	423880	BE278111	Hs.134200	DKFZP564C186 protein	UPF0120,SS,TM	4.9 4.9
75	429545	AI824164		tymphocyte antigen 6 complex.	SS,TM QRPTasa,QRPTasa_N,SS,TM	4.9 4.9
	443044	N28522	Hs.8935	quinolinate phosphoribosyltran	SS,S10_plectin	4.8
	417080	BE392846	Hs.1063	small nuclear ribonucleoprotei zinc/iron regulated transporte	Zio,SS,TM, Cytidylyttransf	4.8
	441455	AJ271671	Hs.7854 Hs.59544	excision repair cross-compleme	HHH,SS,SH3,ank	4.8
80	410182	NM_001983 A1866286	Hs.71962	ESTs. Weakly similar to B36298	SS	4.8
80	456062 439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.8
	408985	BE267317	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	4.8 4.8
	416976	8E243985	Hs.80680	major vauli protein	Vault,SS,TM,kinesin,zf-C2 cNMP_binding,SS,TM,cNMP_b	4.8
	436057	AJ004832	Hs.5038	neuropathy larget esterase	CHAIL THINGS OF LATORIAL TO	7.0
				220		

						40
	424501	AJ470163	Hs.323342	actin related protein 2/3 comp	SS,HhH-GPD	4.8 4.8
	409214	AW405967	Hs.333388	Homo saplens, clone IMAGE:3957	SS,EF1BD,P5CR	4.8
	432716	AI762964	Hs.205180	ESTs .	SS,TM pktnase,SS,WD40	4.8
_	414460	L00727	Hs.898	dystrophia myotonica-protein k	SS,TM,SS,TM,gpdh,gpdh_C	4.7
5	443329	BE262943	Hs.9234	hypothetical protein MGC1936	C2,SS,aminotran_5	4.7
	426120	AA325243	Hs.166887	copine I	SS,TM,hemopexin,Somatomed	4.7
	405356			ENSP00000247029*:SEBOX.	TM, ig. SS, TM	4.7
	437118	AB037857	Hs.300591	CO9 partner 1	SS,TM,GST_C,abhydrolase	4.7
• •	430609	AA302921	Hs.247362	dimethylarginine dimethylamino	SS,TM,pkinese	4.7
10	447131	NM_004585	Hs.17466	ratinoic acid receptor respond	Band_7,Flotillin,TM	4.7
	428469	BE549205	Hs.184488	flotillin 2	SS	4.7
	405189			Target Exon NM_024018*:Homo saplens butyro	SS,TM,SPRY,SPRY,ig	4.7
	404256		11- 404047		SS,zl-B_box,SPRY,SS,Nol1_	4.7
1.5	457955	A1208986	Hs.121647	ESTs hypothetical protein MGC12972	SS,SH2,RhoGAP,SH3,GILT	4.7
15	413201	BE275378	Hs.13972	zinc finger protein 219	zf-C2H2,SS	4,7
	431115	AB015427	Hs.250493	ribonuclease 6 precursor	ribonuclease_T2,SS,ribonu	4.7
	442414	BE408758	Hs.8297 Hs.83951	Hermansky-Pudlak syndrome	SS	4.6
	418289	AW403103	Hs.5300	bladder cancer associated prot	SS	4.6
20	436730	AA045767	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept	4.6
20	444596	BE560662	Hs.279915	translocase of inner mitochond	zf-Tim10_DDP,SS	4.6
	433019	AI208513	Hs.258609	protein tyrosine phosphatase,	fn3,Y_phosphatase,SS,TM	4.6
	431522	A1625859	FIS.230003	sortilin-related receptor, L(D	ldl_recept_a,fn3,ldl_rece	4.6
	400846 422154	T79045	Hs.168812	ESTs	SS	4.6
25	420321	D78761	Hs.96657	hyothetical protein	SS,tsp_1,SS	4.6
23	439921	AL110209	Hs.6770	LCAT-like lysophospholipase	SS,LACT,SS,TM,aa_permease	4.6
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6
	426899	AL043221	Hs.172825	KIAA1037 protein	WD40,TPR,SS,TM	4.6
	408116	AA251393	Hs.289052	Homo saplens, Similar to RIKEN	SS,TM	4.6
30	412974	R18978	Hs.75105	emopamil-binding protein (ster	SS,TM,SS,TM,TBC,rm,FlsJ	4.6
50	426510	AW861225	Hs.110613	BANP homolog, SMAR1 homolog	TM	4.6
	414702	122005	Hs.76932	cell division cycle 34	UQ_con,SS,trypsin,ig	4.6
	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltrans(_4,SS,p450,Ge	4.6
	445637	W58459	Hs.8949	hypothetical protein MGC4172	SS	4.6
35	452190	H26735	Hs.91668	Homo saplens clone PP1498 unkn	SS	4.6
55	409680	W31092	Hs.55847	mitochondrial ribosomal protei	SS,TM,synaptobrevin	4.6
	421140	AA298741	Hs.102135	signal sequence receptor, delt	Herpes_UL3,SS,TM,Sema,pki	4.6
	413407	Al356293	Hs.75339	inositol polyphosphate phospha	SH2,SAM,SS,Folate_rec	4.6
	402463			NM_014624:Homo saplens S100 ca	efhand,S_100,SS,efhand,S_	4.5
40	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA direc	SS,PGAM	4.5
40	406939	M34515		gb:Human omega light chain pro	SS,lg,PH	4.5
	417891	W79410	Hs.82887	protein phosphatase 1, regulat	SS,TFIIS	4.5
	426207	BE390657	Hs.30026	HSPC182 protein	SS	4.5
	423664	NM_004714	Hs.130988	dual-specificity tyrosine-(Y)-	pkinase, SS, Fibrillarin, CK	4.5
45	432562	BE531048	Hs.278422	DKFZP586G1122 protein	zl-C2H2,SS,TM,FG-GAP,inte	4.5
70	427391	W60675		hypothetical protein FLJ 10350	SS,SS	4.5
	432893	NM_016154	Hs.279771	Homo sapiens done PP1596 unkn	ras,arf,SS,2OG-Fell_Oxy,2	4.5
	424954	NM_000546	Hs.1846	tumor protein p53 (U-Fraumeni	P53,SS	4.5
	413815	AL046341	Hs.75562	discoidin domain receptor fami	F5_F8_type_C,pkinase,SS,T	4.5
50	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610	SS,TM	4.5
	416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr,SS	4.5 4.5
	421962	D82061	Hs.288354	FabG (beta-ketoacyl-(acyl-carr	SS,adh_short,SS,TM,zf-C3H	4.5 4.5
	426726	AA488915	Hs.171955	trophinin associated protein (SS	4.5 4.5
	414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-ass	SS,TM	4.5 4.5
55	435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA,SS,TM,spectrin,	4.5 4.5
•	453997	AW247615	Hs.37003	v-Ha-res Harvey rat sarcoma vi	ras,SS	4.5
	449029	N28989	Hs.22891	solute carrier family 7 (callo	ea_permeases,SS,TM,bZIP	4.5
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541	. SS,TM	4.5
	409650	T08490	Hs.288969	HSCARG protein	SS,SS,WD40	4.4
60	412833	AW960547	Hs.298262	ribosomal protein S19	SS,TM,lg,ITAM,Ribosomal_S	
	424133	AA335721	Hs.213628	ESTs	SS,TM	4.4
	414787	AL049332	Hs.77311	BTG family, member 3	SS,Anti_proliferat	4.4
	433046	AA229553	Hs.279945	HSPC023 protein	SS	4.4
	417068	AA451910	Hs.85852	hypothetical protein MGC3169	SS,TM	4.4
65	414814	D14697	Hs.77393	famesyl diphosphate synthase	polyprenyl_synt,SS,TM	4.4
••	418267	BE389537	Hs.83919	glucosidase I	Glyco_hydro_63,SS,PH	4.4
	439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP,SS,G	4.4
	448847	AI587180	Hs.110906	Homo sapiens, Similar to RIKEN	TM,SS	4.4
	452160	BE378541		cystelne sulfinic acid decarbo	SS Authorsforms SS TM CDI	4.4
70	416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acytransferase, SS, TM, GDI	4.4
	449717	AB040935	Hs.23954	cerebral cell adhesion molecul	SS,SS SS.atdo_ket_red	4.4
	425069	AA687465	Hs.298184	potassium voltage-gated channe	55,800_RECTEU	4.4
	413380	Al904232	Hs.75323	prohibiln	Band_7,SS,Band_7,SH3	4.4
	452911	AA541537	Hs.112619	metallothionein 1E (functional	SS,SS,TM,Sec1	4.4
75	436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24,SS,TM,Pepti	4.4
	429218	AA225065	Hs.198269	Target CAT	SS,Nop	4.4
	447987	BE621544	Hs.157160	hypothetical protein MGC2616	SS,NDK,LRRNT,LRRCT,LRR	4.3
	407230	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament SS,PH,RhoGEF,SS,maseA	4.3
	448886	AL137291	Hs.22451	hypothetical protein FLJ10357		4.3
80	421178	BE267994	Hs.102419	zinc finger protein	zI-C2H2,SS,TM	4.3
	454031		Hs.71941	hypothetical protein MGC15677	TM	4.3
	450126		Hs.24447	sigma receptor (SR31747 bindin	SS.jg,fn3	4.3
	446557		Hs.15318	HS1 binding protein	SS,TM,MIP,UBA	4.3
	413781		Hs.850	IMP (Inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD,S	4.5

	433251	AB040955	Hs.322735	KIAA1522 protein	SS,SS,zf-C3HC4,SPRY	4.3
	420531	AI652069	Hs.98614	ribosome binding protein 1 (do	bzip,ss	4.3
	432179	X75208	Hs.2913	EphB3	EPH_tbd,fn3,pkinase,SAM	4.3
	448988	Y09763	Hs.22785	gamma-eminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
5	426526	Al124572	Hs.323879	inhibitor of kappa light polyp	zf-C2H2,SS	4.3
•	432956	AL037895	Hs.279861	CGI-31 protein	thlored,SS,TM	4.3
	428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3,SS,TM	4.3
	428953	AA306610	Hs.348183	turnor necrosis factor receptor	TNFR_c6,SS	4.2
	401128	77303010	15.540100	C12000644:gij5729785[ref]NP_00	SS	4.2
10		NM_005397	Hs.16426	podocalyxin-like	SS,TM,SS,TM	4.2
10	446899			ESTs, Moderately similar to un	SS,TNF	4.2
	407151	H25836	Hs.301527		edh_short,SS	4.2
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro		4.2
	408616	R51604	Hs.300842	KIAA1608 protein	SS,DENN,DENN	4.2
	446616	R65964	Hs.334873	ESTs, Wealthy similar to ALU8_H	SS,Zn_carbOpept	
15	414467	AW903820	Hs.85752	copine II	SS	4.2
	455857	T70192		gb:yc18d03.s1 Stratagene lung	SS,TM,isodh	4.2
	401751			RAN binding protein 3	SS, Orexin, SH2, STAT	4.2
	400563			Target Exon	SS,Pep_M12B_propep	4.2
	430237	A)272144	Hs.236522	DKFZP434P106 protein	abhydrolase,TM	4.2
20	406101	MEIETT	10.20022	C11000273*:gi]12656107 gb AAK0	SS,TM,7tm_1	4.2
20		DE001303	Hs.299148	hypothetical protein FLJ21801	SS,VHP	4.2
	421661	BE281303	16.233140		SS	4.2
	444590	AA457456		hypothetical protein FLJ20435	SS ·	4.2
	408187	AF034373	Hs.43509	ataxin 2 related protein		4.2
0.5	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	SS, Hydrolase, SS, Gal-bind_	4.2
25	400278			_ENSP00000243264:Dolichyl-dipho	SS,TM	
	407394	AF005081		gb:Homo sapiens skin-specific	SS	4.2
	447407	BE387301	Hs.18528	Sjogren's syndrome nuclear aut	\$S,HLH,ras,GSHPx	4.2
	410237	AI750589	Hs.61258	argininosuccinate lyase	lyase_1,SS	4.1
	415410	AF037332	Hs.278569	sorting nextn 17	PX,fn3,pkinase,SAM,EPH_lb	4.1
30	457757	AA434109	Hs.12271	f-box and leucine-rich repeat	SS,F-box,SS,TM,HSF_DNA-bl	4.1
50			Hs.7788	NPD007 protein	SS,TM	4.1
	446388	AA292979		Homo sapiens cDNA FLJ13625 fis	SS	4.1
	412825	AW167439	Hs.190651		SS,C1g,Collagen	4.1
	439737	AJ751438	Hs.41271	Homo saplens mRNA full length		4.1
~ ~	422256	M64673	Hs.1499	heat shock transcription facto	NA,SS,TM,F-box	4.1
35	441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C,SS,RNA_pol_H	
	401727			Target Exon	A_deamin,SS	4.1
	411142	NM_014256	Hs.69009	transmembrane protein 3	GalactosyLT,SS,Ribosomal	4.1
	458176	Al961519	Hs.140309	Homo sapiens, clone IMAGE:3677	SS,pkinase,pkinase_C	4.1
	432178	BE265369	Hs.272814	hypothetical protein OKFZp434E	SS,serine_carbpept	4.1
40	421537	BE383488	Hs.105547	neural proliferation, differen	SS,TM,Glyco_hydro_47	4.1
••	421380	D31833	Hs.1372	arginine vasopressin receptor	7tm_1	4.1
	422702	AJ011373	Hs.119285	chromosome 9 open reading fram	SS,TM,SS,TM	4.1
		U47927	Hs.3759	ubiquitin specific protease 5	z-UBP,UCH-2,UBA,UCH-1,SS	4.1
	434142		115.0100	Sushi domain (SCR repeat) cont	SS,TPR,vwd,sushi,Somatome	4.1
AE	423696	Z92546	11. 477700		BRCT,PARP,zf-PARP,PARP_re	4.1
45	427407	BE268649	Hs.177766	ADP-ribosyttransferase (NAD; p	pkinase,SS,TM,ig	4.1
	413749	A1929320	Hs.75516	tyrosine kinase 2		4.1
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1,SS	4.1
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN R	SS,TM,mm	
	433890	AF103801	Hs.16361	hypothetical protein	DAO,SS .	4.1
50	452603	AW410601	Hs.30026	HSPC182 protein	SS	4.1
•	444496	BE302472	Hs.11314	DKFZP564N1363 protein	SS,GKAP,Band_41	4.1
	422556	NM_006245	Hs.118244	protein phosphatase 2, regulat	B56,SS,TM,Atrophin-1,Exo_	4.1
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KI	TM,SS	4.1
			Hs.183435	NM_004545:Homo sapiens NADH de	SS,TM,Josephin,UIM,Joseph	4.1
55	428284	AA535762		ESTs	SS,sushi	4.0
22	426551	AA381268	Hs.323947		SS.TM	4.0
	417782	T10149	Hs.4243	hypothetical protein FLJ12650		4.0
	443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome,SS,TM,LACT,try	4.0
	410039	AF207989	Hs.58014	Homo saplens, Similar to G pro	SS,TM,7tm_3,SS,TM	4.0
	452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	pkinase	
60	442549	AJ751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF,SS,	4.0
	430603	AA148164	Hs.247280	HBV associated factor	SS,zf-C3HC4,zf-RanBP,pkin	4.0
	427239	BE270447		ubiquitin carrier protein	UQ_con,SS,TM	4.0
	402665	002.01		Target Exon	SS,TM,ig,DSPc	4.0
	413818	BE161405	Hs.79	hypothetical protein MGC15429	SS,KH-domain,WD40,Ribosom	4.0
65			113.73	gh:Homo saplens DNA-binding or	SS,rm	4.0
0.5	406919	M88359	11- 74070		SS,PDZ,DEP,DIX,Dishevelle	4.0
	412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	SS,TM,T-box,GTP_CDC,LRRCT	4.0
	437546	AW074836	Hs.173984	T-box 1		4.0
	419489	AW411280	Hs.90693	replication initiation region	zf-C2H2,LIM,TM	
	410043	D30612	Hs.58167	zinc finger protein 282	zf-C2H2,KRAB,SS,zf-C2H2,K	4.0
70	430067	U79458	Hs.231840	WW domain binding protein 2	GRAMSS	4.0
-	408449	NM_004408	Hs.166161	dynamin 1	PH,GED,dynamin,dynamin_2,	4.0
	448099	BE621839	Hs.61976	Homo sapiens cDNA FLJ12947 fis	SS	4.0
	436656	N35568	Hs.5245	hypothetical protein FLJ20643	SS,TM,sugar_tr,PID	4.0
	424512	X53002	Hs.149846	Integrin, beta 5	integrin_B,EGF,SS,TM	4.0
75		Al923985	Hs.59621	ESTs, Weakly similar to A40815	SS,TM,lg,pkinase	3.9
15	440346			ESTs	SS,TM	3.9
	420065	AW140093	Hs.129926	ubiquitin-activating enzyme E1	Thir, UBACT, SS, pkinase, UCH	3.9
	426636	BE242634	Hs.2055			3.9
	421579	NM_002975	Hs.105927	stem cell growth factor; lymph	lectin_c,SS,TM	3.9
	427498	NM_003926	Hs.178728	methyl-CpG binding domain prot	SS,HLH	
80	457820	AA341497	Hs.31408	RAR (RAS like GTPASE)	SS,TM,Rhomboid	3.9
	439998	BE559554	Hs.61790	hypothefical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	3.9
	438662	AA223599	Hs.6351	cleavage and polyadenylation s	zf-OCHC,zf-CCCH,thaumatin	3.9
		NM_004427	Hs.165263	early development regulator 2	SAMISS	3.9
	414303	F26698	Hs.4884	catcium/calmodulin-dependent p	pkinase, SS, hexokinase, hex	3.9
	435406	1 20030	113.4004			

	414168	AW793296	Hs.103845	ESTs, Moderately similar to 15	SS	3.9
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp5	SS .	3.9 3 . 9
	418181	U37012	Hs.83727	cleavage and polyadenylation s	CPSF_A,SS,TM SS,TM,cyclin,cyclin_C	3.9
5	402793	AA287786	Hs.23449	Terget Exon Insulin receptor tyrosine kina	SS.SH3	3.9
J	418681 412621	L40397	Hs.74137	transmembrane trafficking prot	EMP24_GP25L,SS,TM	3.9
	420631	AW976530	Hs.28355	hypothetical protein FLJ22402	SS,TM	3.9 3.9
	438483	AW966735	Hs.321635	ESTs, Weakly similar to A46302	SS,TM,IP_trans far4_NifH,ParA,APS_kinase	3.9
10	431472	AK001023 AL080092	Hs.256549 Hs.19610	nucleolide binding protein 2 (OKFZP564N1362 protein	SS,TM,SS,TM	3.8
10	447800 436686	AW450205	Hs.305890	BCL2-like 1	TM,8d-2,8H4	3.8
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	SS,TM	3.8 3.8
	441196	BE397802	Hs.7744	NM_007103*:Homo saplens NADH d	Complex1_51K,SNF2_N,helic SS,TM,EMP24_GP25L,SS,TM,G	3.8 3.8
15	433030	AW068857	Hs.279929 Hs.47062	gp25L2 protein potymerase (RNA) II (DNA direc	RNA_POL_M_15KD,SS,COX7a	3.8
13	408721 435049	BE515274 AL122067	Hs.4746	hypothetical protein FLJ21324	SS,pfkB	3.8
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (SS,Insulin,Insulin	3.8 3.8
	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	AriGap, SS, vwa, TSPN, fn3, Co pkinase, SS, pkinase, T-box	3.8
20	414134	X60188 U57059	Hs.861 Hs.83429	mitogen-activated protein kina tumor necrosis factor (ligand)	TNF,SS	3.8
20	418090 448832	AW245212	Hs.22199	ECSIT	SS,rm	3.8
	447256	AW593008	Hs.6126	hypothetical protein dJ1141E15	SS,TM,SS,TM	3.8 3.8
	448107	D45853	Hs.20313	protein tyrosine kinase 2 beta	Focal_AT,pkinase,SS,Pepti TSPN,tsp_3,SS,TM,SEA,TSPN	3.8
25	426433	L38969	Hs.169875	thrombospondin 3 - hypothetical protein DKFZp7611	SS	3.8
23	431626 430956	AL035681 Al183529	Hs.265327 Hs.2706	giutathione peroxidase 4 (phos	GSHPx,SS,TM,ABC_tran	3.8
	450998	BE387614	Hs.25797	splicing factor 3b, subunit 4,	SS,TM,sugar_tr,histone	3.8
	434899	BE613631	Hs.283565	FOS-like antigen-1	bzip,ss,bzip,cofilin_ADF, erg4_erg24,ss,tm	3.8 3.8
20	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	SS,TM,CPSF_A	3.8
30	411090 452135	BE165650 Al492175	Hs.339697 Hs.21446	VPS28 protein KIAA1716 protein	SS,DIX,PDZ,DEP,Dishevelle	3.8
	421339	AA070224	Hs.103561	SRp25 nuclear protein	'SS	3.7
	406535			Target Exon	SS,TM,Ribosomal_S19e,ig,I	3.7 3.7
26	447281	AA017018	Hs.18021	hypothetical protein FLJ20446	SS,SS,Teklin,Piwl,PAZ SS,TM	3.7
35	433126	AB021262	Hs.99816 Hs.155165	beta-catenin-interacting prote zinc finger protein-like 1	PHD,SS,TM,DnaJ,ERG4_ERG24	3.7
	425215 420536	AF030291 AL117455	Hs.275438	histone deacetylase 7A	Hist_deacetyl,SS,Hist_dea	3.7
	417998	AW967420	10.210100	gb:EST379495 MAGE resequences,	SS,TM	3.7
4.0	430890	X54232	Hs.2699	glypican 1	Glypican,SS SS,GTP_CDC,SS,TM	3.7 3.7
40	427863	AF189712	Hs.181002	MLL septin-like fusion Homo saplens ubiquitin conjuga	SS.TM	3.7
	448606 421961	BE613362 AB032993	Hs.109929	likely homolog of rat GRIP-ass	TM,K_tetra,ion_trans,HLH,	3.7
	410293	AK000047	Hs.61960	hypothetical prolein	K_letra,SS	3.7
	425233	Z17861	Hs.155218	E1B-55kDa-associated protein 5	SPRY,SAP,SS,TM,SPRY,SAP,p	3.7 3.7
45	423683	BE388699	Hs.4188	hypothetical protein MGC10812	SS,Peptidase_C15,TGF-beta SS,cpn60_TCP1	3.7
	415697	AI365603 Y18024	Hs.78605 Hs.78877	DKFZP56611024 protein Inositol 1,4,5-trisphosphate 3	SS S	3.7
	415825 418052	AA350659	Hs.83347	angio-associated, migratory ce	WD40,Bacterial_PQQ,TM,UPF	3.7
	444706	AK000398	Hs.11747	hypothetical protein FLJ20391	SS,SS,TM	3.7 3.7
50	407381	AA420659	Hs.183110	ESTs, Weakly similar to ALUC_H	SS,TM TM	3.7
	423432 444982	BE252996 AK002182	Hs.44067 Hs.12211	ESTs GDP-fucose transporter 1	SS,TM,DUF6,SS,TM	3.7
	407777	AA161071	Hs.71465	squalene epoxidase	SS,TM,Monooxygenase	3.7
	422715	AA332178	Hs.119403	hexosaminidase A (alpha polype	Glyco_hydro_20,Glyco_hydr	3.7 3.7
55	422609	Z46023	Hs.118721	sialidase 1 (lysosomal sialida	SS,TM,BNR,SS,TM,SET,HSP70 MCM,RIP,SS,zf-C2H2,KRAB	3.7
	414732 452579	AW410976 AA131657	Hs.77152 Hs.23830	minichromosome maintenance def ESTs	SS,CN_hydrolase	3.7
	419032	W81330	Hs.58643	ESTs, Highly similar to JAK3B	SS.pkinase,SH2,Insulin.pk	3.6
	411165	NM_000169	Hs.69089	galactosidase, alpha	Melibiase, Ribosomai_L44,z	3.6 3.6
60	444000	A1095034	Hs.135528	ESTs Homo sapiens, clone IMAGE:3050	ss,hlh ss,tm	3.6
	441174 429491	BE312775 NM_012111	Hs.294005 Hs.204041	chromosome 14 open reading fra	SS	3.6
	438433	AB018274	Hs.6214	KIAA0731 protein	SS	3.6
	425162	BE514851	Hs.154886	choline kinase-like	Cem_acyltrensf,Choline_k AAA_NB-ARC.TM	3.6 3.6
65	429671	BE379335	Hs.211594	proteasome (prosome, macropain	zt-C2H2,SS,mm,ENTH	3.6
	421018	A1569028 NM_013442	Hs.129888 Hs.3439	hypothetical protein FLJ14768 stomatin-like 2	Band_7,SS,TM,AAA,cdc48_N,	3.6
	433604 451544	AK000429	Hs.26570	hypothetical protein FLJ20422	SS,TM,COX3,SS,TM,SRF-TF	3.6
	444369	AV649296	Hs.282793	ESTs	SS hate textended SC to:	3.6 3.6
70	406660	X65371	Hs.172550	polypyrimidine tract binding p	rm,beta-lactamase,SS,try SS,TM,bromodomain,abhydro	3.6
	456503	AW977779	Hs.194613	ESTs cat eye syndrome chromosome re	SS,SS,TM,A_deaminase	3.6
	451711 425394	AK000461 AA356730	Hs.26890 Hs.323949	kangai 1 (suppression of tumor	SS,TM,transmembrane4	3.6
	428011	BE387514	Hs.181418	KIAA0152 gene product	Acyl-CoA_dh,SS,efhand	3.6 3.6
75	407627	AJ419020	Hs.62620	chromosome 6 open reading fram	SS SS,Syja_N,Exo_endo_phos	3.6
	436437		Hs.5811	chromosome 21 open reading fra tuberous scierosis 2	Rap_GAP,Tuberin,Peptidase	3.6
	419418 440300		Hs.90303 Hs.8859	Homo sapians, Similar to RIKEN	SS	3.6
	448136		Hs.20447	protein kinase related to S. c	pkinase,PBD	3.6 3.6
80	435977	AL138079	Hs.5012	brain-specific membrane-anchor	SS,TM,SS,TM,ubiquilin,Rib pkinase,PH,pkinase_C	3.6
	419095		Hs.188715 Hs.17936	ESTs DKFZP434H132 protein	SS	3.6
	447267 418054		Hs.83354	lysyl coddase-like 2	SRCR,Lysyl_oxidase,SS,TM,	3.6
	444354		Hs.10927	hypothetical protein R33729_1	SS	3.6
				242		

	429098	AF030249	Hs.196176	encyl Coenzyme A hydratase 1,	ECH, Herpes_V23, SS, Gal-bin	3.6
	430622	BE616971	Hs.247478	Homo sapiens, Similar to DNA s	G-patch, SS, TM, ubiquitin, a	3.6
	440675	AW005054	Hs.47883	ESTs, Wealdy stmilar to KCC1_H	pidnase	3.6 ·
	409678	NM_005632	Hs.55836	small optic lobes (Drosophila)	TM,Peptidase_C2	3.6 3.6
5	413097	BE383876	Hs.75196	ankyrin repeat-containing prot	enk,SET,SS,TM,pkinase,SH2 HECT,SS,HECT	3.6
	427579	AA366143	Hs.179669	hypothetical protein FLJ20537 Interferon-Induced protein 35	SS,ras,Ribosomat_L27e,KOW	3.5
	409154	U72882 BE613248	Hs.50842 Hs.172084	Homo sapiens, clone IMAGE:3627	SS,PtD,SH2	3.5
	448528 444426	AL121105	Hs.11170	RNA binding motif protein 14	mm,SS,spectrln,PH,mm,so	3.5
10	409297	R34662	Hs.53066	hsp70-interacting protein	SS	3.5
	441138	T56785	Hs.10101	hypothetical protein FLJ12875	SS	3.5 3.5
	435169	AF148509	Hs.279881	mannosidase, alpha, class 1B,	TM, Glyco_hydro_47	3.5
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	TM,SS,TM,SRCR,Glyco_trans SS	3.5
1.5	403325		11 5000	C2000428*:gij7705383[ref]NP_05	TM,UL21,Lipoprotein_6,GBP	3.5
15	437895	AB014568	Hs.5898 Hs.57100	KIAA0668 protein Homo sapiens mRNA for FLJ00016	SS,Synuclein	3.5
	449030	AI365582 · AF190746	Hs.170310	cat eye syndrome chromosome re	A_deaminase,SS,TM,Hydrola	3.5
	426542 439873	BE159253	Hs.300638	ESTs	SS	3.5
	428950	BE311879	Hs.194673	phosphoprotein enriched in ast	DED,SS,TM,Calsequestrin	3.5
20	421564	AB007864	Hs.105850	KIAA0404 protein	SS CONTRACTOR TELES	3.5
	441094	U33819	Hs.7647	MYC-associated zinc finger pro	SS,zf-C2H2,LIM,PHD,TFIIS.	3.5 3.5
	450007	BE270693	Hs.24301	polymerase (RNA) II (DNA direc	na,ss ss,tm	3.5
	422898	AL043101	Hs.127401	DKFZP434A163 protein; selectiv	WD40,SS,TBC,rrm	3.5
25	444914	AA046947	Hs.12142	`WD repeat domain 13 _lethal glant larvae (Drosophil	WD40,SS,TM	3.5
23	420178 418984	D50550 AA421401	Hs.95659	ribosomal protein L18	SS,TM	3.5
	414166	AW888941	Hs.75789	N-myc downstream regulated	Ndr,abhydrolase,SS	3.5
	409944	BE297925	Hs.57687	four and a half LIM domains 3	LIMSS	3.5
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate	SS	3.5
30	423599	A1805664	Hs.31731	peroxiredoxin 5	AhpC-TSA,SS,hormone_rec,z	3.5 3.5
	427715	BE245274	Hs.180428	KIAA1181 protein	TM,SS,TM,KOW SS,tubulin,SS	3.5
	405496			Target Exon chaperonin containing TCP1, su	cpn60_TCP1,SS,cpn60_TCP1	3.5
	417911	AA333387	Hs.82916 Hs.269468	ESTs, Moderately similar to AL	SS.UCH-2,UCH-1	3.5
35	433620	AA604520 AF052155	ns.205400 Hs.227949	SEC13 (S. cerevisiae)-like 1	WD40,SS,TM,E1-E2_ATPase,C	3.5
22	430053 458687	AW024815	Hs.170088	GLUT4 enhancer factor	SS	3.5
	424679	AL117477	Hs.119960	DKFZP727G051 protein	chromo,SS	3.5
	417360	AW651703	Hs.82023	hypothetical protein similar t	SS,TM,GDA1_CD39,GDA1_CD39	3.5
	439641	AJ251317	Hs.33184	ESTs	SS,TM,GYF,actin,PA	3.5 3.5
40	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,Armadillo_se complex1_49Kd,SS,TM,ITAM,	3.4
	427117	BE258946	Hs.173611	Target CAT	SS;mito_carr,SS,mito_carr	3.4
	422051	AW327546	Hs.111024	solute carrier family 25 (mito ESTs	SS	3.4
	422759	AA316582 U40998	Hs.224571 Hs.81728	unc119 (C.elegans) homolog	SS,glycolytic_enzy	3.4
45	417230 450158	AK001999	Hs.24545	hypothetical protein FLJ11137	SS,zf-C2H2,SCAN,TFIIS,SS	3.4
43	425421	L11669	Hs.157145	tetracycline transporter-like	SS,TM,SS,TM	3.4
	415515	F11327	Hs.167406	gb:HSC2VD101 normalized infant	SS	3.4
	427868	Al360119.comp	Hs.181013	phosphoglycerate mutase 1 (bra	PGAM,SS,TM,ldh	3.4 3.4
	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glu	SS,HSP70,homeobox,Hydanto SS,hemopexin,Filamin,NHL,	3.4
50	413014	AW250533	Hs.75139	partner of RAC1 (arfaptin 2)	SS,P5CR,EF1BD	3.4
	457655	AA622968	Hs.71574	hypothelical protein FLJ 14926 hypothelical protein FLJ 10597	PEP-utilizers,PEP-utilize	3.4
	419432	AK001459	Hs.90375 Hs.101408	branched chain aminotransferas	aminotran_4,TM	3.4
	421066 428038	AU076725 AW134756	Hs.192477	ESTs	SS,Exonuclease,zf-C2H2	3.4
55	430352	AW750535	Hs.50742	Homo saplens cDNA: FLJ23331 fl	TM	3.4
55	432647	Al807481	Hs.278581	fibroblast growth factor recep	lg,pkinase,SS,TM,lg,pkina	3.4
	421310	AW630087	Hs.103315	trinucleotide repeat containin	TM,zf-C2H2,SS,PHD	3.4 3.4
	420999	AA338903	Hs.100915	peroxisomal biogenesis factor	SS SS,TM	3.4
60	409561	U58048	Hs.183138	procollegen (type III) N-endop DKFZP5640243 protein	Herpes_env,SS,TM,Peptidas	3.4
60	419727	AW160796	Hs.92700	ribosomal protein S6 kinase, 7	pkinase,pkinase_C,SS	3.4
	421267 411501	BE314724 AB002368	Hs.103081 Hs.70500	KIAA0370 protein	SS,TM,SS,TM	3.4
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	SS	3.4
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	SS,TM,trypsin	3.4
65	422808	AA449014	Hs.121025	chromosome 11 open reading fra	SS,TM,trypsin,CUB,ubiquit	3.4 3.4
	448173	N95657	Hs.6820	ESTs, Moderately similar to YO	SS SS.TM.homeobox,UM	3.4
	416535	H61851		gb:yr80e10.r1 Soares fetal liv	MHC_I,ig,SS,TM	3.4
	406656	M16714	Hs.181392	major histocompatibility compl	SS,abhydrolase_2	3.4
70	435669	AI867781	Hs.31819 Hs.68257	HT014 general transcription factor (SS,TM,TGF-beta	3.4
70	411077	AW977263 AW327785	Hs.173421	KIAA1564 protein	SS,Peptidase_M24	3.4
	427062 421890	AW959488	Hs.21732	ESTs	SS,zf-C3HC4,SPRY	3.4
	412968	AW500508	Hs.75102	alanyl-tRNA synthetase	DHHA1,SS,IRNA-synt_2c,DHH	3.4
-	439496	BE616501	Hs.32343	Homo saplens, Similar to RIKEN	SS MEDIA CC TM Combania State	3.4 3.3
75	433659	AK001301	Hs.3487	hypothetical protein FLJ10439	WD40,SS,TM,Syntaxin,Synta	3.3
	447578	AA912347	Hs.136585	ESTs, Wealdy similar to JC5314	SS SS,TM	3.3
	441722	AW960504	Hs.173103	FE65-LIKE 2	DSPc,SS,imiC,F-box	3.3
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515 hypothetical protein FLJ20337	SS,TBC,FHA,zI-C3HC4	3.3
80	451714	AK000344	Hs.26898 Hs.346742	hypothetical protein MGC3260	SS,TM	3.3
90	410633	8E546789 BE298441	Hs.287361	ADP-ribosylation factor relate	arf,ras,SS,arf,Stathmin	3.3
	410609 414775		Hs.172702	ESTs, Weakly similar to (defil	SS.PCI	3.3
	428495		Hs.184640	hypothetical protein MGC10781	SS,TM,XPG_N,XPG_L,5_3_exo	3.3 3.3
	429215		Hs.2364	GLI-Kruppel family member HKR3	zf-C2H2,BTB,TP2,K_tetra,S	2.3

	446618	AL110307	Hs.15591	COP9 subunit 6 (MOV34 homolog,	MOV34,SS,zI-C2H2,SCAN	3.3
	444858	BE560471	Hs.12101	hypothetical protein	SS,PCI	3.3
	430041	AW247237	Hs.227835	KIAA1049 protein	SS,TM,7tm_1,tubulin	3:3 · 3.3
_	416950	AL049798	Hs.80552	dermatopontin	SS AAA_Sigma54_activat_SS,TP	3.3
5	431203	AW248421	Hs.250758 Hs.278675	proteasome (prosome, macropain bromodomain-containing 4	bromodomain, SS, TM, SNF2_N,	3.3
	432714 415674	Y12059 BE394784	Hs.78596	proteasome (prosome, macropain	SS,proteasome,SS,TM,Cadha	3.3
	426152	BE299190	Hs.167246	P450 (cytochrome) oxidoreducta	flavodoxin,FAD_binding,SS	3.3
	418440	NM_006936	Hs.85119	SMT3 (suppressor of milf two 3,	ublquitin,SS,UQ_con	3.3 3.3
10	410545	U32324	Hs.64310	Interleutin 11 receptor, alpha	lg,fn3,SS,TM,GalP_UDP_tra transmembrane4,cyclin,SS,	3.3
	409428 443121	M33680 Z19287	Hs.54457 Hs.9006	CD81 antigen (target of antipr VAMP (vesicle-associated membr	TM,MSP_domain	3.3
	453856	AAB04789	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb	3.3
	430137	NM_005456	Hs.234249	millogen-activated protein kina	SS,SH3,PID,SS,PID	3.3
15	446427	AW295863	Hs.119632	ESTs	SS fn3,lg	3.3 3.3
	400747	AE467670	Hs.12912	Target Exon skb1 (S. pombe) homolog	SS,SS	3.3
	445580 452568	AF167572 AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp5	SS,mm,Ephrin,pkinase,ATP	3.3
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via d	death, DED, SS, TM	3.3
20	401655			Target Exon	SS 22 225	3.3 3.3
	429460	D56263	Hs.203238	phosphodiesterase 1B, calmodul	PDEase,SS,PDEase	3.3 3.3
	416448	L13210	Hs.79339	lectin, galactoside-binding, s mitochondrial carrier homolog	SRCR,SS,TM TM,mito_carr,TM	3.3
	433038 440251	AF192559 AW796016	Hs.279939 Hs.332012	Homo saplens, clone IMAGE:3687	SS,TM,SS,TM,IRK	3.3
25	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo b	SS,homeobox,SS	3.3
	432941	W04803	Hs.279851	hypothetical protein FLJ10241	SS,RNase_PH,RNase_PH_C	3.3
	441244	BE612935	Hs.184052	PP1201 protein	SS,TM,WD40	3.3 3.3
	438175	AJ376727	Hs.122110	ESTs	SS,TM,trypsin,kringle,fn2 SS,TM,CD36,CD36	3.3
30	423024	AA593731 AW675298	Hs.325823 Hs.233694	ESTs, Moderately similar to AL hypothetical protein FLJ11350	SS	3.3
20	430120 419571	AW674962	Hs.91146	protein kinase D2	pkinase,DAG_PE-bind,PH,DC	3.3
	413019	BE281604	Hs.75140	low density lipoprotein-relate	SS	3.3
	400299	X07730	Hs.171995	kaliikrein 3, (prostale specif	trypsin,SS,trypsin,trypsi	3.3 3.2
25	433519	BE263901	11 1000	ESTs, Weakly similar to S37431	SS,TM Peplidase_M16,HCO3_cotran	3.2
35	434702	AL039734	Hs.4099 Hs.273385	nardilysin (N-arginine dibasic guanine nucleotide binding pro	G-alpha,arf,SS,G-alpha	3.2
	422242 430480	AJ251760 AL079399	Hs.241543	DKFZP586F1524 protein	SS,TM,hemopexin,Somatomed	3.2
	452438	BE514230	Hs.29595	JM4 protein	8S,TM,KOW,HLH	3.2
	456939	AA431633	Hs.163867	NM_002488*:Homo saplens NADH d	SS,tRNA-synt_2b,WHEP-TRS,	3.2 3.2
40	421009	AL049709	Hs.343357	Human DNA sequence from clone	TM SBF,SS,TM,G6PD,G6PD_C,hex	3.2
	411969	X12458 N54708	Hs.72980 Hs.303025	Protein P3 chromosome 11 open reading fra	6S	3.2
	409197 417896	AA379770	Hs.82890	defender against cell death 1	DAD,SS,TM	3.2
	418026	BE379727	Hs.83213	fatty acid binding protein 4,	lipocalin,SS,lipocalin	3.2
45	409057	AA702305	Hs.180060	ESTS	SS,TGFb_propeplide,TGF-be	3.2 3.2
	437869	W91976	Hs.290834	ESTs	SS,TM,SH3,zf-C3HC4 SS,TM	3.2
	413211	AW967107 Al393498	Hs.109274	hypothetical protein MGC4365 Inositol 1,4,5-triphosphate re	SS,CTF_NFI	3.2
	425080 445363	NM_005993	Hs.12570	tubulin-specific chaperone d	ATP-synt_B,HEAT_PBS,SS,TM	3.2
50	421943	BE616520	Hs.343912	Homo sapiens, Similar to RIKEN	SS,TM,SS,TM	3.2
	443337	Y07604	Hs.9235	non-metastatic cells 4, protei	NDK,SS,adh_short,NDK	3.2 3.2
	418885	D17530	Hs.89434	drebrin 1	cofilin_ADF,SS,cofilin_AD pkinase,SS	3.2
	411817	BE302900 BE271020	Hs.72241	mitogen-activated protein kina tumor suppressor deleted in or	SS,TM	3.2
55	413891 449455	T60748	Hs.278408	hypothetical protein	TM	3.2
<i>JJ</i> .	419193	D29643	Hs.34789	dolichyl-diphosphooligosacchar	SS,TM,DDOST_48kD,VP7,SS,T	3.2
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	SS,TM,UDPGT	3.2 3.2
•	436467	AW450278	Hs.91681	ESTs, Weakly similar to DCHUO	SS,tRNA-synt_1b,tRNA_bind S1,SS	3.2
60	446334 410270	U52427	Hs.14839 Hs.195727	polymerase (RNA) II (DNA direc tumor endothellal marker 1 pre	SS,TM,EGF,lectin_c,sushi,	3.2
UU	445411	AF279142 AL137255	Hs.12646	hypothetical protein FLJ22693	SS,hormone_rec,zf-CCCH	3.2
	458018	A)199575	Hs.37716	ESTs	SS,TM,OxysteroLBP	3.2
	426530	U24578	Hs.278625	complement component 4A	SS,A2M,NTR,A2M_N,prenyltr	3.2 3.2
65	445604	T08566	Hs.12956	Tax interaction protein 1	PDZ,SS,TM,P2X_receptor,FG SS,PDZ,LIM,pkinase	3.2
65	443402	U77846 BE410937	Hs.2985	elastin (supravalvular aortic emerin (Ernery-Dreifuss muscula	LEM, SS, Ribosomal_L10e, Acy	3.2
	432416 429662	AI929701	Hs.211586	phospholnosilide-3-kinase, reg	SH2,SH3,RhoGAP,SS,GILT,SH	3.2
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolo	SS,TM,Fz,Frizzled,7tm_2,S	3.2
	427729	AB033100	Hs.300646	KIAA1274 protein (similar to m	SS Phoces DOVIDUOS TM Dibon	3.2 3.2
70	418151	AA864238.comp	Hs.83583	actin related protein 2/3 comp mitochondrial ribosomal protei	RhoGEF,REV,PH,SS,TM,Ribos Ribosomal_S2,SS,lipocalin	3.2
	448250	NM_016034	Hs.20776 Hs.136280	Homo sapiens cDNA: FLJ22288 fi	SS.Exonuclease	3.2
	431158 414292	AW859138 BE388407	Hs.75875	ubiquilin-conjugating enzyme E	UQ_con,SS,TM,SAM_PNT	3.2
	406307			Target Exon	SS,TM,7tm_2,SS,TM,7tm_2,G	3.2
75	423325	R55565	Hs.347286	hypothetical protein FLJ22427	SS,TM,Surp,ubiquitin,TBC	3.2 3.1
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis vir	na,ss Ss	3.1
	419069	AA233801 BE396150	Hs.6945	ESTs, Weakly similar to CA13_H mitochondrial ribosomal protei	SS,TM	3.1
	431717 448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp4	RhoGAP,SS,TM,SET,zf-CXXC,	3.1
80	419394	AB011124	Hs.90232	KIAA0552 gene product	SS,lg	3.1
	436240	BE388673	Hs.5086	hypothetical protein MGC10433	SS,TM,Ets,COX6B,transmemb TPR,SS,TM,DnaJ	3.1 3.1
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein adenosine monophosphale deamin	A_deaminase,SS,G-alpha,GS	3.1
	417920 421819	S47833 NM_013403	Hs.82927 Hs.108665	zinedin	WD40,pkinase,pkinase	3.1
	741013					

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	426362	BE267158	Hs.169474	DKFZP586J0119 protein	IF-2B,SS,PP2C	3.1
	408917	AW249025	Hs.7768	fibroblast growth factor (acid	SS,bZIP,cofiln_ADF,EGF	3.1
	443099	A1372836	Hs.9003	hypothetical protein FLJ13868	TM	3.1
-	427022	AW245839	Hs.173255	small nuclear ribonucleoprotei	mm, SS, rm, SH3, res, 20G-Fe	3.1
5	452711	AW967047	Hs.293224	ESTs, Weakly similar to T00375	SS	3.1
	407236	W79485	Hs.173980	nuclear matrix protein NMP200	WD40,SS,TM,PTR2,7tm_1	3.1
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	SS,SNF2_N,helicase_C	3.1
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fi	SS	3.1
	447629	AF034790	Hs.19105	translocase of Inner mitochond	Tim17,SS,TM,pkinase,OTU	3.1
10	401097			C12000858*:gi]7353437[ref]NP_0	SS,TM,7tm_1,SS	3.1
	452736	C01164	Hs.4232	Homo sapiens PAC clone RP1-130	SS,SS,TM,TBC,Surp,ubiquit	3.1
	435507	Al143579	Hs.26510	vacuolar protein sorting 338 (SS,Sec1,Sec1	3.1
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial	PPR,SS,TM,cNMP_binding,RN	3.1
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6	SS,TM,kazal,Ribosomal_S8,	3.1
15	409858	NM_006586	Hs.56828	trinucleotide repeat containin	SS,SS,TM,B56	3.1
	424582	AF026849	Hs.150922	BCS1 (yeast hornolog)-like	AAA,SS,PI-PLC-X,PH,PI-PLC	3.1
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	SS	3.1
	417947	AA323563	Hs.325309	hypothetical protein FLJ14598	SS,TM,PTPA	3.1
	409283	NM_004860	Hs.52788	fragile X mental retardation,	KH-domain,SS,TM,HMG_box	3.1
20	412813	AF086947	Hs.74617	dynactin 1 (p150, Glued (Droso	CAP_GLY,SS	3.1
-	456535	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B,SS,p450,actin	3.1
	432482	L19267	Hs.275924	dystrophia myotonica-containin	WD40,SS,pkinase,pkinase	3.1
	437256	AL137404	Hs.97871	Homo sapiens, clone IMAGE:3845	TM,SS	3.1
	440191	AJ990417		tubulin, beta 5	SS,formiminotr,prenyltran	3.0
25	407972	AA827639	Hs.18587	- KIAA1588 protein	SS,TM	3.0
	420890	AA434058	Hs.100071	6-phosphogluconolactonase	Glucosamine_Iso,SS	3.0
	440060	AI696387	Hs.126451	ESTs, Weakly similar to A46302	SS	3.0
	452222	AW806287	Hs.21432	SEX gene	SS,TM,Sema,TIG,PSI,GDI	3.0
	401772			NM_014520:Homo saplens MYB bin	SS	3.0
30	453754	AW972580	Hs.172753	ESTs	SS,TM,ras,Ribosomal_S19,T	3.0
	423865	H05202	Hs.133968	FGF receptor activating protei	SS,TM	3.0
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma	SS,TM	3.0
	441954	AI744935	Hs.8047	Fanconi anemia, complementatio	TPR,SS,TM,AAA,cdc48_N,Ban	3.0
	412787	D87452	Hs.74579	KIAA0263 gene product	zf-CCCH,SS,TM,NTP_transfe	3.0
35	422034	AC006486	Hs.333069	Ets2 repressor factor	Ets,SS,pkinase,PAF-AH_lb	3.0
	450788	AI738410	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	ESTs	SS,TM	3.0
	452511	BE408178	Hs.285165	Homo saciens cDNA FLJ20845 fis	SS, Ihiored, P5CR	3.0
	414380	BE391815	Hs.75981	ubiquilin specific protease 14	UCH-2,UCH-1,ubiquitin,SS	3.0
	407597	AA043925	Hs.339352	Homo saplens brother of CDO (B	SS,TM,SS,TM	3.0
40	434955	BE276128	Hs.284286	mitochondrial ribosomal protei	SS	3.0
••	435632	AF220049	Hs.43549	uncharacterized hematopoletic	SS.UQ_con	3.0
	432465	D56165	Hs.275163	non-metastatic cells 2, protei	NDK.SS.NDK	3.0
	430526	AF181862	Hs.242407	G protein-coupled receptor, fa	7tm_3,homeobox,SS,TM	3.0
	453412	AJ003290		gb:AJ003290 Selected chromosom	pkinase	3.0
45	446456	BE613933	Hs.15106	chromosome 14 open reading fra	UPF0143.SS	3.0
73	433180	AB038651	Hs.31854	K562 cell-derived leucine-zipp	TM,Acetyltransf,TM,Acetyl	3.0
	447322	BE617649	Hs.77690	RAB5B, member RAS oncogene fam	SS.oxidored_molyb,heme_1,	3.0
	422268	N25485	Hs.330310	matemal G10 transcript	G10,SS,WD40	3.0
	419578	AF064853	Hs.91299	quanine nucleolide binding pro	WD40.SS.EPO_TPO	3.0
50	446929	AA076132	Hs.9460	Homo sapiens mRNA; cDNA DKFZp5	SS,TM,WD40	3.0
20	770323	747010104	16.5700	Transcription to an alama and about	2-11	

TABLE 218: Pkey: Unique Eos probeset Identifier number CAT number: Gene duster number

55	Accession:	Genbank acces	sion numbers
60	Pkey 408215	CAT Number 10478_1	Accession BE614290 AA307674 N35629 AA338538 A1193603 AA781096 A1680061 A1613258 AW276647 BE221263 A1348910 A1965031 A1090078 A1359617 AA666391 A160210 A1446461 A1355345 A1343638 A1343640 A1275091 M78746 AW262795 AW250002 AA503756 A1934519 AW272086 N26520 AA626639
	409938 411674	116091_1 1253746_1	AW974648 AA652153 AA649671 AA078582 AW861123 AW861125 AW856717 AW861116 AW856706 AW856788 AW856774 AW856787 AW856780 AW856782 AW856789 AW856772 AW856784 AW856786 AW856776 AW856635 AW856767
65	413052 413837	1347214_1 139363_1	BE249841 BE062657 BE062771 BE052636 BE062813 BE062699 BE062895 BE062747 BE062719 BE293541 AW163525 AW163285 AW163385 AI929359 BE279279 AA132590 AW157329 AA584408 AW157252 AI692198 AW003514 T24436 AI765658 AW157459 AI810740 AI659582 AI969924 AI929284 AI340993 AI349083 AW299522 AW664650 AW299513 AA132529 AI340991 AI912836 AI341283 AI650609 AA279
70	413891	139759_1	BE271020 A1763358 AJ925430 AJ806151 AW003726 T15590 AA649945 AW129911 AJ570748 T57492 AA828002 AW237602 AW003539 AJ139045 AJ950958 BE042625 AW778973 AJ287859 AJ983931 AW515101 AW150029 AJ358496 AJ621173 AA846016 AJ470921 AW169748 AJ991000 AW513748 AJ04058
	414023 416535	1410860_1 1599332_1	BE243828 BE245081 BE247016 BE241984 BE241534 BE246091 BE245679 BE243620 BE245998 BE242329 BE241417 BE241457 BE242522 BE241989 BE241464 H61851 H74099 T67099
75	417998 418984	171375_1 181094_1	AW967420 AA210915 AA236991 AA210916 AA421401 T49326 AA330568 AA328941 W63573 AA758023 AA976306 H52254 AA877107 BE207784 AW664584 AI924890 AA458586 AI422142 AI891097 AI811174 R69866 T49327 AA233722 AA631138 AA910314 AI379416 AI129321 AA861574 AA635649 AI339443 AW009533 AA677036 AA948287 AA62
	419069	181650_3	AA233801 BE383487 AA913939 AI632681 AI813277 AI373652 AW134802 AI863574 AW305364 AI858557 AI670746 AI015036 AI935384 AI935317 AW138668 AW204971 AI765223 AA884146 AA973341 AA234062
80	419250	183289_2	AW770185 AW296271 H11254 AW403510 Al032786 AA767048 AI376115 Al582209 AA460965 Al886663 Al016900 R05715 Al127382 Al660953 Al023644 H00465 AW959578 AA815039 AW292253 R05714 AA815462 AA235654 AA481274 W24933 AA300091 H00515
	420160 421572	191054_1 204022_1	A1492840 A1287657 AA255989 A1698206 A1468558 AA531607 A1565370 A1376907 A1811618 AW138145 AW139465 AA421658 AA293069 AW118141 A1214980 AW663502 A1343486 A1553789 AA650416 A1498947

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Z92546 AA330586 AI570568 AW341487 AI8Z7050 AW298668 AI792189 AU015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA6Z7504 H16914 AA358477 AA338009 AI393498 R42314 AI088818 AI696468 AA18641 AA573152 F08817 AI910796 AW338934 R39024 AA729145 BE245956 AI093722 AA541730 F08835 AI24Z755 AA350447 AA855667 T93903 AW081029 AA493711 AA650030 N35995 N21491 T57002 Z25379 AI906851 BE270447 AW409921 BE207248 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719 BE268715 BE518716 BE31876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879 BE296373 BE510736 A200724
                   423696
                                            23112_1
                    425080
                                             246559_1
  5
                                             27647 1
                   427239
                                                                       BE269633 BE621936 AA290724
W60675 AK001212 AA155752 AA878366 AA090872 AB033013 AW249107 AA031890 AA112820 AW366388 N55156 AA326756 AW952294
AA180820 C03570 C04358 W60678 AW248674 AA034989 AA044781 AA074274 H26212 AI800572 AI127583 AI951785 AA856557 AI571746
                    427391
                                             27815_1
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10
                                                                       AW879141 AA421182 A1734104 A1733923 AA430600
AI824164 AI676005 AW129612 AI825903 AA773987 AI823645 AI823860 AA456229 AI824295 AA454622 AI264049 AI090237 AI669787 AI804012
AI306153 W96164 AI298273 AW884073 AW883986
                    428092
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                    429545
                                               305902_1
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                    430168
                                              313927_1
15
                    433519
                                               368801_2
                                               46360_1
                     438707
                     440191
                                               48804 3
                                                                        U77846 AA479373 AA346348 AA348194 M26867 AA728901 AA715367 AA377787 R64236 Al752721 R77311 AA339685 BE074254 AW938712 AW068444 AA330624 AA347098 AA327507 AW391973 AA495763 AA479278 AW605018 T19644 Al204484 AW834745 AW081309 AW090002
20
                    443402
                                               5681_1
                                                                         AJ095659 AJ131556 AJ56
                                                                         AA457456 AA907921 Al567715 AA579472 T64216 AA373128 F35533 AA722113 T64403 AA653738 F28806 AA595689 AA047537 AA022499
                      444590
                                               6116 1
                                                                         AW440532 F36782 Al554180 Al183767 Al806052 AA160379 AA481678 Al185031 Al148988 Al174482 AA868833 Al674395 AA481440 Al914985
                                                                         AIG98771 AA44
BE246743 AA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 AI399986 R50073 R48743 AI769689
AI863005 AA317806 AI678000 AW189963 AI986207 AW471273 R73463 AI335104 AI590161 AI469257 AI954604 H21954 T25141 AA856793
 25
                      445625
                                               64558_1
                                                                          R50074 Al708253 Al2
                                                                          BE613362 AA447862 H72036 AA393664 AI681334 AW139128 AA932579 AI302241 AI936800 AW960628 AI492148 C06192 AA336107 AA808008
AW615212 BE297403 BE298978 AI187207 AA928695 AI820631 AA938128 AI346527 AI040261 AA808401 AW130326 AI440313 AA868693
                      448606
                                               77159 1
 30
                                                                          Al653329 Al33246
                                                                          Al560769 Al857497 AW151454
                      448677
                                                775217_1
                                                                          Al738410 AW016905 AJ971725
                      450788
                                                846840_1
                                                                          BE378541 Al853051
                       452160
                                                901991_1
                                                                          AJ003290 AJ003288 AW276947
T70192 BE147696
 35
                       453412
                                                966264_1
                      455857
                                                1376021_1
                                                                          BE170313 BE158339 BE158290
                                                 1383899_1
                       455928
                                                                          AW377258 BE067468 BE067511 BE067515 BE067467 BE067514 AA397442
                                                274445_1
                       457022
  40
                       TABLE 21C:
                      Presy: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
                       Strand: Indicates DNA strand from which exons were predicted
                       Nt_position: Indicates nucleotide positions of predicted exons
  45
                                                                                                      Nt_position
                                                                            Strand
                                                  Ref
                        400460
                                                  8389428
                                                                           Plus
                                                                                                      35559-36295
                                                                                                      81941-82434
                        400563
                                                 9844011
                                                                           Plus
  50
                       400747
400846
                                                  7329330
                                                                            Minus
                                                                                                      71249-71441
                                                  9188605
                                                                            Plus
                                                                                                      39310-39474
                                                                                                      60356-61096
                        401097
                                                  9965518
                                                                            Minus
                                                  8699792
                                                                                                      37349-37885
79556-80132
                        401128
                        401655
                                                  9099093
                                                                            Plus
    55
                                                  8134856
9828651
                                                                                                       54342-54482
                         401727
                                                                            Plus
                                                                                                        139165-139322
                                                                            Plus
                         401751
                                                                                                        183917-184042
                                                  9966243
                                                                             Plus
                         401772
                         402365
                                                   9454515
                                                                             Minus
                                                                                                       70928-71185
                                                   9796896
                                                                             Minus
                                                                                                       8818-8952
                         402463
                                                                                                        11824-12090,14290-14544
    60
                                                  8077033
6136940
                         402665
                                                                             Minus
                                                                                                        69012-69165
                                                                             Minus
                         402793
                                                                                                        361-474,541-687
                                                   7406502
                                                                             Minus
                         402916
                                                                                                        114150-114272
109763-109926
                         403028
                                                    7670577
                                                                             Minus
                         403325
                                                   8440025
                                                                             Minus
                                                                                                         146931-147796
     65
                                                                             Plus
                         404256
                                                   9367203
                                                                                                         168236-168795
                                                    7229907
                                                                             Minus
                         405189
                          405325
                                                    6094661
                                                                              Minus
                                                                                                        25818-26380
                                                                                                        36116-36276
                                                    2155224
                                                                             Plus
                          405356
                                                                                                         147706-148062
                          405496
                                                    8468968
                                                                             Plus
     70
                                                                                                         125325-125831
```

Table 22A lists about 811 genes up-regulated in ovarian cancer compared to normal adult lissues that are likely to encode extracellular or cell-surface proteins. These were Table 2ZA usis about this genes up-regulated in ovarian cancer compared to normal adult issues that are likely to encode extracerular or cau-surface proteins. These were selected as for Table 2OA, except that the ratio of "average" ovarian cancer to "average" normal adult lissues was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 95th percentile value amongst various ovarian cancer spectmens, the "average" normal adult lissue level was set to the 75th percentile value amongst various normalignant lissues, the "average" ovarian cancer value was greater than or equal to 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of transducing an intracellular signal, or of being modulatable by small molecules (e.g., pkinase, peptidase, phosphatase, or ion_transporter). Predicted protein 75 80 domains are noted.

TABLE 22A:

406101

406307

406535

Pkey: Unique Eos probeset identifier number

9124019

8576099

7711477

Plus

Plus

95473-95585,98900-99180

B3135-B3362

ExAcon: Exemplar Accession number, Genbank accession number

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UnigenelD: Unigene number Unigene Title: Unigene gene title Protein Dom.: Predicted protein domain R1: Ratio of turnor to normal body tissue

5	111. 14000 01	W.1101 W 1701111	- 000, 000			
J	Pkey	ExAcon	UniGene ID	Unigene Titla	Protein Dom.	R1
	407223	H96850		gb:yw03b12.s1 Soares malanocyt		58.9
	430281	AI878842	Hs.237924	CGI-69 protein	milto_carr	46.7
	410418	D31382	Hs.63325	transmembrane proteasa, serine	ldi_recept_a,trypsin	41.0
10	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH	37.1
	438424	At912498	Hs.25895	hypothetical protein FLJ14996		35.3 35.2
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3	28.2
	453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C	28.2
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB	27.9
15	451721	NM_006946		spectrin, beta, non-erythrocyt	spectrin,PH,CH	27.9
	416819	U77735	Hs.80205	pim-2 oncogene	pkinase HCO3_cotransp	27.7
	430397	AI924533	Hs.105607	bicarbonate transporter relate	PAP2	26.7
	450334	AF035959	Hs.24879	phosphatidic acid phosphatase	lipoxygenase,PLAT	25.3
20	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	MAPEG	25.1
20	424420	BE614743	Hs.146688	prostaglandin E synthase	efhand	24.4
	412674	X04106	Hs.74451	calpain 4, small subunit (30K)	FKBP	24.3
	430023	AA158243	Hs.227729	FK508-binding protein 2 (13kD) laminin, alpha 5	laminin_EGF.laminin_G.EGF	24.0
	444672	Z95636	Hs.11669	annexin A11	annexin	23.1
25	413726	AJ278465	Hs.75510	inositol 1,3,4-triphosphate 5/	oxidored_nitro	23.0
25	438951	U51336	Hs.6453 Hs.196177	phosphorylase kinase, gamma 2	pkinase	23.0
	429099	BE439952 AF124249	Hs.268541	novel SH2-containing protein 1	SH2	22.4
	431765	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase	22.4
	422645	AF238083	Hs.68061	sphingosine kinase 1	DAGK¢	22.3
30	413436 422639	AI929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	21.5
20	429869	Al907018	Hs.15977	Target CAT		21.3
	418891	NM_002419		mitogen-activated protein kina	SH3,pkinase,pyridoxai_deC	21.1
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal	RYDR_ITPR,RyR,SPRY,lon_tr	21.0
	432866	BE395875	Hs.279609	mitochondrial carrier homolog	mito_carr	20.9
35	452875	BE275760	Hs.30928	DNA segment on chromosome 19 (Euk_porin	20.8
55	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cy	pro_isomerase	20.8
	402916	02020.00		ENSP00000202587*:Blcarbonate t	HCO3_cotransp	20.8
	425760	D17629	Hs.159479	galactosamine (N-acetyi)-6-sui	Sulfatase	20.7
	400419	AF084545		Target	EGF,ig,lectin_c,sushi,Xli	20.0
40	419444	NM_002490	5 Hs.90443	Target CAT	fer4	19.5
••	459133	U40343	Hs.29656	cyclin-dependent kinase inhibi	ank _	19.2
	447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	19.2
	422708	AB017430	Hs.119324	kinestn-like 4	kinesin,homeobox	19.0
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	18.8
45	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6	18.5
	425848	BE242709	Hs.159637	valyl-IRNA synthetase 2	GST_C,GST_N,Tropomyosin	18.4
	451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	18.1
	447859	AK002194	Hs.19851	peroxisornal biogenesis factor	040.051:-101-040	17.5 17.3
	426457	AW894667		chimerin (chimaerin) 1	DAG_PE-bind,RhoGAP	17.1
50	421612	AF161254	Hs.106196	8D6 antigen	kd_recept_a	16.9
	421363		1 Hs.103854	docking protein 1, 62kD (downs	PH,IRS	16.8
	442739		4 Hs.8679	cytosolic acyl coenzyme A thio	Acyl-CoA_hydro	16.8
	420568	F09247	Hs.247735	protocadherin alpha 10	cadherin	16.8
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp pkinase,KA1,UBA	16.7
55	425424		4 Hs.157199	ELKL motif kinase	kazal,OATP_N,OATP_C	16.5
	446329		2 Hs.14805	solute carrier family 21 (orga	myosin_head,Myosin_tail,I	16.4
	406620	M81105	Hs.146550	myosin, heavy polypepiide 9, n	PX,SH3,OPR	16.3
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4	PH,OxysteroLBP	16.2
κ'n	429183	AB014604		KIAA0704 protein	DSPc,Rhodanese	16.2
60	444664	N26362	Hs.11615	map kinase phosphatase-like pr	MIF Jate_protein_L2	16.2
	427640	AF058293		D-dopachrome tautomerase phosphomannomutase 2	PMM	16.0
	425123	AW205274		branched chain keto acid dehyd	E1_dehydrog	15.8
	416006	AA324251		mitogen-activated protein kina	pkinase	15.8
65	412942	AL120344		acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
U.S	423366	Z80345 AW16105	Hs.127610 Hs.169811	second mitochondria-derived ac	70). 00. Carp 0). 00. Care.	15.7
	426391			cytochrome P450, subfamily XXV	p450	15.5
	424568	AF005418 BE258876		polyamine-modulated factor 1	aldo_ket_red	15.5
	420029	AF234887		cadherin, EGF LAG seven-pass G	7tm_2,EGF,cadherin,lamini	15.4
70	433573 407619	AL050341		collagen, type IX, alpha 2	Collagen	15.3
70	427326	A1287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	7tm_1	15.2
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	_	15.1
	458130	AA11581		ras homolog gene family, membe	ras,ari	15.0
	449936	AA93829		hypothelical protein MGC11314	•	15.0
75	409230	AA85243		NM_021074:Homo saptens NADH de	complex1_24kD	14.7
, ,	423801	NM_0150		GTPase regulator associated wi	RhoGAP, SH3, PH	14.0
	419639	AK00150		hypothetical protein		13.6
	419298	AA85347		pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	13.6
	426108	AA62203		programmed cell death 5	DUF122	13.5
80	448133	AA72315		folate receptor 1 (adult)	Fotate_rec	13.5
50	418736	T18979	Hs.87908	Snf2-related CBP activator pro	helicase_C,AT_hook	13.5
	436543		212 Hs.5215	integrin beta 4 binding protei	elF6	13.3
	431515		152 Hs.258583	endothelial differentiation, I	7tm_1_	13.3
	429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDC-P	13.2

	431462	AW583672	Hs.256311	granin-like neuroendocrine pep		13.2
	444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	13.2 13.1
	423464	NM_016240		CSR1 protein	Collagen MIP	13.0
5	450787		Hs.25475 Hs.184877	equaporin 7 solute carrier family 25 (milto	mito_can	13.0
,	428539 436014		Hs.283741	exosome component Rrp46	RNasa_PH_RNase_PH_C	12.9
	416866		Hs.80324	serine/threonine protein phosp	Metallophos	12.9
	433867	AK000598	Hs.3618	hippocalcin-like 1	efhand	12.9 12.8
10	411408		Hs.69949	calcium channel, voltage-depen	ion_trans S_100,efhand	12.7
10	432329	NM_002962		S100 calcium-binding protein A caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	12.7
	447887 427448		Hs.19949 Hs.2157	Wiskoti-Aldrich syndrome (ecze	WH1,PBD,WH2	12.7
	428820		Hs.172631	integrin, alpha M (complement	FG-GAP	12.7
	446603	NM_014835		oxysterol-binding protein-rela	Oxysterol_BP	12.6
15	422633		Hs.118804	enolase 3, (beta, muscle)	endase	12.6 12.6
	445839		Hs.16244	mitotic spindle colled-coll re	Troponin HIT	12.5
	414757		Hs.77252 Hs.185973	fragile histidine triad gene degenerative spermatocyte (hom	141	12.5
	428593 432370		Hs.274424	N-acetylneuraminic acid phosph	Antifreeze, NeuB	12.5
20	401542	77 20000		C15001413*:gi]10645199[ref[NP_		12.4
	428782	X12830	Hs.193400	interleukin 6 receptor	fn3,ig	12.3
	425999		Hs.332981	ESTs, Weakly similar to 138022	FAD_binding_2	12.3 12.2
	. 422301	AI752163	Hs.114599	collagen, type VIII, alpha 1	C1q,Collagen RGS,G-gemma,DEP	12.2
25	410720	AF035154	Hs.65756 Hs.332329	regulator of G-protein signali EST	1/00/0-Agriniahon	12.1
23	407143 421321	C14076 NM_005309		glutamic-pyruvate transaminase	aminotran_1_2	12.1
	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	PWWP,PHD	12.0
	420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	12.0 12.0
30	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-	ig,ITAM,Zn_clus MATH	12.0
	427336	NM_005658		TNF receptor-associated factor phosphoserine phosphatase-like	Hydrolase	11.9
	409799 436319	D11928 H90727	Hs.76845 Hs.5123	inorganic pyrophosphatase	Pyrophosphatase	11.9
	400748	1100127	12.0125	NM_022122:Homo septens matrix		11.9
35	428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	11.8
• -	401215			C12000457*:gi[7512178[pir][T30	trypstn	11.7 11.7
	401281		455050	DKFZP586N2124 protein	efhand,RmaAD	11.7
	427397	A1929685	Hs.177656	calmodulin 1 (phosphorylase ki solute carrier family 2 (facil	supar_tr	11.7
40	453496 409608	AA442103 AF231023	Hs.33084 Hs.55173	cadherin, EGF LAG seven-pass G	7tm_2,cadherin,GPS,lamini	11.7
40	424415	NM_001975		enolase 2, (gamma, neuronal)	enolase	11.7
	447495	AW401864	Hs.18720	programmed cell death 8 (apopt	pyr_redox	11.6
	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-c)	adh_short	11.6 11.5
45	405371			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ Xlink	11.4
45	416282	R86664	Hs.167257	brain link protein-1 programmed cell death 10	Addik	11.4
	452295 430390	BE379936 AB023186	Hs.28866 Hs.241161	KIAA0969 protein	PH	11.4
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	PH	11.2
	443814	BE281240	Hs.9857	carbonyl reductase		11.2
50	440242	AW295871		glucose transporter protein 10	SH3,PH,RhoGEF	11.1 11.1
	447365	BE383676	Hs.334	Rho guanine nucleotide exchang NM_003105°:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	11.1
	400843 422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	11.0
	400232	ANOU 1300	113,110000	NM_001895":Homo saplens casein	pkinase	10.9
55	426828	NM_000020	Hs.172670	activin A receptor type II-lik	pkinase,Activin_recp	10.9
	431157	A1823969	Hs.132678	ESTs	MAPEG	10.8 10.8
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	AIRS,AIRS_C	10.8
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg olfactory receptor, family 2,	7tm_1 ·	10.8
60	400389	AL135841		Taget Exon	A2M_N,A2M	10.8
00	402207 435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	10.8
	435615 452434	D30934	Hs.29549	C-type tectin-like receptor-1	lectin_c	10.7
	402053			C11001722°:gi 11436283 ref XP_	net to Superbula Da	10.7 10.6
	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin, Reprolysin, Pe	10.6
65	431512	BE270734	Hs.2795	lactate dehydrogenase A NM_019595:Homo sapiens Interse	ldh,ldh_C SH3,efhand,C2,PH,RhoGEF	10.6
	403213	DE241740	Hs.785	integrin, sights 2b (platelet g	FG-GAP,integrin_A	10.6
	412158 423673	BE241740 BE003054	Hs.1695	matrix metalloproteinase 12 (m	Peplidase_M10,hamopexin	10.6
	403949	800000	12.1000	C10000813*:gi[5453992]ref[NP_0		10.6
70	457670	AF119666	Hs.23449	insulin receptor tyrosine kina	SH3	10.5
	418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	10.4 10.4
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding	BRCT BIRTK	10.4
	422765	AW409701		baculoviral IAP repeat-contain	Kunitz BPTI	10.4
75	453023	AW028733		serine protease inhibitor, Kun hexokinase 3 (white cell)	hexokinase, hexokinase 2	10.4
75	425694 438800	U51333 AB037108	Hs.159237 Hs.6418	seven transmembrane domain orp		10.3
	438800	ADUST 100	13.0710	Target Exon	Carn_acyltransf	10.3
	444202	AL031685	Hs.12785	KIAA0939 protein	Na_H_Exchanger,ABC2_membr	10.3
	425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3 10.2
80	413431	AW24642		ubiquitin-conjugating enzyme E	UQ_con SNF2_N,helicase_C,bromodo	10.2
	415200	AL040328		SWI/SNF related, matrix essoci inositol 1,4,5-triphosphate re	RYDR_ITPR.ton_trans,MIR	10.2
	414874	D26351 AF055989	Hs.77515 Hs.129738	potassium voltage-gated channe	ion_trans,K_letra,thaumat	10.2
	423524 457558			G protein-coupled receptor	7tm_1,globin	10.2
	-0,000					

	445629	Al245701	Hs.193326	fibroblast growth factor recep		10.1
	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,ari	10.1 10.1
	402497	AF006823	Hs.24040	C1001261*:gij2695979jemb(CAA70 potassium channet, subfamily K	lon_trans	10.0
5	449853 427672	AA356615	Hs.336916	death-associated protein 6		10.0
•	412048	AW866863	Hs.73090	nuclear factor of kappa light	RHD,TIG,ank,death	10.0 10.0
	410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8 ras,arf	10.0
	420319 420332	AW406289 NM_001756	Hs.96593 Hs 1305	hypothetical protein serine (or cysteine) proteinas	serpin	9.9
10	420532	MICOTIO	113.1000	NM_001093":Homo saplens acetyl	CPSase_L_chain,biotin_lip	9.9
••	401507			C15000810°:gij11131272[sp[P793		9.9 9.9
	431434	BE267696	Hs.254105	enolase 1, (alpha)	enolase	9.8
	447232	AW499834 NM_002960	Hs.327	interleukin 10 receptor, atpha S100 calcium-binding protein A	S_100	9.8
15	432343 408931	AA251995	Hs.334648	poly(A) polymerase alpha	NTP_transf_2	9.8
13	421542	AA411607	Hs.118964	ESTs, Wealdy similar to KIAA11		9.8
	430323	U40714	Hs.239307	tyrosyl-IRNA synthetase	DUF101	9.8 9.7
	412270	AC005262	Hs.73797	guanine nucleotide binding pro embryonic ectoderm development	G-alpha,arf WD40	9.7
20	424649 400772	BE242035	Hs.151461	NM_003105*:Homo sapiens sortil	kdi_recept_a,fn3,ldi_rece	9.7
20	450493	M93718	Hs.166373	nitric oxide synthese 3 (endot	flavodoxin,FAD_blnding,NO	9.7
	401510			NM_017434:Homo saplens dual ox	efhand,Ferric_reduct	9.7 9.7
	404596			Target Exon	aldanna	9.7
25	451367	AA923729	Hs.26322	cell cycle related kinase hydroxymethylbilane synthase	pkinase Porphobil_deam	9.6
25	417810 432855	D28419 AF017988	Hs.82609 Hs.279565	secreted frizzled-related prot	Fz,NTR	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,lg,lRK	9.6
	430398	AF105202	Hs.241376	potassium voltage-gated channe	ion_trans,KCNQ1_channel	9.6
••	424339	BE257148		endoglycan	MCM	9.6 9.6
30	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase gb:H.sapiens DAT1 gene, partia	PGAM SNF	9.6
	407065 433938	Y10141 AF161536	Hs.284292	ubiquinol-cytochrome c reducta		9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc	9.6
	404968			C4001170:gij6863176 gb AAF3040	-	9.5
35	400833			C11000890:gij3746443jgbJAAC639	7tm_1	9.5 9.5
	410191	A1609645	Hs.286218	NM_021075*:Homo sapiens NADH d junctional adhesion molecule 1	ig	9.4
	444633 427747	AF111713 AW411425		serine/threonine kinase 12	pkinase	9.4
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F	9.4
40	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD	9.4 9.4
	422328	X60459	Hs.1513	Interferon (alpha, beta and om	pkinase	9.4
	445143	U29171	Hs.75852	casein kinase 1, delta death-associated protein kinas	pkinase	9.4
	450883 414625	AA335738	8 Hs.25619 Hs.76686	glutalhione peroxidase 1	GSHPx	9.3
45	401935	10000100	113.70000	Target Exon	PH	9.3
	418329	AW247430) Hs.84152	cystathionine-beta-synthase	PALP,CBS	9.3
	425242	D13635	Hs.155287	KIAA0010 gene product	HECT,IQ	· 9.3 9.2
	400404	AF161221		kaliikrein 14 Terget CAT	trypsin fer2,molybdopterin,bac_dn	9.2
50	442332 431534	A1693251 AL137531	Hs.8248 Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	ional incompany in a second	9.2
50	402823	AL101001	110.220000	C1002456*:gij9930918jemb CAC05		9.1
	404527			peptide YY, 2 (seminalplasmin)	GDA1_CD39	9.1 9.1
	439963	AW24752		platelet-activating factor ace	PAF-AH_Jb,Lipase_GDSL Rhodanese,DSPc	9.1
55	412970	AB026436 AL040535		dual specificity phosphalase 1 ATP-binding cassette, sub-fami	ABC_tran	9.1
23	443553 400933	ALUHUUU	115.5570	NM_004347:Homo saplens caspase	ICE_p20,ICE_p10,CARD	9.0
	403268			NM_002210*:Homo sapiens integr	FG-GAP	9.0
	446673		61 Hs.15871	LPAP for lysophosphatidic acid	acid_phosphat	9.0 9.0
60	422531	AW96728		ESTs, Weakly similar to HERC2 frequenin (Drosophila) homolog	pkinase efhand	9.0
60	421658	X84048	Hs.301760	Target Exon	kinesin	9.0
	401885 402651		•	NM_000721°:Homo sapiens calciu	ion_trans	9.0
	457432	NM_0051	36 Hs.268538	potassium voltage-gated channe	ISK_Channel	9.0
	433146	AB03300		solute carrier family 12, (pot	Theread 1740	9.0 9.0
65	420090	AA22023		ribonuclease P (38kD) hydroxyacyl glutathione hydrol	Ribosomal_L7Ae lactamase B	9.0
	425281 410855	AA44439 X97795	0 Hs.155482 Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C	9.0
	407986	U32659	Hs.41724	interleukin 17 (cytotoxic T-ly	-	9.0
	431131	N84730	Hs.250616	Isocitrate dehydrogenase 3 (NA	isodh	. 9.0 9.0
70	422802	NM_0042		phosphatidylinositol glycan, c	DUF158	9.0
	447958	AW7965		Homo sapiens microsomal signal ESTs. Wealthy similar to ALUC_H		9.0
	438080 418843	AA77738 AJ25101		polassium intermediate/small c	CaMBD,SK_channel	9.0
	419244	A143656		ATP synthase, H transporting,	ATP-synLDE	8.9
75	404676			Target Exon	110	8.9 8.9
-	428744	BE26703		ubiquitin-conjugating enzyme E	UQ_con SDF	8.9
	421474	U76362	Hs.104637	solute carrier family 1 (gluta CD79B antigen (immunoglobulin-	ig,itam	8.9
	419056	M89957 AF20706	Hs.89575 59 Hs.153357	procollagen-lysine, 2-oxogluta	20G-Fell_Oxy,Glycos_trans	8.9
80	424825 444628	U01120	Hs.242	glucose-6-phosphatase, catalyt	PAP2	8.9
5 0	404199	5540		ENSP00000211797*:Helicase SKI2	RasGAP,PH	8.9 8.9
	428826	AL0488		attractin	lectin_c,CUB,Kelch,PSI,EG ethand	8.8
	410681	AW2468		calbindin 1, (28kD) edenosine A1 receptor	7tm_1	8.8
	415056	AB0046	62 Hs.77867	, aconomic in recopier		

	400471			Target Exon		8.8
	406591			NM_003888*:Homo saplens retina	eldedh	8.8 8.8
	425427	A1652662	Hs.157205	Digital local designation of the second	aminotran_4	8.7
_	410839		Hs.66581		ihiored,Rho_GDI,gnIR pkinase	8.7
5	430037		Hs.227789 Hs.428		fit3_fig	8.7
	450848 414534	A1677994 BE257293	Hs.76366	BCL2-antegonist of cell death		8.7
	401454	DC201200	1.0	NM_014226°:Homo sapiens renal	pkinase	8.7 · 8.7
	408493	BE206854	Hs.46039	histophich longer are memore a func	PGAM homeobox,pkinase,PH,pkina	8.7
10	433333	Al016521	Hs.71816		Patched	8.7
	430432	AB037758	Hs.241419	NM_002920":Homo sapiens regula	Oest_recep,zf-C4,hormone_	8.7
	406128 419493	AF001212	Hs.90744	protessome (prosome, macropain	PCI	8.7
	439569	AW602166	Hs.222399	CEGP1 protein	CUB,EGF	8.6 8.6
15	401134	•		C12001198:glj3183183[sp[Q92142	blopterin_H	8.6
	442286	W31847	Hs.50335 Hs.184011	cytochrome P450 monocxygenase pyrophosphalase (inorganic)	Pyrophosphatase	8.6
	428376 433494	AF119665 AB029396	13.104011	bela-1,3-glucuronyltransferase	Glyco_trant_43	8.6
	433494	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-	pkinase	8.6
20	437278	AA748017	Hs.290145	ESTs	cNMP_binding	8.6 8.6
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin	lipocalin, Kunitz_BPTI Starold_dh	8.6
	421871	AK001416	Hs.306122	glycoprotein, synaptic 2 protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM	8.6
	447827	U73727	Hs.19718	Target Exon	DNA_pol_A	8.6
25	403379 446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7tm_1	8.6
23	432857		Hs.279582	GTP-binding protein Sara	arf,ras	8.5 8.5
	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	8.5
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHL A2M_N,A2M	8.5
20	402209			Target Exon C10002057*:gf[3211705[gb]AAC21	rencipe	8.5
30	400518	U52112	Hs.158331	renin-binding protein		8.5
	425606 437965	AA843222	Hs.193534	ESTs, Moderately similar to AL	RasGEF	8.5
	433392	AF038535	Hs.127588	svnantotagmin VII	C2	8.5 8.5
	402191			NM_021733*:Homo saplens testis		8.5
35	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras PARP,PARP_reg	8.5
	431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p HRAS-like suppressor	Man h von Doğ	8.5
	457579	AB030816	Hs.36761 3 Hs.288626	RCE1, prenyl protein protease	Abi	8.5
	409656 456373	BE247706	Hs.89751	membrane-spanning 4-domains, s		8.4
40	432499	BE276633	(10.001.01	RAB6B, member RAS oncogene fam	ras,arf	8.4 8.4
• •	400565			Target Exon	Branch	8.3
	401960			Target Exon	cyclin	8.3
	432545	X52486	Hs.3041 Hs.12503	urecil-DNA glycosylase 2 Interleukin 15 receptor, alpha	sushi	8.3
45	445303 404528	AW362198	rts.12300	peptide YY, 2 (seminalplasmin)	GDA1_CD39	· 8.3
43	428542	079989		KIAA0167 gene product	ank,PH,ArfGap,ras	8.3 8.3
	406868	AA505445	Hs.300697	immunoglobulin heavy constant	COCasa I shain histin ila	8.3
	405473			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,blotin_lip 7tm_1	8.3
50	408601	U47928	Hs.86122	protein A proteinase 3 (serine proteinas	trypsin	8.3
50	415008	NM_00277 AU076644		protein phosphatase 2A, regula	-11	8.3
	430258 436483	AJ272063	Hs.283010	vanilloid receptor subtype 1	ank,ion_trans	8.3
	459302		4 Hs.36566	LIM domain kinase 1		8.3 8.3
•	437644	AA748575	Hs.136748	lectin-like NK cell receptor	lectin_c Latrophilin,OLF,7tm_2,Gal	8.2
55	421707		21 Hs.107054	lectomedin-2	COesterase	8.2
	414629	AA345824		carboxylesterase 1 (monocyte/m arachidonate lipoxygenase 3		8.2
	453898	AW003513 AF057036		collagen-like tall subunit (si	Collagen	8.2
	424053 457398	BE258532		CTP synthase	GATESO	8.2
60	421504	AW40299		adaptor protein with plackstri	SH2,PH	6.1 8.1
•••	406495			Target Exon	SRCR DEAD,helicase_C	8.1
	453610	AW36888		RecQ protein-like 5 retinitis pigmentosa GTP ase re	RCC1	8.1
	424880 -		28 Hs.153614 Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4	8.1
65	423847 409829	U16997 M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon	8.1
05	401180	WI33332	113.001 23	eukaryotic translation elongat	ion_trans.IQ	8.1 8.1
	452072	BE25885	7 Hs.27744	RAB3A, member RAS oncogene fam	res,erf	8.1
	426484	AA37965	8 Hs.272759	KIAA1457 protein	IP_trans 7tm_1	8.1
70	402453			C1002496:gi[7363439 ref[NP_039 nuclear receptor subfamily 2,	ruiC1	8.1
70	457310	W28363	Hs.239752 3 Hs.343603	titin-cap (telethonin)	globin,cNMP_binding,pkina	8.1
	422069 400275	AJ01006	3 (15.54500)	NM_006513°:Homo sapiens seryi-	NA	8.0
	434357	AW7322	B4 Hs.3828	mevalonata (diphospho) decarbo	GHMP_kinases	8.0 8.0
_	430299	W28673	Hs.106747	serine carboxypeptidase 1 prec	EVED TEO	8.0
75	413762	AW4114	79 Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR 4 Rhogef,PH	8.0
_	402393		000 11- 400040	ENSP00000085284°:CDNA FLJ2040 RAS protein activator like 1 (C2.PH.RasGAP.BTK	8.0
	429252		658 Hs.198312 Hs.1030	ras inhibitor	RA,SH2,VPS9	7.9
	456181 431493	h		ESTs, novel cytochrome P450	p450	7.9
80	451558		089 Hs.26630	ATP-binding cassetta, sub-fami	ABC_tran,SRP54	7.8 7.8
	415758	BE2704	65 Hs.78793	protein kinase C, zeta	ptinase,DAG_PE-bind,pkina EPH_lbd,pkinase,SAM,fn3	7.8 7.8
	419270	NM_005	232 Hs.89839	EphA1	7tm_1	7.8
	422837		Hs.121478	dopamine receptor D3 . Target Exon	pkinase	7.8
	401118	•		•	250	

	426440		Hs.169902	solute carrier family 2 (facil	sugar_tr	7.8
	418635		Hs.1183	dual specificity phosphatase 2	DSPc,Rhodanese,Y_phosphat PMP22_Claudin	7.8 7.8
	432747 403672	NM_014404	MS.278907	calcium channel, voltage-depen C4001244:pij539933[pirljA61275	tubulin	7.8
5	437806	AJ424921	Hs.122487	ESTs, Wealdy similar to AS4854	RasGAP	7.7
•	456890	U48213	Hs.155402	D site of albumin promoter (al	DAGKc,bZIP	7.7
	424107		Hs.139648	kinesin family member 1C	kinesin,FHA	7.7 7.7
	452695 433262		Hs.30327 Hs.284171	milogen-ectivated protein kina KIAA1535 protein	cNMP_binding,ion_trans	7.7
10	424198		Hs.143026	KIAA1087 protein	Na_Ca_Ex,Calx-beta	7.6
	406496	,		Target Exon	SRCR	7.6
	425423	NM_005897	Hs.157180	intracistemal A particle-prom	BTB,Kelch	7.6
	402211	V400CC	11. 47007	KIAA0430 gene product	ion_trans,K_tetra	7.6 7.5
15	408710 457615	Y10256 W56321	Hs.47007 Hs.111460	mitogen-activated protein kina calcium/calmodulin-dependent p	pkinase,SAM_decarbox pkinase	7.5
13	402760	1130021	113.111100	NM_021797*:Homo saplens eosino	Glyco_hydro_18,CBM_14	7.5
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	C1q,Collagen	7.4
	423579	NM_004121		gamma-glutamyltransferase-like	G_ghu_transpept	7.4 7.4
20	413104	L42374 BE280337	Hs.75199 Hs.194693	protein phosphatase 2, regulat solute carrier family 7 (catio	856 aa_permeases	7.4
20	419660 424774	BE244179	Hs.153022	TATA box binding protein (TBP)	and permitted the second	7.4
	402632	GCZTTTT	10.1000	Target Exon	Fz,kringle,ig	7.4
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like	ARID, SNF	7.4
25	405714	44007464	11-0000	ENSP00000221137:Olfactory rece	7tm_1	7.3 7.3
25	442732 421758	AA257161 BE397336	Hs.8658 Hs.1422	hypothetical protein DKFZp434E Gardner-Rasheed feline sarcoma	EGF,laminin_EGF,Xiink,S_m SH2,SH3,pkinase	7.3
	421756	NM_004573	115.1422	phospholipase C, bela 2	PI-PLC-X,PI-PLC-Y,C2	7.3
	405137	***************************************		Target Exon		7.3
•	402460			C1001261*:gij2695979jembjCAA70	2	7.3
30	431398	BE616547	Hs.2785	keratin 17	filament	7.3 7.3
	429592 429225	AB029041 BE250337	Hs.209646 Hs.198273	KIAA1118 protein Target CAT	Troponin	7.2
	423215	U18548	Hs.123034	G protein-coupled receptor 12		7.2
	454373	NM_005133		RCE1, prenyl protein protease	Abi	7.2
35	440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK	7.2
	432920	U37689	Hs.3128	polymerase (RNA) II (DNA direc	V	7.2 7.2
	446143 422201	BE245342 NM_001505	Hs.306079	sec61 homolog G protein-coupled receptor 30	secY 7tm_1	7.2
	440869	NM_014297		protein expressed in thyroid	lactamase_B	7.1
40	435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_I,5_3_exonuclea	7.1
	437161	AA054477	Hs.25391	ESTs	t 4 Dtt- D 1440D	7.1
	429683	AF148213	Hs.211604	a disintegrin-like and metallo	tsp_1,Reprolysin,Pep_M128 pkinase	7.1 7.1
	426268 445087	AF083420 AW893449	Hs.168913 Hs.12303	serine/threonine kinase 24 (St suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
45	416377	AA179930	Hs.293867	caspase recruitment domain pro	o vior retressorium Zezarbren.	7.1
	421748	NM_014718		KIAA0726 gene product	cadherin	7.1
	426691		Hs.171834	PCTAIRE protein kinase 1	pkinase	7.0
	428599	AB033078	Hs.186613	sphingosine-1-phosphate lyase	pyridoxal_deC	7.0 7.0
50	411898 427010	BE409714 AW138332	Hs.44856	hypothetical protein FLJ12116 muscle RAS oncogene homolog	ras	7.0
50	457305	BE268048	Hs.236494	RAB10, member RAS oncogene fam	ras,arf	7.0
	431630	NM_002204		integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	7.0
	457764	AW028284	Hs.4815	nudix (nucleoside diphosphate	NUDIX	6.9 6.9
55	435575 456488	AF213457 AW015098	Hs.44234 Hs.301946	triggering receptor expressed ESTs, Wealdy similar to T30867	ig	6.9
55	428761	AF236119	Hs.193076	GRB2-related adaptor protein 2	SH2,SH3	6.9
	430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF	6.9
	422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Semia	6.9
60	445937	A1452943	Hs.321231	UDP-Gal:belaGlcNAc beta 1,4- g hypothetical protein FLJ20260	Galactosyl_T_2 PH	6.9 6.8
60	457499 400845	AA953015	Hs.274370	NM_003105":Homo saptens sortil	ldl_recept_a,fn3,ldl_rece	6.8
	416931	D45371	Hs.80485	edipose most abundant gene tra	C1q,Collagen	6.8
	414915	NM_002462		myxovirus (influenza) resistan	dynamin_2,dynamin,GED	6.8
~	432990	AL036071	Hs.279899	tumor necrosis factor receptor	TNFR_c6	6.8
65	458128	W32474	Hs.301746	RAP2A, member of RAS oncogene	ras,ari,idh Goloofond T. 2 lo	6.8 6.8
	429542 401488	AF038660	Hs.206713	UDP-Gal:belaGlcNAc beta 1,4- g Target Exon	Galactosyl_T_2,lg Gtyco_hydro_1	6.7
	456243	Al345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	6.7
	424321	W74048	Hs.1765	lymphocyte-specific protein ty	SH2,SH3,pkinase	6.7
70	405187			NM_014272Homo saplens a disin	Reprolysin,tsp_1,Pep_M12B	6.7
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450 NADHdh_2	6.7 6.7
	448496 419667	BE379077 AU077005	Hs.130849 Hs.92208	ESTs, Weakly similar to 138022 a disintegrin and metalloprote	disintegrin, Reprotysin, Pe	6.7
	417103	Z33905	Hs.81218	hypothetical protein MGC3597	TPR_zf-C3HC4,PHD	6.7
75	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	FAD_Synth	6.7
-	456469	NM_005109	Hs.95220	oxidative-stress responsive 1	zf-C2H2.pkinase	6.7
	449546	W86248	Hs.58819	ESTs	hexokinase	6.6 6.6
	428926	NM_00170	2 Hs.194654	brain-specific angiogenesis in C1002000*:gij12735712 ref XP_0	7tm_2,lsp_1,GPS,HRM	6.6
80	404953 449401	AL135401	Hs.23557	semiogically defined colon ca	pro_isomerase	6.6
-	429962	M69113	Hs.226795	glutathione S-transferase pl	GST_C,GST_N	6.6
	421547	AA489908	Hs.1390	proteasome (prosome, macropain	Clathrin_lg_ch,proteasome	6.6
	430035	NM_00346		protein tyrosine phosphalase t	Y_phosphatase,DSPc	6.6 6.6
	406867	AA157857	Hs.182265	keralin 19	filament,bZIP	0.0

	404946			Target Exon	3Beta_HSO	6.5
	435213	AA092510	Hs.5985	non-kinase Cdc42 effector prot	_	6.5
	411201	T74588	Hs.8509	ESTs, Weakly similar to C3HU c	A2M_N,A2M	6.5
_	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank DAGKa DAGKc DAG_PE-bi	6.5
5	426194	T50872	Hs.2001	thromboxane A synthase 1 (plat	p450	6.5 6.5
	424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK	6.5
	417903 408905	NM_002342 AV655783		lymphotoxin beta receptor (TNF Target CAT	TNFR_c6	6.5
	438646	AV655765 AI973076	Hs.661 Hs.231958	matrix metalloproteinase 28		6.5
10	431530	X61615	Hs.2798	leukemia inhibitory factor rec	fn3	6.5
10	428883	AA436959	Hs.258802	ATPase, (Na)/K transporting, b	Na_K-ATPase	6.5
	404757			Target Exon	_	6.4
	406370			interleukin 11	trypsin	6.4
	443611	NM_014397		NIMA (never in mitosis gene a)	pkinase	6.4
15	424008	R02740	Hs.137555	putative chemokine receptor, G	7tm_1	6.4 6.4
	444912	AW247380	Hs.12124	putative prostate cancer susce	lactamase_B	6.4
	454460	X66945	Hs.748	fibroblast growth factor recep	ig,pkinase pkinase,Sema,PSI,TIG,A4_E	6.4
	432269 458718	NM_002447 Al359476	Hs.157699	macrophage stimulating 1 recep ESTs	planaso,ocina,i ottiosa-e	6.4
20	405282	MOOSHIU	113.101033	Target Exon	Cache	6.4
20	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	6.3
	442297	NM_006202		phosphodiesterase 4A, cAMP-spe	PDEase	6.3
	400894		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	C11000129:gij9938014 ref NP_06	7tm_1	6.3
	440446	NM_013385	Hs.7189	plackstrin homology, Sec7 and	PH,Sec7	6.3
25	430886	L36149	Hs.248116	chemokine (C motif) XC recepto	7tm_1	6.3
	451394	NM_003595		tyrosylprotein sulfotransferas	Sulfotransfer	6.3
	436523	BE612990	Hs.5212	single-strand selective monofu	DU10004	6.3 6.3
	422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221	6.3
30	408924	AW295606	Hs.236131 Hs.76394	homeodomain-interacting protei encyl Coenzyme A hydratase, sh	ECH_Peptidase_U7	6.3
30	414551 413254	Al815639 U40272	Hs.75253	isocitrate dehydrogenase 3 (NA	isodh	6.3
	415010	NM_004203		membrane-associated tyrosine-	pkinase	6.3
	449761	AB009698	Hs.23965	solute carrier family 22 (orga	sugar_tr	6.3
	432221	M21191	Hs.273415	aldolase A, fructose-bisphosph	glycolytic_enzy,Adeno_E3_	6.3
35	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS.pkinase_C	6.2
	458516	BE010749	Hs.255097	ESTs	•	6.2
	417985	AA187545	Hs.83114	crystallin, zeta (quinone redu	adh_zinc	6.2
	447507	H59696	Hs.18747	POP7 (processing of precursor,	M. I. States BOD-	6.2
40	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibi	Y_phosphatase,DSPc	6.2 6.2
40	428443	BE618106	Hs.184326	CDC10 (cell division cycle 10,	GTP_CDC,M	6.2
	423229	AC003965	Hs.125532	protease, serine, 26	trypsin SQS_PSY,dsrm,z-elpha	6.2
	408903	BE244377	Hs.48876	famesyl-diphosphate famesylt SH3-domain binding protein 2	PH,SH2	6.1
	426176 421395	AB000462 D90084	Hs.167679 Hs.1023	pyruvata dehydrogenase (lipoam	E1_dehydrog	6.1
45	430517	S80071	Hs.241597	solute carrier family 6 (neuro	SNF	6.1
-13	435906	AI686379	Hs.110796	SAR1 protein	erf,ras	6.1
	402758	, 110000.0		C1001899*:gl 12722636 ref XP_0	Glyco_hydro_18	6.1
	434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
	402115			NM_021624:Homo sapiens histami	7tm_1	6.1
50	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gat	ASC	6.1
	404679			Target Exon		6.0
	450739	A1732707		ESTs, Wealthy similar to ALU7_H	V1R	6.0 6.0
	439888	AB040949	Hs.6733	pancreas-enriched phospholipas	C2,PI-PLC-Y,PI-PLC-X,RasG Peolidase_M3	6.0
55	415742	BE410243	Hs.78769	thimet ofigopeptidase 1	PH,PHD,RUN	6.0
23	453190	AB002354 AW328081	Hs.32312 Hs.6817	KIAA0356 gene product Inosine triphosphatase (nucleo	Ham1p_like	6.0
	439975 412800	AW950852		polymerase (DNA directed), del	homeobox	6.0
	432805	X94630	Hs.3107	CD97 antigen	7tm_2,GPS,EGF	6.0
	418964	174640	12.5107	gb:yc57c12.r1 Stratagene liver	A2M_N,A2M	6.0
60	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
	419755	H18444	Hs.134846	BAI1-associated protein 3	CZ .	6.0
	457276	AF235097	Hs.227583	Homo saplens chromosome X map		6.0
	423908	AJ006422	Hs.135183	centaurin-elpha	PH,ArfGap	6.0
65	432118	N98718		gb:yy65g02_r1 Soares_multiple_		5.9 5.9
65	427334	R44789	Hs.33191	Homo saplens, Similar to trans	pkinase.SH3	5.9
	424959		1 Hs.153937	activated p21cdc42Hs kinase	ton_trans	5.9
	453082	H18835 AF182277	Hs.31608 Hs.330780	hypothetical protein FLJ20041 cytochrome P450, subfamily IIB	p450	5.9
	421168 422287	F16365	Hs.114346	cytochrome c oxidase subunit V	COX7a,Phage_G	5.9
70	401736	1 10000	113.117070	C16000492":gi 3127193lgb AAD05	AMP-binding	5.9
. 0	434755	AA648502		ESTs	-	5.9
	414962	AF273304		XPMC2 protein	Exonuclease	5.8
	407338	AA773213		gb:ab66f10.s1 Stratagene lung	ig	5.8
	448426	BE018315		tankyrase, TRF1-interacting an		5.8
75	409586	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp4	ABC_tran	5.8
	450778	U81375	Hs.25450	solute carrier family 29 (nucl	Nucleoside_tran	5.8
	423612		7 Hs.1686	guanine nucleotide binding pro	G-alpha,arf	5.8
	430845	AF024690		G protein-coupled receptor 43	7tm_1	5.8 5.8
90	424741	AF051941		nucleoside diphosphate kinase	NDK	5.8
80	412958	BE391579		Fas-activated serine/threonine gamma-glutamyl hydrolase (conj	GATase	5.8
	415701	H97991	78 Hs.78619 Hs.193313	gamma-gustanyi nyolokasa (cok) Targel CAT	MoaA_NiiB_PqqE	5.8
	423158 414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	5.8
	412915	AW08772		NM_004541:Homo saplens NADH de	•	5.7
				-		

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					h	5.7
	420904	AL035964	Hs.100221	nuclear receptor subfamily 1.	hormone_rec,zf-C4 Sulfotransfer	5.7
	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransfer8	DEAD,helicase_C,dsm,Vira	5.7
	433074	AL045019 AW292809	Hs.323462 Hs.50727	Homo sapiens cONA FLJ11214 fis N-ecetylglucoseminidase, alpha	OPACHEROSO_CACOMINATO	5.7
5	409124 428270	BE501549	Hs.50727 Hs.107040	ESTs		5.7
,	435114	AA775483	Hs.288936	mitochondrial ribosomal protei	ODC_AZ	5.7
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	asp	5.7
	453054	AI878908	Hs.31547	Target CAT	•	5.7
	420730	NM_002691		polymerase (DNA directed), del	ICL.	5.7
10	415117	AF120499	Hs.78016	polynucieotide kinase 3'-phosp	Viral_helicase1	5.7
	400985			Target Exon		5.7
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase	5.7
	413858	NM_001610	Hs.75589	acid phosphatase 2, lysosomal	acid_phosphat	5.7
	457308	AI416988	Hs.238272	inositol 1,4,5-triphosphate re	ton_trans,RYDR_ITPR,MIR	5.7
15	400551			C10001991*:gi[6624920]emb]CAB6	SRCR	5.7 5.7
	433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	5.7
	409531	BE384319	Hs.54702	xylosylprotein beta1,4-galacto	GalactosyL_T_2 neur	5.7
	449139	BE268315	Hs.23111 Hs.14716	phenylalanine-IRNA synthetase- ESTs	iica	5.7
20	450207 400266	T87615	13.14710	NM_002858*:Homo sapiens ATP-bi	ABC_tran	5.6
20	430713	AA351647	Hs.2642	eukaryolic translation elongat	GTP_EFTU,GTP_EFTU_D3,GTP_	5.6
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (TPR	5.6
	405683	511410		Target Exon		5.6
	449181	X96783	Hs.23179	synaptotagmin V	C2	5.6
25	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synt_C	5.6
	415193	AL048891	Hs.12185	hypothetical protein MGC14333		5.6
	434883	AW381538	Hs.19807	hypothetical protein MGC12959		5.6
	433135	AA443873	Hs.110477	dolichyl-phosphate mannosyltra		5.6
••	413049	NM_002151		hepsin (transmembrane protease	trypsin	5.6
30	420899	NM_001629		arachidonale 5-lipoxygenase-ac	MÅPEG	5.6
	423397	NM_001838		chemokine (C-C motif) receptor	7tm_1	5.5 5.5
	443759	BE390832	Hs.134729	FXYD domain-containing ion tra	integrin_A,FG-GAP	5.5
	454112	NM_000885	HS.40034	integrin, alpha 4 (antigen CD4 NM_021949:Homo saplens ATPase,	E1-E2_ATPase,Hydrolase	5.5
35	405594	05010404	Hs.79217	pyrroline-5-carboxylate reduct	P5CR,Octopine_DH_N	5.5
33	416322 446755	BE019494 AW451473	Hs.16134	serine/threonine kinase 10	pkinase,TYA	5.5
	411030	BE387193	Hs.67896	7-60 protein	production of the production o	5.5
	431498	AK001777	Hs.258551	aspartyl aminopepiidase	Peptidase_M18	5.5
	433012		Hs.279910	ATX1 (antioxidant protein 1, y	HMA	5.5
40	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	pkinase,POLO_box	5.5
	424572	M19650	Hs.92909	2,3-cyclic nucleotide 3' pho		5.5
	406617			Target Exon	efhand,Ferric_reduct	5.5
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil, Glyco_hydro_31	5.4
4.0	419525	179257	Hs.1259	asialoglycoprotein receptor 2	tectin_c	5.4
45	448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	adh_short	5.4 5.4
	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF	5.4 5.4
	406432			CD1E antigen, e polypeptide	Sulfotransfer	5.4 5.4
	428921	Z43809	Hs.194638	polymerase (RNA) II (DNA direc	efhand	5.4
50	430337	M36707 AB011133	Hs.239600	calmodulin-like 3 KIAA0561 protein	pktnase,PDZ	5.4
50	427162 414216	D86970	Hs.173864 Hs.75822	TGFB1-induced anti-apoptotic f	oxidored_q4,myosin_head,b	5.4
	422083		Hs.111256	arachidonate 15-lipoxygenase,	lipoxygenase,PLAT	5.4
	424373	AJ133798	Hs.146219	copine VII	C2	5.4
	449405	AA001350	131110	gb:zh83h05.r1 Soares_fetal_liv	mito_car .	5.4
55	409983	D50922	Hs.57729	Ketch-like ECH-associated prot	BTB,Kelch	5.4
	455818	AI733747	Hs.71174	Interleukin 21 receptor		5.4
	424357	AW961058		hypothetical protein FLJ12116		5.4
	423606	AB011094	Hs.129892	KIAA0522 protein	PH,bZIP,IQ,Sec7	5.3 5.3
CO	432311	BE083080	Hs,274323	similar to sialyltransferase 7	Glyco_transf_29	5.3
60	450080	AB037831	Hs.24372	ESTs, Weakly similar to dJ207H	DEAD,GSPILE	5.3
	423778	Y09267	Hs.132821	flavin containing monooxygenas Target Exon	гмонию,рут_гевох p450	5.3
	402338	ornenent	Ua 72700	macrophage migration inhibitor	MIF	5.3
	412276	BE262621 BE277414	Hs.73798 Hs.5947	mai transforming oncogene (der	ras,arf	5.3
65	437967 424766	BE388855	Hs.152978	proteaseome (prosome, macropai	PA28_slpha,PA28_beta	5.3
05	447766		1 Hs.19513	CGI-63 protein	adh zinc	5.3
	453660	X98507	Hs.286226	myosin IC	myosin_head,IQ	5.2
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	HLH, Myc_N_term, Myc-LZ	5.2
	432336		9 Hs.274382	protein kinase, Interferon ind	dsrm,pkinase	5.2
70	445139	AB037848		synaptotagmin XIII	C2 _	5.2
	429214	AB012722	Hs.198256	kinesin-like 3	kinesin	5.2
	432462	AK000013		thymidine kinase 2, mitochondr	dnk	5.2
	424387	A1739312	Hs.284163	ANKHZN protein		5.2 5.2
76	405697		11-01016	gb:Human homeobox-like mRNA	Odishdimne Adena 181	5.2 5.1
75	450321	Y16521	Hs.24812	CDP-diacytglycerol synthase (p	Cytidylyltrans,Adeno_VII	5.1
	412939	AW411491		eukaryotic translation elongat	SHMT GDA1_CD39	5.1
	445109	AF039916		ectonucleosida triphosphata di Homo sapiens cDNA FLJ12797 fis	ig,tsp_1,ZU5	5.1
	419073	AW372170		hyaturonan synthase 1	Glycos_transf_2	5.1
80	409958 442599	AF078037	23 Hs.57697 Hs.324051	RelA-associated inhibitor	SH3,ank	5.1
30	424305	BE386095		histone deacetylase 8	Hist_deacetyl	5.1
	427247	AW50422		integrin, alpha L (antigen CD1	wwa.integrin_A,FG-GAP	5.1
	429061	Y14039	Hs.195175	CASP8 and FADD-like apoptosis	DED,ICE_p20	5.1
	420849	X52221	Hs.99987	excision repair cross-complame		5.1

	453337	R73417	Hs.25391	gbtyi92g12_r1 Soares breast 2N	GSPIL_III	5.1
	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH	5.1
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyro	SH2,SH3,pkinase,PH,BTK	5.1
_	405202			NM_021734*:Homo saplens deaxyn	mito_carr	5.1
5	451452	BE560065	Hs.26433	dolichyl-phosphate (UDP-N-acet	Glycos_transt_4	5.0 5.0
	418231 425165	AA326895	Hs.83848 Hs.154899	tricsephosphate isomerase 1 Target CAT	TIM	5.0
	407876	NM_004519		potassium voltage-gated channe	ion_trans,KCNQ1_channel	5.0
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antig	tg .	5.0
10	404716			NM_007313":Homo saplens v-abl	SH2,SH3,pkinase	5.0
	405020			Terget Exon	7tm_1	5.0
	426236		Hs.168212	kinesin family member 38	kinesin	5.0 5.0
	433178	AB038269	Hs.253706	cysteinyl teukotriene Cyst.T2 r RAB7, member RAS oncogene fami	7tm_1 erf,res	5.0
15	422340	AW296219 NM_001183		ATPase, H transporting, lysoso	a1,165	5.0
13	439414 425846	AA102174	Hs.159629	myosin IXB	myosin_head,DAG_PE-bind,I	5.0
	413599	AJ006239	Hs.75438	quinoid dihydropteridine reduc	adh_short	5.0
	424168	L29277	Hs.321677	signal transducer and activato	SH2,STAT,STAT_bind,STAT_p	5.0
	436042	AF284422	Hs.119178	cation-chloride cotransporter-	aa_permeases	5.0
20	410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	KhH-GPD	5.0
	428734	BE303044	Hs.192023	eukaryotic translation initiat	WD40	5.0 4.9
	420340	NM_000734		CO3Z antigen, zeta potypeptide	ITAM BNR	4.9
	433075	NM_002959 X03363		sortilin 1 HER2'receptor tyrosine kinase	pkinase	4.9
25	400300 426811	BE259228	Hs.172609	nucleobindin 1	efhand	4.9
23	401577	DELLOCATIO	10.112000	NM_000761:Homo saplens cytochr	p450	4.9
	409637	AA323948	Hs.55407	Homo saplens mRNA; cONA DKFZp4	Collagen	4.9
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase	4.9
0.0	430904	U65402	Hs.248124	G protein-coupled receptor 31	7tm_1	4.9
30	423552	AF107028	Hs.129783	sodium channel, voltage-gated,	lg,Adeno_E3_CR2	4.9 4.9
	421487	AF027406	Hs.104865	serine/threonine kinase 23 NM_004491*:Homo sapiens glucoc	pkinase FF	4.5 4.9
	402183 456748	AW137749	Hs.125902	ubiquitin specific protesse 2	UCH-1,UCH-2	4.9
	424771	BE397151	Hs.153003	serine/threcnine kinase 16	pkinase	4.9
35	406441	00037131	15.150000	Target Exon	Aa_trans	4.9
55	437053	AU077018	Hs.3235	keratin 4	filament,bZIP,Tropomyosin	4.9
	443044	N28522	Hs.8935	quinolinate phosphoribosyltran	QRPTase,QRPTase_N	4.9
	431204	F28841	Hs.250760	cytochrome c oxidase subunit V	dUTPase,COX6A,ras,ATP-syn	4.9
40	456417	L36531	Hs.91296	Integrin, elpha 8	integrin_A,FG-GAP	4.8 4.8
40	436735	L48489	11. 7054	mannosyl (beta-1,4-)-glycoprot	7ln	4.8 4.8
	441455	AJ271671	Hs.7854 Hs.299629	zinc/iron regulated transporte peroxisomal long-chain acyl-co	Ζφ	4.8
	446948 451564	BE409053 AU076698	Hs.132760	hypothetical protein MGC15729	suger_tr,Condensation	4.8
	403771	Y0010030	115.152700	NM_003061:Homo saplens slit (D	EGF,laminin_G,LRR,LRRNT,L	4.8
45	403248			ESTs, Wealthy similar to 178885	SLT	4.8
	410214	L29555	Hs.301698	slalyltransferase 4A (beta-gal	Glyco_transf_29	4.8
	407047	X65965		gb:H.saplens SOD-2 gene for ma	sodfe	4.8
	422668	AF199364	Hs.119120	E3 ubiquitin ligase SMURF1	C2,WW,HECT	4.8
50	436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_blading	4.8 4.8
50	431262	NM_00667		solute carrier family 22 (orga stearoyt-CoA desaturase (dalta	sugar_tr FA_desaturase	4.8
	406625 428659	Y13647 U66579	Hs.119597 Hs.188859	G protein-coupled receptor 20	1 ~_ucsamaso	4.8
	432716	Al762964	Hs.205180	ESTs		4.8
	414460	L00727	Hs.898	dystrophia myotonica-protein k	pkinase	4.8
55	400287	S39329	Hs.181350	kallikrein 2, prostatic	trypsin	4.8
	428946	D42046	Hs.194665	DNA2 (DNA replication helicase	UvrD-helicase,Viral_helic	4.7
	420028	AB014680	Hs.8788	carbohydrate (N-acetylglucosam	Sulfotransfer	4.7 4.7
	402912			Target Exon	pkinase	4.7
60	443329	BE262943		hypothelical protein MGC1936	C2	4.7
UU	426120	AA325243 AA302921	Hs.166887 Hs.247362	copine I dimethylaminine dimethylamino	~	4.7
	430609 451320	AW118072		diacylglycerol kinase, zeta (1	zf-C2H2,BAR,SH3	4.7
	447131		5 Hs.17466	retinolc acid receptor respond		4.7
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A	zona_pellucida	4.7
65	406458			C14000133":gi[1082739[pir]]C44	proteasome	4.7
	427804	AL049654	Hs.180871	protein kinase C, alpha bindin	PDZ	4.7 4.7
	450748	AI733093	Hs.247686	ESTs	7tm_1 efhand	4.7
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1 phosphodiesterase 1A, calmodul	PDEase	4.7
70	407978	AW385125 BE256238		bridging integrator 1	SH3.BAR	4.7
70	428773 456444	AAB84517		ESTs, Weakly similar to KIAA14	Of Iofan a c	4.7
	405574	(VIDOW)	15.01000	Target Exon	pkinase	4.7
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	ribonuclease_T2	4.7
	418289	AW40310	3 Hs.83951	Hermansky-Pudlak syndrome		4.6
75	421601	A1660190		cyclin-dependent kinase inhibi	COI	4.6
	422795	AB033109		KIAA1283 protein	kazala2Ma2M_N	4.6 4.6
	433019	AI208513		translocase of inner mitochond	zf-Tim10_DDP fn3,Y_phosphatase	4.6
	431522	A1625859	Hs.258609	protein tyrosine phosphatase,	idi_recept_a_fn3,idi_rece	4.6
80	400846	AW02830	2 Hs.155079	sortilin-related receptor, L(D protein phosphatase 2, regulat	856	4.6
90	456881 418172	X61157	Hs.83636	adrenergic, beta, receptor kin	pkinase,PH,RGS	4.6
	408433	AW16293		ras-related C3 botulinum toxin	ras	4.6
	439921	AL110209		LCAT-like lysophospholipase	LACT	4.6
	427122	AW05773		HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6
				•		

	427945	AW137156	Hs.181202	hypothetical protein FLJ 10038	Collagen	4.6
	451777		Hs.459	solute carrier family 18 (vesi	sugar_tr	4.6
	429938		Hs.226377	phosphate cytidylyltransferase	Cytidytyttranst,COX6C	4.6
_	412974		Hs.75105	emopamil-binding protein (ster		4.6
5	414702		Hs.76932	cell division cycle 34	UQ_∞n	4.6
	425795		Hs.159543	endothelial differentiation, G	7tm_1	4.6
	422454		Hs.161362	protein (peptidyl-protyl cis/t	Rotamase,WW Methyltransf_4	4.6 4.6
	408135 457388		Hs.42957 Hs.264157	methyltransferase-like 1 cadherin-like 22	cadherin,Cadherin_C_term	4.6
10	421140		Hs.102135	signal sequence receptor, delt	Herpes_UL3	4.6
10	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-a	Acyltransferase	4.6
	413407	Al356293	Hs.75339	inositol polyphosphate phospha	SH2,SAM	4.6
	402463			NM_014624:Homo saplens S100 ca	efhand,S_100	4.5
	417891	W79410	Hs.82887	protein phosphatase 1, regulat		4.5
15	421681	AA384922	Hs.195175	CASP8 and FADD-like apoptosis	ICE_p20,DED	4.5
	426516	BE262660	Hs.170197	glutamic-oxaloacetic transamin	aminotran_1_2	4.5
	418963	BE304571	Hs.89529	aldo-keto reductase family 1,	aldo_ket_red	4.5 4.5
	423664 427681	NM_004714	Hs.180338	dual-specificity tyrosine-(Y)- tumor necrosis factor receptor	pkinase TNFR_c6,death,PH,Xlink,Rh	4.5
20	432893	AB018263 NM_016154		Homo saplens clone PP1596 unkn	ras,arf	4.5
20	413815	AL046341	Hs.75562	discoldin domain receptor fami	F5_F8_type_C,pktnase	4.5
	405546			NM_018833*:Homo saplens transp	ABC_membrane,ABC_tran	4.5
	416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr	4.5
0.5	421962	D82061	Hs.288354	FabG (beta-ketoacyl-(acyl-carr	adh_short	4.5
25	415341	R00602		gb:ye74c04.r1 Soares fetal liv	pkinase	4.5
	456668	W81526	Hs.118329	ESTs, Moderately similar to GA	Neur_chan_LBD,Neur_chan_m	4.5
	456652	AW327546	Hs.111024	solute carrier family 25 (mito	mito_carr	4.5
	407863	AA317089	Hs.597	glutamic-oxaloacetic transamin	aminotran_1_2 sodcu,HMA	4.5 4.5
30	435891	AW249394 AW247615	Hs.5002 Hs.37003	copper chaperone for superoxid v-Ha-res Harvey rat sarcoma vi	FBS	4.5
20	453997 449029	N28989	Hs.22891	solute carrier family 7 (catio	aa_permeases	4.5
	424829	NM_002507	Hs.1827	nerve growth factor receptor (death,TNFR_c6	4.5
	429362	T25833	Hs.200478	ublquitin-conjugating enzyme E	UQ_con	4.5
	429133	N31854	Hs.197116	solute carrier family 7 (catio	aa_permeases	4.5
35	426079	D31220	Hs.166168	peter pan (Drosophila) homolog	7tm_1	4,4
	414814	D14697	Hs.77393	famesyl diphosphate synthase	polyprenyl_synl	4.4
	433261	AB040967	Hs.112034	KIAA1534 protein	PH,Oxysterd_BP	4.4
	402915	0.000000	11- 00010	ENSP00000202587*:Bicarbonate t	HCO3_cotransp	4.4 4.4
40	418267	BE389537	Hs.83919	glucosidase i Homo sapiens, Similar to myosi	Glyco_hydro_63 efhand	4.4
40	430716 420874	BE387257 X66357	Hs.247831 Hs.336478	cyclin-dependent kinase 3	pkinase	4.4
	439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP	4.4
	400223	74 11 T-133	113.0707	Eos Control	Skp1	4.4
	450611	NM_004405	Hs.419	distal-less homeo box 2	homeobox	4.4
45	412965	L06419	Hs.75093	procollagen-lysine, 2-oxogluta	2OG-Fell_Oxy	4.4
	435564	AF210652	Hs.16614	5(3)-deoxyribonucleotidase (dN		4.4
	416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase .	4.4
	423323	AI951628	Hs.127007	potassium channel, subfamily K	ion_trans	4.4
50	448191	NM_005881		branched chain alpha-ketoacid	HATPase_c	4.4
50	456217	BE253181	Hs.81687	non-metastatic cells 3, protei	NDKArteri_glycop	4.4 4.4
	436415	BE265254	Hs.343258	proliferation-associated 2G4, Target CAT	Peptidase_M24	4.4
	429218 407433	AA225065 AF209923	Hs.198269	gb:Homo sapiens orphan G-prote	7tm_3	4.4
	425955	T96509	Hs.248549	ESTs, Moderately similar to S6	74.20	4.4
55	407230	AA157857	Hs.182265	keratin 19	filament,bZIP	4,3
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coe	HMG_CoA_synt	4.3
	416409	R61573 .	Hs.79300	ubiquitin-conjugating enzyme E	UQ_con	4.3
	447957	NM_014821		KIAA0317 gene product	Filamin, HECT	4.3
60	421771		Hs.108131	caspase 2, apoptosis-related c	ICE_p20,CARD,ICE_p10	4.3
60	448886	AL137291	Hs.22451	hypothetical protein FLJ10357	PH,RhoGEF	4.3 4.3
	414821	M63835 AA324358	Hs.77424 Hs.249227	Fc fragment of IgG, high affin Homo saplans DNA, cosmid clone	ig	4.3
	431096 429892	NM_003803		myomesin 1 (skelemin) (185kD)	łg,fn3	4.3
	450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin	ig,iiio	4.3
65	413781	J05272	Hs.850	IMP (Inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD	4.3
-	406530	V002.12		NM_005546*:Homo septens IL2-in	SH2,SH3,pkinase,PH,BTK	4.3
	428363	AK000284	Hs.183860	hypothetical protein FLJ20277	GNT-1	4.3
	413954	AL037111	Hs.75641	galactose-1-phosphate undylyl	GalP_UDP_transf,GalP_UDP_	4.3
70	432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3,pkinase,SAM	4.3
70	456529	AF014643	Hs.100072	connextn46.6	connexin	4.3
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m zf-C2H2	4.3 4.3
	426626	A1124572	Hs.323879	inhibitor of kappa light polyp CGI-31 protein	zi-uznz thlored	4.3
	432956 428970	AL037895 BE276891	Hs.279861 Hs.194691	retingic acid induced 3	7tm_3	4.3
75	428953	AA306610	Hs.348183	tumor necrosis factor receptor	TNFR_c6	4.2
, 5	423922	AK001663	Hs.135458	muscle-specific beta 1 Integri		4.2
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro	adh_short	4.2
	426566	AF131836	Hs.170453	tropomodulin	Tropomodulin,pkinase	4.2
	425179	AJ224442	Hs.155020	putative methyltransferase		4.2
80	412715		7 Hs.74519	primase, polypeptide 2A (58kD)		4.2
	459298	R86701		gb:ym86d09.r1 Soares adult bra		4.2
	404879			NM_030807:Homo saplens glucose	Analinaaratala	4.2
	400836	776 470	U= 34044E	Terget Exon	Apolipoprotein	4.2 4.2
	430940	Z25470	Hs.248145 .	melanocortin 5 receptor		4.2

	400563			Towned Com-	Dec 44400	40
	430237	AJ272144	Hs.236522	Target Exon DKFZP434P106 protein	Pep_M12B_propep sbhydrolase	4.2 4.2
	425175		Hs.155001	UNC13 (C. etegans)-like	DAG_PE-bind,C2	4.2
	409067		Hs.50267	putative GTP-binding protein s	res	4.2
5	419982		Hs.55610	solute carrier family 30 (zinc	-	4.2
	428394	AU076472	Hs.184141	glutaryl-Coenzyme A dehydrogen	Acyl-CoA_dh_Acyl-CoA_dh_M	4.2
	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase	4.2
	454034	NM_000691		aldehyde dehydrogenase 3 famil	aldedh	4.2
10	410237		Hs.61258	argininosuccinate lyase	tyasa_1 .	4.1
10	451478 415410	NM_012331 AF037332	Hs.278569	methionine sulfoxide reductase sorting nextin 17	PMSR PX,fn3,pkinase,SAM,EPH_lb	4.1 4.1
	406538	Arustusz	ns.210000	Target Exon	typsin	4.1
	424349	AF141289	Hs.145550	solute carrier family 7 (catlo	6a_permeases	4.1
	441164		Hs.7724	KIAA0963 protein	helicase_C	4.1
15	421318	U63973	Hs.103501	rhodopsin kinase	pkinase,pkinase_C,RGS	4.1
	439340	AB032436	Hs.6535	brain-specific Na-dependent in	sugar_tr.BT1	4.1
	417447		Hs.293267	ESTs	Glyco_hydro_31	4.1
	409693	AA010233	Hs.55921	glutamyt-protyt-tRNA synthetas	WHEP-TRS,GST_C,HGTP_antic	4.1
20	403655			NM_003071:Homo sapiens SWI/SNF	SNF2_N,heficase_C,zf-C3HC	4.1
20	411142	NM_014256		transmembrane protein 3	GalactosyLT	4.1
	437016		Hs.5398	guarine monphosphate synthetas	- GMP_synt_C,GATase	4.1
	422699		Hs.119257	ems1 sequence (mammary tumor a	SH3,HS1_rep	4.1 4.1
	427202 421380	BE272922 D31833	Hs.173936 Hs.1372	interleukin 10 receptor, beta arginine vasopressin receptor	Tissue_fac 7tm_1	4.1
25	434142	U47927	Hs.3759	ubiquitin specific protease 5	zf-UBP,UCH-2,UBA,UCH-1	4.1
23	427407		Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,re	4.1
	413749	AI929320	Hs.75516	tyrosine kinase 2	pkinase	4.1
	411927		Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1	4.1
	419726	U50330	Hs.1274	bone morphogenetic protein 1	EGF, CUB, Astacin	4.1
30	423814	AF105020	Hs.132989	putative protein O-mannosyltra	PMT,MIR	4.1
	451355	NM_004197	Hs.444	serina/threonine kinase 19		4.1
	422556	NM_006245	Hs.118244	protein phosphalase 2, regulat	856	4.1
	428284		Hs.183435	NM_004545:Homo saplens NADH de		4.1
25	431968	AF117222	Hs.272261	UDP-Gat:betaGlcNAc beta 1,3-ga	GalactosyLT	4.0
35	443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome	4.0
	410039	AF207989	Hs.58014	Homo saplens, Similar to G pro	7tm_3	4.0
	431066	AF026273	Hs.249175	interteukin-1 receptor-associa	pkinase,death	4.0
	452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	pkinase	4.0 4.0
40	403692 442549	AI751601	Hs.8375	NM_007037*:Homo sapiens a disi TNF receptor-associated factor	Reprolysin,tsp_1,Pep_M12B zf-C3HC4,MATH,zf-TRAF	4.0
70	427239	BE270447	rs.03/3	ubiquitin carrier protein	UQ_con	4.0
	451125	AAD15779	Hs.226923	ESTs	Y_phosphatase	4.0
	425081	X74794	Hs.154443	minichromosome maintenance def	MCM	4.0
	402171	A14134	13.101110	Target Exon	C2	4.0
45	402665			Target Exon		4.0
	420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B	myosin_head,IQ,MyTH4,SH3,	4.0
	412187	U68487	Hs.73739	5-hydroxytryptamine (serotonin	7tm_1	4.0
	412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	POZ,DEP,OIX,Dishevelled	4.0
50	425786	. U35234	Hs.159534	protein tyrosine phosphatase,	fn3,lg,Y_phosphatase,DSPc	4.0
50	424288	AW137198	Hs.278682	Phosphatidylglycerophosphale S		4.0
	452230	AW135360	Hs.224170	ESTs	pkinase	4.0
	408449	NM_004408		dynamin 1	PH,GED,dynamin,dynamin_2	4.0 4.0
	423883 422676	AF250238	Hs.134514	ATP-binding cassette, sub-fami	ABC_tran,pholoRC,SRP54,Ca 7tm_1	4.0
55	458639	D28481 BE247683	Hs.1570 Hs.14611	histamine receptor H1 dual specificity phosphatase 1	DSPc	4.0
33	400726	BL247003	113.14011	C13000717*:gi[129376]sp]P26196	DEAD,helicase_C	4.0
	405370			NM_005569*:Homo sapiens LIM do	pkinase, LIM, PDZ	4.0
	413654	AA331881	Hs.75454	peroxiredoxin 3	AhpC-TSA	4.0
	432917	NM_014125		PRO0327 protein		4.0
60	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L	sugar_tr	4.0
	424512	X53002	Hs.149846	Integrin, beta 5	integrin_B,EGF	4.0
	TABLE 22B:					
65			t identifier number			
ÇÜ		. Gene cluster				
	Accession:	Genbank acces	ssion numbers			
	Pkey	CAT Number	Acenaelan			
	410191	11824_1		A A D A D D D A A 1970070 A A CODORC A A D COD	70 E31073 WIDERAN AWKDEREAA VOOTS	6 AAA31579 AA970887 AI885085 AI767835
70	410151	11024_1		24 Al000871 AW242322 AW007204 W68		
, ,			AA776726 AI04097		EUS ANNO 1100 ATT 100510 DEELEGTT	**************************************
	415341	1534442_1				
	415995	1584_1			02206 AA774879 AW630959 AI43962	3 AI933994 AW751282 AW374413 AA578823
	110000					098 AI416986 AW769231 AI767111 AA293723
75			Al422290 AA46503			
• •	418984	1809680_1		•••		
	424339	23827_1	BE257148 BE3121			T66208 BE255806 BE254484 AA324163 H07952
		-		2 Al204971 Al282924 AW192547 Al6527		
0.0	427010	27436_1	AW138332 AW207	450 AW138931 AW136963 NM_012219 A	4F043938 AA931386 A1084600 AA975	999 BE551105 AA450260 Al080368 AA324154
80				01 AL118847 W44458 AI765270 AA4531		
	427239	27647_1				BE292738 BE261776 BE314300 BE267719
				76 BE295291 BE297066 AA210923 BE40	17519 H51344 BE622905 AW248281 A	WZ50313 T19021 AA355115 AA316879
			BE269633 BE6219			
	427326	277229_1	A1287878 A180416	AA400787		
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D79989 NM_014770 U81031 AA352392 AA984512 H38328 AL120358 AL134787 AL134589 AI637763 AI671506 AA526909 AI651627 AW243560
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BE266413 BE278348 BE280885 BE278833 BE281417 BE407786 BE378176 BE392818 AW377597 BE395951 BE393978 AW327483 BE394175
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                                      BE385795 BE275663 BE3
           432118
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A7767195 AA339439 R13005 R23431 AW961069 AA233819 AA224118 R19518 AJ890314 Z46184
NM_002959 X98248 AA233278 AA846376 AJ470560 AJ470533 BE327147 AW291971 AA017125 AJ198417 AJ365213 AJ168442 AJ337018
           432499
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           433075
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10
                                      AH75049 H85459 AA969895 AA888000 AA418326 AA418378 N71981 AL043634 AA426361 AA418275 AA232975 AL036861 BE277220 BE387505
                                      N99710 AW375004 A
                                      AB029396 T04934 R21715 R19005 H11563 H14256 R46605 Z40857 BE218899 AI457785 BE550988 AI693847 AA961017 H40944 M78617
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                                      H40089 AA018091
15
                                      AA648502 AA814365 AW976711 AA746117
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                                      L48489 AL022312 D13789 AT761974 AW173260 AW271715 AA837437 AU075278 Al367012 Al953032 Al571173 H44868 AA743691 H47026
AA837368 AA829826 AA713585 AW502618 AW500856 AW501353 AW499765 AA339125 H19141 H29645 R18883 AW450375 AA326081
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20
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                                      AI732707 AI742120
AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088
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25
           459298
                                      R86701 R84600 AL157655...
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           TABLE 22C
           Pkey: Unique number corresponding to an Eos probeset
           Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495
30
           Strand: Indicates DNA strand from which exons were predicted
           Nt_position: Indicates nucleotide positions of predicted exons
                                                    Nt_position
105629-105760
                                      Strand
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           400471
                        9931670
                                      Minus
           400518
                        9796703
                                                    37240-37774
                                      Plus
                                                    40629-40934
            400551
                        9801071
                                      Minus
            400563
                         9844011
                                      Plus
                                                    81941-82434
            400565
                        9863505
                                      Minus
                                                    93178-93429
51524-51786
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                        8131629
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                                      Minus
            400833
                         8705148
                                                     187599-188138
                                       Minus
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                                      Plus
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                        9188605
                                      Plus
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            400846
                        9188605
                                      Plus
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            400894
                         9958307
                                       Minus
            400933
                         7651935
                                       Minus
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                         8085497
                                      Minus
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                         9966714
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                         7210005
                                       Plus
                          9438648
                                                     150981-152128
            401180
                                       Minus
            401215
                         9858408
                                       Plus
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                         9800073
                                                     13622-15130
            401281
                                       Minus
            401454
                                                     114659-114832
                         9186923
                                       Minus
            401488
                         7341775
                                       Plus
                                                     54523-54686,55364-55451,55737-55846,58047-58175,58261-58356
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                         8072607
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            401577
                                                     139377-139674,141195-141281,142217-142340
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            401736
                                                     1771-1894
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402115
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                                       Minus
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            402209
                                       Minus
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                                                      174215-174380
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                                       Minus
                                                      87638-87924
            402758
                          9213869
                                       Plus
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	402760	9213869	Plus	136829-136952,137336-137521
	402823	8217451	Phrs	57916-58170,58475-58759,59580-59867
	402912	7263904	Plus	145965-146257,150876-151368
5	402915	7406502	Minus	140-278
J	402918 403213	7406502 7630897	Minus	361-474,541-687
	403213	7656833	Minus Minus	162572-162739,164442-164540
			Minus	167439-167606 73832-73962
	403268 403379	7230852 9438244	Minus	117348-117560
10	403578	8736093	Plus	65668-65859
10	403672	7283286	Minus	96600-95881,96951-97280,97393-97594
	403692	7387384	Minus	93803-93938
	403092	7770492	Plus	112901-113045
	403771	7711972	Minus	1731-1941
15	403949	6010176	Minus	1669-2740
IJ	404199	8152087	Plus	127737-127796,128080-128210,129888-130054,132545-132869
		8152087		135325-135486
	404528		Plus	
	404596	9958262	Minus	104807-105043
20	404676	9797204	Minus	56167-56342,58066-58189,58891-59048,60452-60628
20	404679	9797204	Plus	125964-126092,126691-127011,127774-127893
	404716	9838068	Minus	123145-123417
	404757	7706327	Plus	100933-101083,101580-101782
	404879	5103013	Plus	78346-78473,78693-78893
25	404946	7382189	Plus	134445-134750
25	404953	7387324	Plus	16588-17031,
	404968	6899755	Plus	39287-39506
	405020	7137674	Plus	106606-107309
	405137	8570507	Ptus	158969-159423
30	405187	7229826	Plus	117025-117170,118567-118736
20	405202	7230116	Plus	40209-40429
	405282	3810573	Minus ·	10482-10689
	405370	2078469	Minus	38980-39111
	405371	2078469	Minus	47657-47766,48461-48596 153074-153343,154501-154598,156879-156999,158863-159051,159910-160053,161109-161229,163035-163131,165163-
35	405473	8439781	Ptus	165259,165868-166003,167375-167552,169252-169364,171127-171281
	405474	8439781	Plus	172005-172175
	405546	1054740	Plus	124010-124183
	405574	3820491	Minus	33200-33646
40	405594	6960456	Plus	161628-161734,162823-163014,164439-164652
40	405683	4508157	Minus	21701-21844
	405697	4309923	Minus	56765-57010,57696-58016
	405714	4156179	Minus	42789-43553
	406128	9159110	Plus	50425-50876
4.5	406370	9256130	Plus	125320-125482
45	406432	9256504	Plus	3804-3930,4026-4120,4929-5109
	406441	9280715	Ptus	26200-26458
	406458	9756020	Ptus	145874-146911
	406495	7711328	Minus	174661-174978
	406496	7711328	Minus	178947-179264,181779-182087
50	406530	7711474	Minus	11703-11860,14711-14829,14920-14984,16232-16448,16916-17087
	406538	7711478	Plus	35196-35367,38229-38476,40080-40216,43522-43840
	406591	8224230	Minus	2117-2257,2436-2540
	406617	8439858	Plus	36430-36552
55				
	Table 22/	Litele about 770	O GORGO HIS O	endated in overian cancer compared to non-malianant adult overies. These were selected as for Table 20A, except that the railo of

Table 23A lists about 779 genes up-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer lo "average" normal ovaries was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 93rd percentile value amongst various non-malignant adult ovaries, the "average" ovarian cancer value was greater than or equal to 200 units.

60

TABLE 23A:
Pksy: Unique Eos probeset identifier number
Ex. Accn: Exemplar Accession number, Genbank accession number
UG ID: UniGene number
Title: UniGene gene title
Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal ovaries

65

37.8 29.2
27.6
27.2
26.5
25.9
25.8
25.0
23.3
22.8
22.7
22.6
21.4
21.4
21.2

					************	20.7
	424420 422645		Hs.146688	prostaglandin E synthese glycogen synthase kinase 3 glo	MAPEG,SS,TM,MAPEG pkinase,SS,Ets	20.7 20.7
	436725		Hs.118890 Hs.136912	hypothetical protein MGC10796	pariaso,oo,co	20.4
	422098		Hs.111497	similar to mouse neuronal prot	TM	20.2
5	429556		Hs.98988	ESTs	SS.pkinase,PMP22_Claudin	20.1
_	434068		Hs.127274	ESTs	SS	20.0
	423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	19.9
	423652		Hs.130712	Homo sapiens clone 23929 mRNA	ABC1,SS,PID,PID	19.8
10	422179		Hs.112667	dynein, exonemal, intermediate	WD40,SS	19.3 18.5
IU	441356		Hs.182885	ESTs, Weakly similar to JC5024	SS,TM,ank SH3,SH3	17.2
	418969 432631	W33191 H08379	Hs.28907 Hs.165563	hypothetical protein FLJ20258 hypothetical protein OKFZp434N	TM, DnaJ, UBA, Arl Gap, homeob	17.2
	439108	AW163034	Hs.6467	synaptogyrin 3	Synaptogyrin, SS, TM, PDZ, WD	17.2
	451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF, RhoGAP, PH, C2	17.2
15	434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	16.9
	413244		Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	16.3
	456642		Hs.109752	putative c-Myc-responsive		16.2
	421612	AF161254	Hs.106196	8D6 antigen	kd_recept_a,SS,TM	16.0
20	456177		Hs.79414	prostate epithelium-specific E	Ets,SAM_PNT	15.7 15.6
20	409261	BE315042	Hs.19210	hypothelical protein MGC11308	aldedh	15.6
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famili Target Exon	Band_41	15.4
	401278 444804	AI084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,1	15.1
25	421495	AI583067	Hs.149152	ESTs, Weakly similar to RHOP M		15.0
	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	15.0
	442620	C00138	Hs.8535	Homo sepiens mRNA for KIAA1668	\$S,RNA_pol_K	14.9
	406901	M14624		gb:Human 4-beta-galactosyltran		14.6
20	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
30	455557	AW995839		gb:QV4-BN0044-110200-108-h07 B	Metallophos	14.4
	416819	U77735	Hs.80205	plm-2 oncogene	pkinase,SS,TM,OTU,K_letra	14.3
	444441	AW613841	Hs.301394	hypothetical protein MGC3101	zf-C2H2,SS	14.0 14.0
	405918 407605	M88357 W03512	Hs.6479	gb:Homo sapiens DNA-binding pr hypothetical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	13.6
35	447304	Z98883	Hs.18079	phosphalidylinositol glycan, c	SS.Peptidase_C2	13.6
55	402365	250003	118.10075	Target Exon	SS,SS,TM,ig	13.4
	407767	W15398	Hs.38628	hypothetical protein	SS,zI-CCCH	13.3
	432931	AF174487	Hs.293753	Bci-2-related ovarian killer p		12.7
	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
40	423801	NM_015071	Hs.132942	GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
	430397	A1924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.6
	411570	BE144584	Hs.314341	ESTs	20.00.00	12.5
	400206	4100 4505		Eos Control	SS,SS,Glyco_tranf_43,COLF	12.3 12.2
45	457941	A1004525	Hs.14587	ESTs, Weakly similar to AF1518 calpain 4, small subunit (30K)	SS,TM,SS,TM efhand,SS,CAP_GLY	12.0
73	412674 400460	X04106	Hs.74451	C11002253*:gij129091 spjP23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
	417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.6
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	11.5
	424707	BE061914	Hs.10844	Homo saplens cDNA FLJ14476 fis	SS,SS,TM,Sema	11.5
50	444359	AI697160	Hs.143594	ESTs, Weakly similar to HS4L_H		11.5
	435158 -	AW663317	Hs.65588	DAZ associated protein 1	mm,SS,mm	11.3
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA		11.3
	450503	R35917	Hs.301338	hypothetical protein FLJ 12587	SS	11.2
55	427448	BE246449	Hs.2157	Wiskolt-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2 11.2
22	406230	41.040403	11- 400404	Target Exon	SS,TM,cys_rich_FGFR	11.2
	432143	AL040183 AF234887	Hs.123484 Hs.57652	Homo saplens, clone IMAGE:4178 cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	11.1
	433573 413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	11.1
	431974	AW972689	Hs.200934	ESTs	bZIP	11.0
60	428167	AA770021	Hs.16332	ESTs	SS,lg,fn3	11.0
- •	450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS ·	10.9
	412738	N34731	Hs.74562	siah binding protein 1; FBP in	homeobox	10.9
	445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,flpoc	10.9
~~	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.7
65	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS STORY STREET	10.6
	444607	AW405635	Hs.293587	ESTS	SS,PI-PLC-X,PH,PI-PLC-Y,C	10.6
	404333			C7001735*:gij7768636jdbjjBAA95	wwd	10.5 10.5
	401210	A1202440		C12000519:gij7710046 ref NP_05 ribosomal protein S18	SS,TM	10.5
70	434743	Al363410	Un 2700	low molecular mass ubiquinone-	SS SS	10.4
70	434030 450029	AW162336 AW073380	Hs.3709 Hs.267963	hypothetical protein FLJ10535	SS_Pyridox_oxidase,zI-C2H	10.4
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	SS,TM,transmembrane4	10.3
	438185	Y19188	Hs.320461	ESTs	SS	10.2
	432031	AF039196	Hs.272367	hairless protein (putative sin	jmjC	10.2
75	405371			NM_005569°:Homo saptens LIM do	pkinase,UM,PDZ	10.1
	456741	W37608	Hs.184492	ESTs	SS,pkinase	10.1
	458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	10.0
	456977	AK000252	Hs.169758		alde first and DO THE ale	10.0
00	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	10.0 9.9
80	445625	BE246743	U= 403040	hypothetical protein FLJ22635	SS,TM Amd-CoA dh Amd-CoA dh M	9.8
	423366	ZB0345	Hs.127610		Acyl-CoA_dh,Acyl-CoA_dh_M	9.8
	458216 451721	AW024282	Hs.104938 5 Hs.26915	specifin, beta, non-enythrocyt	spectrin, PH, CH, SS, Peptida	9.7
	421445	AA913059	Hs.104433		asp,SS,TM,lon_trans,K_tet	9.7
	761770				259	
					/ 14	

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	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS.PWWP.PHD	9.7
	443780	NM_012068		activating transcription facto	bZIP,NTP_transf_2,SS,TBC	9.7
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.7
5	444202 427640	AL031685 AF058293	Hs.12785 Hs.180015	KIAA0939 protein D-dopactirome tautomerase	SS,TM,Na_H_Exchanger,ABC2 MIF,late_protein_L2,SS,GS	9.7 9.6
,	419167	AL589535	Hs.94875	ESTs, Weakly similar to A35363	SS	9.6
	424518	L29472	Hs.1802	major histocompatibility compl	TM.ig,MHC_II_beta,SS,TM,A	9.6
	427497 · 420423	AW139476 AA827718	Hs.31240 Hs.88218	ESTs ESTs	SS	9.6 9.6
10	414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	9.6
	407893	BE408359	Hs.43621	Homo saplens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.5
	408294	BE141732	Un 227460	gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp SS,TM,TGFb_propeptide,TGF	9.5 9.4
	442232 416866	Al357813 AA297356	Hs.337460 Hs.80324	ESTs, Weakly similar to A47582 serine/threonine protein phosp	Metallophos, Metallophos	9.4
15	419823	AW271708	Hs.118918	ESTs, Wealty similar to M2OM_H	SS,TM	9.4
	422625	AW504698	Hs.155976	cullin 48	SS,SS,Cutlin,Cutlin	9.3
	401264 407507	U73799		C18000090*:gl[6678656]ref[NP_0 gb:Human dynactin mRNA, partia	SS,laminin_Nterm,laminin_ SS,TM,HCO3_cotransp,CAP_G	9.3 9.2
	400833	010133		C11000890:gi[3746443]gb[AAC639	SS,TM,7tm_1	9.2
20	422064	AW452589	Hs.335742	ESTs	ТМ	9.2
	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2 9.1
	421363 427397	NM_001381 AI928685	Hs.103854 Hs.177656	docking protein 1, 62kD (downs calmodulin 1 (phosphorylase ki	PH,IRS,TM,PH,IRS,trypsin, efhand,RmaAD,SS,efhand	9.1
	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	9.0
25	434798	AAB12046		ESTs -	SS,myb_DNA-binding,myb_DN	9.0
	422639	AI929377 AI525268	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt TM	9.0 9.0
	447867 442472	AW806859	Hs.164303	ESTs gb:MR0-ST0020-081199-004-c03 S	SS,TM,inos-1-P_synth,Occl	8.9
	455588	Al129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.9
30	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
	429527 432603	AA454184 AA554920	Hs.289014 Hs.105794	ESTs UDP-glucose:glycoprotein gluco	SS,TM	8.9 8.9
	410338	W03445	Hs.38205	gb:za05g11.r1 Soares melanocyt	pkinase	8.9
	452833	BE559681	Hs.30736	KIAA0124 protein	WD40	8.9
35	407363	AF035032	Hs.181125	gb:Homo sapiens clone MCA1L my	SS,tg,SS,G_glu_transpept	8.8
	414413 431765	BE294877 AF124249	Hs.268541	gb:601174162F1 NIH_MGC_17 Homo novel SH2-containing protein 1	SS SH2,88,TM	8.8 8.8
	421694	BE387430	Hs.106880	bystin-like		8.8
40	453683	AL079854	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.8
40	418736	T18979	Hs.87908	Snt2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.7 8.7
	450958 419725	AL137669 U66048	Hs.348012 Hs.92683	Homo sapiens mRNA; cDNA DKFZp4 Homo sapiens clone 161455 brea	•	8.7
	415126	D60945	110.02000	gb:HUM141D04B Clontech human f	SS,TM	8.7
15	406301			Target Exon	TM CAMPOOK Abased TM	8.6
45	418843 433396	AJ251016 AJ742071	Hs.89230 Hs.133205	potassium intermediate/small c ESTs	TM,CaMBD,SK_channel,TM SS,TM	8.6 8.6
	434333	AA186733	Hs.292154	stromal cell protein	00,1111	8.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
50	452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6 8.6
50	422418 447859	AK001383 AK002194	Hs.116385 Hs.19851	hypothelical protein FLJ10521 peroxisomal biogenesis factor	RhoGEF	8.6
	420836	AW958453	Hs.204959	hypothelical protein FLJ 14886	SS,ras	8.6
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	8.6
55	419639	AK001502	Hs.91753	hypothetical protein	authored of CC TH em	8.6 8.5
22	429712 452554	AW245825 AW452434	Hs.211914 Hs.58006	ENSP00000233627*:NADH-ubiquino ESTs, Weakly similar to ALU5_H	oxidored_q8,SS,TM,rrm SS,PAS,HLH	8.5
	441076	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343		8.5
	428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
60	421901	AB014554 AW450211	Hs.109299 Hs.126825	protein tyrosine phosphalase, ESTs, Weakly similar to A46302	SAM, SS, TM, mm, PDZ SS, TM, HSP20, 7tm_1	8.4 8.4
00	441363 443801	AW206942	Hs.253594	intron of: trichorhinophalang	GATA	8.4
	432862	AW004958	Hs.236720	amnionless protein	SS,MATH,ZETRAF,ZEC3HC4	8.4
	431849	A1670823	Hs.85573	hypothetical protein MGC10911	SS,TM	8.4 8.3
65	423662 404365	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc Target Exon	SS SS	8.3
05	425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,he	8.3
	423098	AA321980	Hs.204682	ESTs		8.3
	434552	AAB39618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
70	418361	AW505368	Hs.12460	gb:UI-HF-BNO-atu-d-03-0-UI.r1 chromosome 4 open reading fram	SS,pkinase	8.2 8.2
70	·427433 420138	D82070 BE268854	Hs.177972 Hs.177729	ESTs	SS	8.2
	426391	AW161050	Hs.169611	second mitochondria-derived ac	SS	8.1
	457613	AA598869	Hs.173770	ESTS	00 TH ADO 44 - 05 5	8.1
75	427502	AJ811865 AL117488	Hs.7133	Homo saplens, clone IMAGE:3161 Human clone 23564 mRNA sequenc	SS,TM,ABC_tran,Glyco_tran SS	8.1 8.1
13	437215 423384	AL117488 AL133632	Hs.127808	Homo sapiens mRNA; cDNA DXFZp4	~	8.1
	447151	AJ022813	Hs.92679	Homo saplens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	8.0
	431898	AK000020	Hs.272018	hypothetical protein FLJ20013	CO VECCE ALDERET Inches	8.0
80	454291	AW384847	Hs.213534 Hs.239784	ESTs, Weakly similar to MUC2_H human homolog of Drosophila Sc	SS,XRCC1_N,BRCT,lactamase SS,TM,fg	8.0 8.0
υU	430354 459302	AA954810 NM 00231	4 Hs.36566	LIM domain kinase 1	- Control of the Cont	8.0
	422765	AW409701		bacutoviral IAP repeat-contain	BIR,TK,SS,TM	8.0
	425944	AK000664	Hs.164256		SS,zI-C2H2,mm	7.9 7.9
	450873	BE464016	Hs.238956	ESTs ·		1.9
					260	

	454946	414046406	11- 0000	FOT-		7.0
	454246 450635	AW245185 AW403954	Hs.6996 Hs.25237	ESTs	4HBT	7.9 7.9
	422305	AI928242	Hs.293438	mesenchymal stem cell protein ESTs, Highly similar to AF1984	SS	7.9
	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase,SS,TM	7.9
5	413534	BE146961		gb:QV4-HT0222-011199-019-b12 H	SS,TM	7.8
	446931	A1348856	Hs.21627	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho		7.8
	421726	AK001237	Hs.319088	hypothetical protein FLJ 10375	TM	7.8
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	7.8
10	448993	AJ471630	11 0040	KIAA0144 gene product	5	7.8
10	443136	NM_001440		exostoses (multiple)-like 3	Exostosin,SS,TM	7.8
	427725 400923	U66839	Hs.180533	mitogen-activated protein kina Target Exon	pkinase SS,TM,DUF289	7.8 7.8
	419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
	458834	AI566883	Hs.196446	ESTs	00,1111	7.8
15	427899	AA829286	Hs.332053	serum emyloid A1	SS,SAA_proteins,SS,SAA_pr	7.7
	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	7.7
	436543	NM_002212	Hs.5215	integrin beta 4 binding protei	elF6	7.7
	431811	AB040972	Hs.301696	hypothetical protein FLJ11560	SS,TM,Band_7,AAA,cdc48_N,	7.7
20	414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	7.7
20	455885	BE153524		gb:PM0-HT0339-241199-002-C03 H	SS.pkinase	7.7
	427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	7.6
	430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6 7.6
	427273 450334	AW139032 AF035959	Hs.107376 Hs.24879	hypothetical protein DKFZp434N phosphalidic acid phosphatase	SS,SS,TM PAP2,SS	7.6 7.6
25	413564	BE260120	NS.24019	gb:601146990F1 NIH_MGC_19 Homo	PAP 200	7.6
20	410397	AF217517	Hs.63042	DKFZp564J157 protein	6S,homeobox,UPF0160,DUF23	7.6
	439539	BE348395	Hs.121589	EST8	SS,Fork_head	7.5
	400286			C16000922:gi[7499103[pir][T209	TM,ABC_tran,ABC_membrane	7.5
	416472	AA180756	Hs.340316	ESTs, Moderately similar to Al.	zf-C2H2	7.5
30	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin, Reprolysin, Pe	7.5
	419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	7.5
	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX58	7.5
	406495			Target Exon	SRCR,TM,Acetyltransf	7.5
35	448043	A1458653	Hs.201881	ESTs	PHD	7.4
33	401724	177640	U. 4767	C16001374:gi[6755086]ref[NP_03	TMPLATISS	7.4 7.4
	424263 428092	M77640 AW879141	Hs.1757	L1 cell adhesion molecule (hyd ESTs	fn3,lg,lRK,SS,TM,fn3,lg,R SS.TM	7.3
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	7.3
	400137	711020100	110.01400	Eos Control	resuzzor repotrațios cub	7.3
40	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	7.3
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
	448859	BE272446	Hs.265317	hypothetical protein MGC2562	SS,TPR	7.3
45	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.3
45	429299	A1620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	7.3
	401674	*********	11. 470400	C16001417*:gij7500345[pir][T21	FAD-oxidase_C,FAD_binding	7.2
	412289	AW935967	Hs.170162	KIAA1357 protein	SS CS TMNs Co Fr Colubeia	7.2
	424198 412173	AB029010 171071	Hs.143026	KIAA1087 protein gb:yc50b05.r1 Stratagene liver	SS,TM,Na_Ca_Ex,Calx-beta, CPSase_L_chain	7.2 7.2
50	438113	AI467908	Hs.8882	ESTs	SS,TM,7Im_1	7.2
50	429869	AI907018	Hs.15977	Target CAT	um	7.2
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_lb,Lipase_GDSL,SS,	7.2
	425041	Al377150	Hs.150914	ESTs	SS	7.2
	448340	AJ492910	Hs.32362	ESTs		7.1
55	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	7.1
	431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
	421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	7.1
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	7.0
60	430281	A1878842 Z95636	Hs.237924	CGI-69 protein	mito_carr,SS,TM laminin_EGF,laminin_G,EGF	7.0 7.0
00	444672	295030	Hs.11669	iaminin, alpha 5	00 17 0	7.0
	405928 421321	NY UUESUG	Hs.103502	Target Exon glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.9
	439905	AW799755	Hs.110953	refincic acid induced 1	HLH	6.9
	451937	AF119664	Hs.27299	transcriptional regulator prot	SS,Integrin_B,fn3,Calx-be	6.9
65	426675	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.9
-	438627	AI087335	Hs.123473	ESTs	TM,Reticulon	6.9
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,addored_nitro,SS	6.8
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	6.8
70	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.8
70	405346	A A CO (C40	U- 24204	Rag C protein	RCC1	6.8 6.8
	432746	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF1BD	6.7
	452798 426315	Al918771 AA854219	Hs.257170 Hs.348137	ESTs Homo sapiens, clone IMAGE:3542	SS,TM,TNFR_c6 SS,crystall	6.7
	440317	BE561888	113.040101	gb:601346093F1 NIH_MGC_8 Homo	- July Jum	6.7
75	438857	Al627912	Hs.130783	Forssman synthetase	SS.RA.RasGEF.RasGEFN	6.7
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase	6.7
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.7
	423106	N52572	Hs.13702	ESTs, Moderately similar to AL		6.7
00	453101	AW952776	Hs.94943	ESTs	TM	6.7
80	420307	AW502869	Hs.66219	EST8	SS,TM	6.7
	415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.7
	454262	AW612232		ESTs	SS,TM,voltage_CLC,CBS	6.7
	409227 413908	AA806165 BE409966	Hs.130323	Homo saplens, clone IMAGE:3960	CC -4 (*31)	6.6 6.6
			Hs.323813	Homo sapiens, clone MGC:2867,	SS,zf-C2H2	0.0

	457274	AW674193	Hs.227152	mannani-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	6.6
	419157 431424	AA234540 AI222969	Hs.23871	ESTs ESTs	pkinase SS	6.6 6.6
_	412464	T78141	Hs.22826	ESTs, Wealty similar to 155214	SS,cadherin,crystall	6.6
5	430168 455035	AW968343 AW851734		DKFZP434I1735 protein gb:MR2-CT0222-011199-007-e10 C	SS,TM,efhand,efhand	6.6 6.6
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.6
	453367 450593	AW732847 AF129085	Hs.70573 Hs.25197	PKCI-1-related HIT protein STIP1 homology and U-Box conta	SS,TM TPR,SS,TM,Rhombold,lactam	6.6 6.6
10	420319	AW406289	Hs.96593	hypothetical protein .	ras,arf	6.6
	431131 431297	N84730 AA651771	Hs.250616 Hs.3076	isocitrate dehydrogenasa 3 (NA ESTs	isodh,isodh	6.6 6.6
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	SS,HECT,phostip	6.5
15	441307 454682	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM filament	6.5
13	407299	AW816029 AA460205	Hs.289770	gb:MR3-ST0220-151299-027-510 S ESTs, Wealdy similar to 138022	Manent	6.5 6.5
	422837	U25441	Hs.121478	doparnine receptor D3	7tm_1,SS,TM,7tm_1	6.5
	407722 417810	BE252241 D28419	Hs.38041 Hs.82609	pyridoxai (pyridoxine, vitamin hydroxymethylbilane synthase	pfkB,SS Porphobil_deam	6.4 6.4
20	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
	402197 419390	Al701162	Hs.90207	Target Exon hypothetical protein MGC11138	SS,TM,ATP1G1_PLM_MAT8,lg, SS,TM,PMP22_Claudin,PMP22	6.3 6.3
	447754	AW073310	Hs.163533	intron of HER4		6.3
25	444664 421190	N26362 U95031	Hs.11615 Hs.102482	map kinase phosphatase-like pr mucin 5, subtype 8, tracheobro	DSPc,Rhodanese,SS,TM Cys_knot,vwc	6.3 6.3
	432872	Al908984	Hs.279623	selenoprolein X, 1	DUF25,SS,Ribosomal_L3,PDZ	6.3
	430023 413343	AA158243 BE392026	Hs.227729 Hs.334346	FK506-binding protein 2 (13kD) hypothetical protein MGC13045	SS,FKBP,SS,PDGF,C2,PI-PLC SS,DnaJ	6.3 6.2
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.2
30	403128	ALICEETOS	U- 75102	KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_t	6.2
	413055 427812	AV655701 AA770424	Hs.75183 Hs.98162	cytochrome P450, subfamily IIE ESTs	p450 SS	6.2 6.2
	457761	AW401809	Hs.4779	KIAA1150 protein	SS,UM,SS	6.2
35	453099 426048	H62087 A1768853	Hs.31659 Hs.134478	thyroid hormone receptor-assoc ESTs	SS TM	6.2 6.2
-	407223	H96850		gb:yw03b12.s1 Soares melanocyt	SS,TM,SS,TM,DDOST_48kD	6.2
	445634 441197	A1624849 BE244638	Hs.344612 Hs.166	ESTs, Weakly similar to NEL1_H sterol regulatory element bind	W.d.	6.2 6.1
40	421707	NM_014921		lectomedin-2	Latrophilin,OLF,7tm_2,Gal	6.1
40	435750 432353	AB029012 NM_016558	Hs.4990 Hs.274411	KIAA1089 protein SCAN domain-containing 1	SS,TM SCAN	6.1 6.1
	427326	Al287878	115.274411	gb:qv23i06.x1 NCL_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	· 6.1
	447128	AI271898	U- 00/42	cyclin K	ford CC TALLY ATDees sub a	6.1
45	419444 457978	NM_002496 AA776638	ns.30443	Target CAT gb:ae78g04.s1 Stratagene schlz	fer4,SS,TM,V_ATPase_sub_a SS,PH,IQ,RasGEF,RasGEFN,R	6.1 6.1
2	410445	AA199830	11 074740	gb:zq75h01.r1 Stratagene hNT n		6.1
	431857 407143	W19144 C14076	Hs.271742 Hs.332329	ADP-ribosyltransferase (NAD; p EST	PARP,PARP_reg,SS,TM,Pepti SS,TM	6.1 6.0
50	408724	AI685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	6.0
50	436685 441583	W28661 AJ791499	Hs.5288 Hs.205742	Homo sapiens mRNA; cDNA DKFZp4 ESTs, Weakly similar to ALUA_H	SS,TM,pkinase,Activin_rec	6.0 6.0
	418802	AB028989	Hs.88500	mitogen-activated protein kina	WD40,Pico_P2A,M,SS	6.0
	414927 434314	T83587 BE392921	Hs.186476 Hs.3797	ESTs RAB26, member RAS oncogene fam	SS,Sulfatase ras,arf,SS	6.0 6.0
55	414157	BE297801	Hs.103845	ESTs, Moderately similar to i5	SS	6.0
	424415 406487	NM_001975	Hs.146580	enolase 2, (gamma, neuronal) Target Exon	enolase,SS,Atrophin-1,Atr SS,TM	6.0 6.0
	447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	6.0
60	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,ig	6.0 5.9
UU	442297 426440	NM_006202 BE382756	Hs.169902	phosphodiesterase 4A, cAMP-spe solute carrier family 2 (facil	PDEase sugar_tr,SS,TM,sugar_tr	5.9
	418256	AW845318	Hs.12271	f-box and leucine-rich repeal	SS,SS,TM,HSF_DNA-bind	5.9 5.9
	431543 430344	AW969619 AA476827	Hs.259768 Hs.171012	adenylate cyclase 1 (brain) hypothetical protein FLJ22349	TM HLH	5.9
65	428539	AW410063	Hs.184877	solute carrier family 25 (mile	mito_carr,SS,TM,profilin,	5.9
	403938 456950	AF111170	Hs.306165	Target Exon Homo sapiens 14q32 Jagged2 gen	Ephrin SS,TM,DSL	5.9 5.9
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.9
70	434357 443553	AW732284 AL040535	Hs.3828 Hs.9573	mevalonate (diphospho) decarbo ATP-binding cassette, sub-fami	GHMP_kinases,SS,TM ABC_tran,SS	5.9 5.9
	433333	AI016521	Hs.71816	v-ald murine thyrnoma vtrat onc	homeobox,pldnase,PH,pldna	5.9
	430600 409034	AW950967 AI684149	Hs.274348 Hs.172035	HLA-B associated transcript-3 hypothetical protein similar t	ubiquitin,SS,TM,G-patch,a SS	5.9 5.9
	421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11	SS,SS	5.9
75	431534	AL137531 AF231023	Hs.258890	Homo saplens mRNA; cDNA DKFZp4	SS,TM,ras SS,TM,ras SS,TM,ras SS,TM,ras	5.9 5.9
	409608 423464		Hs.55173 Hs.128856	cadherin, EGF LAG seven-pass G CSR1 protein	SS,TM,7tm_2,cadherin,GPS, Collagen,SS	5.9 5.9
	422379	AA932860	Hs.133864	ESTs	≠ pcn	5.8
80	443887 450122	NM_004729 BE313765	Hs.9933 Hs.343443	Ac-like transposable element ESTs, Weakly similar to 138022	zf-BED SS,TM,Y_phosphatase,LON,A	5.8 5.8
	404807			Target Exon	UPF0027	5.8
	445303 445631	AW362198 AK001822	Hs.12503	Interleukin 15 receptor, alpha Homo saptens cDNA FLJ10950 fis	SS,sushi,SS	5.8 5.8
	412091	R06185		gb:ye94d03_r1 Soares fetal liv	SS,TM,IBR,IBR	5.8
				•	262	

	446536	W74413	Hs.15251	hypothetical protein	SS	5.8
	432866	BE395875	Hs.279609	mitochondrial carrier homolog	milo_carr	5.8
	402393			ENSP0000085284*:CDNA FLJ20404	RhoGEF, PH, SS, zf-CCCH, vwd	5.8
5	413041	BE061580	Hs.61622	gb:MR0-BT0249-091299-201-c07 B	SS	5.8
,	414356 402916	AW505085	Hs.335147	gb:UI-HF-BN0-als-a-10-0-UI.r1 ENSP00000202587*:Bicarbonate t	SS,TM HCO3_cotransp,SS	5.8 5.7
	459133	U40343	Hs.29656	cyclin-dependent kinase Inhibi	ank,SS,Adap_comp_sub	5.7
	404757	0.5000 100		Target Exon	TM_zf-C2H2	5.7
10	409879 411219	BE083422 AW832917	Hs.56851	hypothetical protein MGC2668 gb:QV2-TT0003-161199-013-h06 T	SS,TM	5.7 5.7
10	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM_Steroid_dh,SS	5.7
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.7
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	h	5.7
15	446562 407117	BE272686 AA146625	Hs.15356	hypothetical protein FLJ20254 gb:zo71c07.s1 Stratagene pancr	hormone,SS,pfkB SS	5.7 5.7
1.5	444855		Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.7
	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
	407757	BE048414	Hs.165215	hypothetical protein MGC5395	SS,EF1G_domain,GST_C,GST_	5.7 5.7
20	419125 437141	AA642452 BE304917	Hs.130881 Hs.31097	B-cell CLL/lymphoma 11A (zinc hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.7 5.7
20	408905	AV655783	Hs.661	Target CAT	00,111,01,000_00	5.7
	450787	AB006190	Hs.25475	aquaporin 7	MIP,SS,TM	5.7
	432496	D45576	Hs.187959	ESTs	Camp DELTIC CC TIATIC Co	5.7 5.7
25	429367 422708	AB007867 AB017430	Hs.278311 Hs.119324	plexin 91 kinesin-like 4.	Sema,PSI,TIG,SS,TM,TIG,Se kinesin,homeobox,SS,TM,zf	5.7 5.7
	417442	AA199940	Hs.124039	ESTs		5.7
	432751	AF152099	Hs.278911	Interleukin 17C	SS	5.7
	432004	BE018302 AA047169	Hs.2894	placental growth factor, vascu	PDGF,SS SS,TM,Gtycos_transf_4	5.7 5.7
30	454151 456145	BE299427	Hs.154088 Hs.21446	hypothetical protein FLJ22756 KIAA1716 protein	SS, DIX, PDZ, DEP, Dishevelle	5.6
-	417677	NM_016055		CGI-118 protein		5.6
	451558	NM_001089		ATP-binding cassette, sub-famil	ABC_tran,SRP54,SS,TM,ECH	5.6
	408795	AW749126	Hs.170345	hypothetical protein FLJ13710	hormone_rec,zf-C4 SS,histone,histone	5.6 5.6
35	407204 452849	R41933 AF044924	Hs.140237 Hs.30792	ESTs, Wealty similar to ALU1_H hook2 protein	bZIP,SS,AhpC-TSA	5.6
-	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	and the same	5.6
	459271	AL045934		gb:DKFZp434M116_r1 434 (synony	SS,PI3_PI4_kinase,PI3Ka	5.6
	401609	122202	11- 40940	C16001614:gij7801278[emb]CAB91	V shaashalaaa fa2 la MAM	5.6 5.6
40	447827 409125	U73727 R17268	Hs.19718 Hs.343567	protein tyrosine phosphatase, axonal transport of synaptic v	Y_phosphatase,fn3,lg,MAM, SS,kinesin,PH,FHA,kinesin	5.6
••	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.6
	415514	F11301	Hs.138329	ESTs	SS,TM	5.6
	437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	5.6
45	406663 421678	U24683 AA419008	Hs.106730	Immunoglobulin heavy constant chromosome 22 open reading fra	SS SS,TM,UBA,Rhombold,SS,TM	5.6 5.6
-15	422472	R59096	Hs.279939	mitochondrial carrier homolog	mito_carr	5.6
	414918	Al219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	5.6
	434906	BE410573	Hs.283636	Homo sapiens, cione IMAGE:4053	SS,TM,Exo_endo_phos,BNR,A	5.6 5.6
50	414757 436014	U46922 AF281134	Hs.77252 Hs.283741	fragile histidine triad gene exosome component Rrp46	HIT RNase_PH,RNase_PH_C,SS,TG	5.6
50	421696	AF035306	Hs.106890	Homo saplens clone 23771 mRNA	inimo] infinimo] (Colochid	5.6
	408015	AW136771	Hs.244349	epidermal differentiation comp		5.6
	445871	Al702901	Hs.145582	ESTs, Weakly similar to FOR4 M	SS,TM,efhand,efhand	5.5 5.5
55 .	411813 425098	NM_014931 AW295349	Hs./21/2 Hs.8038	KIAA1115 protein ESTs	SS,TM,Y_phosphatase SS,TM	5.5
<i>33</i> .	429720	M79091	115.0000	gb:EST01239 Subtracted Hippoca	00,111	5.5
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	SS,TM,lipoxygenase,PLAT,s	5.5
	449225	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
60	423233 432538	BE048021 BE258332	Hs.11067 Hs.278362	ESTs, Highly similar to T46395 male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5 5.5
O	408215	BE614290	113.210002	syntaxin 10	SS,SS,TM,HLH,TRM,zFCCCH	5.5
	406244			Target Exon		5.5
	436041	AIB03516	Hs.272891	hippocalcin-like protein 4	SS,efhand,TGF-beta,TGFb_p	5.5 5.5
65	422013 442451	N92696 A1498080	Hs.293354 Hs.129616	ESTs ESTs	SS,TM SS	5.5 5.5
05	427859	AA416856	Hs.98170	ESTs	SS,TM,DUF60,trypsin,CUB,u	5.5
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	5.5
	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase,SS,TM,synaptobrev	5.4 5.4
70	441456 431630	Al458911	Hs.127765 Hs.265829	ESTs Integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	5.4 5.4
70	415976	R43144	Hs.21919	ESTs	TM	5.4
	447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tall,M	5.4
	431275	T56571	Hs.10041	ESTs	SS,HLH	5.4
75	404343	BE299671	Hs.256310	C7002191*:gi[5053028]gb]AAD388	SS,ABC_tran	5.4 5.4
13	431461 421779	A)879159	Hs.108219	likely artholog of mouse ZFP28 wingless-type MMTV integration	SS,wnt.SS	5.4
	418678	NM_00132		cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.4
	457310	W28363	Hs.239752	nuclear receptor subfamily 2,		5.3
90	417193	AJ922189	Hs.288390		SS audia SS audia	5.3 5.3
80	432545 455573	X52486 Al279811	Hs.3041	uracil-DNA glycosylase 2 Homo sapiens, clone IMAGE:3953	cyclin,SS,cyclin	5.3
	456573 409164	AA706639		gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hint,HH_signal,tubu	5.3
	442296	NM_00727	5 Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.3
	438670	Al275803	Hs.123428	ESTs		5.3

	400257			ENSP00000000452:BAD protein (B	SS,hormone_rec,zf-C4	5.3
	449514	AW970440	Hs.23642	protein predicted by clone 236	SS,PX,art,lipocalln,PHD,z	5.3
	427336	NM_005658		TNF receptor-essociated factor	MATH, SS, MATH, A2M_N, A2M, NT	5.3 5.3
5	414551 447960	AI815639 AW954377	Hs.76394 Hs.26412	encyl Coenzyme A hydratase, sh ring finger protein 26	ECH_Peptidase_U7,SS,TM SS,TM_Cbl_N,Cbl_N2,Cbl_N3	5.3
•	430605	AJ245433	Hs.247323	G4 protein	SS,TM,G-patch,ubiquitin,a	5.3
	456849	AA622394	Hs.153177	ribosomal protein S28	SS,TM	5.2
	430513	AJ012008 BE244700	Hs.241586 Hs.147049	G6C protein	SS,TM,GST_C,abhydrolase	5.2 5.2
10	424437 427815	BE072019	Hs.12851	cut (Orosophila)-like 1 (CCAAT phosphatidylserine synthase 2	CUT,homeobox,beta-lactama SS,TM,7tm_1	5.2
	417903	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.2
	420476	AW575863	Hs.136232	ESTs	SS,HLH	5.2
	409960	BE261944	Hs.7393	hexoldnase 1	SS,TM	5.2 5.2
15	436325 444439	AL390088 AI458883	Hs.143545	hypothetical protein from EURO hypothetical protein MGC11303	SS,Synapsin_C,SS SS,TM,PAF-AH_p_li	5.2
13	412915	AW087727	Hs.74823	NM_004541:Homo saptens NADH de	041114711111111111111111111111111111111	5.2
	418891	NM_002419		mitogen-activated protein kina	SH3,pkinase,pyridoxal_deC	5.2
	430323	U40714	Hs.239307	tyrosyl-tRNA synthetase	DUF101,SS,tRNA-synt_1b,tR	5.2
20	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	SS	5.2 5.2
20	457843 429252	AW138211 NM_004658	Hs.128746	ESTs RAS prolein activator like 1 (C2,PH,RasGAP,BTK,SS,C2,PH	5.1
	429225	BE250337	Hs.198273	Target CAT	WD40	5.1
	412104	AW205197	Hs.240951	Homo saplens, Similar to RIKEN	SS,TM	5.1
25	449750	H28586	Hs.32325	ESTs	SS,ras	5.1
25	442725	AI935786	Hs.131035	ESTs, Wealdy, similar to CA24_H	SS,SS,TM,PX,PH,PLDc,arres PH,SS,TM	5.1 5.1
	430390 421658	AB023186 X84048	Hs.241161 Hs.301760	KIAA0969 protein frequenin (Drosophila) homolog	efhand	5.1
	426928	AF037062	Hs.172914	retinal dehydrogenase 5 (11-ci	adh_short,SS,adh_short,TG	5.1
••	428924	AI016405	Hs.98959	ESTs, Wealthy similar to JC5314	SS,TM,lectin_c	5.1
30	458876	A1650896	Hs.195347	ESTs		5.1
	402632	AUDIA 4 4 7 7 7	Un 040	Target Exon	Fz,kringle,ig FKBP,TPR,SS	5.1 5.1
	413762 419451	AW411479 AI907117	Hs.848 Hs.90535	FK506-binding protein 4 (59kD) syntaxin binding protein 2	Sec1,SS,TM	5.1
	456155	R85182	Hs.7175	ESTs, Weakly similar to AF1568	SS ·	5.1
35	422396	W21872	Hs.7907	ESTs, Weakly similar to T19486		5.1
	413983	BE348384	Hs.279194	ESTs		5.0
	447598	A1799968	Hs.199630	ESTS	SS,TM	5.0 5.0
	425858 440511	AA364923 AF132959	Hs.7236	gb:EST75602 Pineal gland II Ho eNOS interacting protein	SS,TM,Peptidase_M10,fn2,h SS,TM,MAGE,Ribosomal_S17,	5.0
40	452661	AW449413	Hs.257152	ESTs	00,11141121004112001120011	5.0
	412800	AW950852	Hs.74598	polymerase (DNA directed), del	homeobox,SS,efhand,hexoki	5.0
	446603	NM_014835	Hs.15519	oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
	402884	A11624C000,	Un 24762	ENSP00000164597:PR00566.	taminin_Nterm,laminin_Nte	5.0 5.0
45	448580 431515	AW245890 NM_012152	Hs.21753 Hs 258583	JM5 protein endothelial differentiation, I	WD40,SS,TM,KOW,HLH 7tm_1	5.0
1.5	427204	AA405404	Hs.215725	ESTs	SS,SS	5.0
	425169	AW292500	Hs.128514	ESTs	SS	5.0
	412940	8E295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
50	440839	A1142078	Hs.135562	ESTs	SS 1	5.0 5.0
30	443814 434243	BE281240 AA628062	Hs.9857 Hs.200358	carbonyl reductase ESTs, Moderately similar to AL	SS,TM	5.0
	435605	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC_	5.0
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	5.0
E E	403055			C2002219 :gij12737280 ref XP_0	t and 60 mate allows	5.0
55	420856 405594	BE513294	Hs.205736	HLA class II region expressed	kazal,SS,TM,lg,pklnase E1-E2_ATPase,Hydrolase,SS	4.9 4.9
	405334			NM_021949:Homo sapiens ATPase, Target Exon	SS,TM,MIP	4.9
	419493	AF001212	Hs.90744	proteasome (prosome, macropaln	PCI,SS,CDK5_activator	4.9
60	413764	BE162704		gb:PM1-HT0454-301299-001-d08 H	SS ·	4.9
60	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light	CO THE I. FOE III HATH	4.9
	446933 409139	AL137659 Al681917	Hs.297214 Hs.3321	HSPC141 protein ESTs, Highly similar to IRX1_H	SS,TM,ank,EGF,notch,MATH, SS,homeobox	4.9 4.9
	456672	AK002016	Hs.114727	Homo septens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	4.9
	420842	A1083668	Hs.50601	hypothetical protein MGC10986	SS	4.9
65	421909		Hs.109428	TATA-binding protein-binding p		4.9
	419667	AU077005	Hs.92208	a distritegrin and metalloprote	disintegrin, Reprolysin, Pe	4.9 4.9
	443496 400933	AJ006973	Hs.9482	target of myb1 (chicken) homol NM_004347:Homo saptens caspase	VHS,GAT,TM,Heme_oxygenase ICE_p20,ICE_p10,CARD,SS,I	4.9 4.9
	456143	H11097	Hs.61960	hypothetical protein	SS,pkinase	4.9
70	427527	AI809057	Hs.153261	Immunoglobulin heavy constant	SS,TMJg	4.9
	414265	BE410411	Hs.75864	endoplasmic reticulum glycopro		4.9
	433933	AI754389	U= 00000	Homo saplens clone TCCCIA00164	SS,TM,SS,TM,SH2,Y_phospha	4.9 4.9
	452302 409938	AF173867 AW974648	Hs.28906	glucocorticold modulatory elem gb:EST386752 MAGE resequences,	SAND,SS SS.Adap_comp_sub.GYF	4.9 4.8
75	409336	OPOPICITA		NM_003105":Homo sepiens scriil	ldl_recept_a,fn3,ldl_rece	4.8
	425976	C75094	Hs.334514	NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	4.8
	452969	W92792	Hs.77575	hypothetical protein MGC3136	tion V should see on T	4.8
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3.jg,Y_phosphatase,SS,T	4.8 4.8
80	434962 418572	AK001574 AI751740	Hs.4291 Hs.86172	golgi perepheral membrane prot paired related homeobox protei	homeobox	4.8
50	440869	NM_01429		protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	4.8
	453446	8E299996		gb:600944574F1 NIH_MGC_17 Homo	•	4.8
	412159	AF286598	Hs.9271	KIAA1071 protein	bzip	4.8
	438999	AW276811		gb:xp66c02_x1 NCI_CGAP_Ov39 Ho		4.8

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	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	88	4.8
	414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin, SS, TM, G6PD, G6PD	4.8
	433669	AL047879	Hs.80475	ESTs, Weakly similar to ALU2_H	SS,TM,RNA_pol_L,RasGAP,C2	4.8
5	448984 426912	AW751955 AL043054	Hs.22753 Hs.256657	hypothetical protein FLJ22318 ESTs, Wealthy similar to A46302	SS SS	4.8
•	418945	BE245762	Hs.89499	arachidonate 5-lipoxygenase	lipoxygenase,PLAT,SS	4.8 4.8
	440333	A1378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans.pkinase.pk	4.8
	425615 458040	AF023614 BE280562	Hs.158341 Hs.287711	transmembrane activator and CA	TM	4.8
10	458367	AA088470	Hs.83135	hypothetical protein FLJ22692 Homo sapiens, Similar to RIKEN	SS,tRNA-synt_2d	4.8 4.8
	433294	AA582082	Hs.199410	ESTs	00,84040,110,24	4.8
	437671	AA535047	Hs.9850	hypothetical protein MGC1842		4.8
	425338 447946	H16716 Al566164	Hs.182648 Hs.165827	Homo saplens cDNA FLJ14444 fis ESTs	SS,PTN_MK,7tm_1,DAGKc,DAG	4.8
15	447205	BE617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	4.7 4.7
	416880	H99640	Hs.53687	EST		4.7
	440150	AW975738	Hs.7001	Homo saplens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	4.7
	426268 429253	AF083420 Y11739	Hs.168913 Hs.198313	serine/threonine kinase 24 (St winged-helix nude	pkinase,pkinase Fork_head,SS,TM,glycolyti	4.7 4.7
20	450261	AA788727	Hs.34068	ESTs, Weakly similar to A43932	SS	4.7
	439246	AJ498072		membrane-associated tyrosine-	SS,SS,TM	4.7
	419120	8E271922	11- 70047	ESTs, Weakly similar to zinc f	SS,TM,DENN,Cytidylyltrans	4.7
	416487 413837	AW190458 AW163525	Hs.79347	KIAA0211 gene product filin-cap (telethonin)	SS,zf-C2H2 SS,Methyltransf_3	4.7 4.7
25	419887	AW292562	Hs.187628	ESTs .	TM	4.7
	410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	4.7
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	4.7
	410892 407754	AW809762 AA527348	Hs.222056 Hs.288967	Homo saplens cDNA FLJ11572 fis Homo saplens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,tsp_3,SE	4.7 4.7
30	409877	AW502498	Hs.15220	zinc finger protein 106	00,114,00,114,10FH,6P_0,0E	4.7
	431629	AU077025	Hs.265827	interferon, alpha-inducible pr	pkinase,SH2,SH3	4.7
	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	4.7
	420823 418900	R95881 8E207357	Hs.63609 Hs.3454	Hpall tiny fragments locus 9C KIAA1821 protein	TM SS	4.7 4.7
35	402400	OLLOVO	113.0131	Target Exon	SS,TM,RNase_HII,bZiP,DUF2	4.7
	419625	U91616	Hs.91640	nuclear factor of kappa light	ank,SS,TM	4.7
	433319	AA583232	11- 450007	ESTs	SS	4.7
	424959 432750	NM_005781 NM_014440		activated p21cdc42Hs kinase interleukin 1, epsilon	pkinase,SH3 IL1	4.7 · 4.7
40	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	4.7
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	4.7
	427101	R87591	Hs.172884	ESTs	SS,TM	4.6
	447544 400266	AA401573	Hs.288284	hypothetical protein FLJ22378 NM_002858*:Homo saplens ATP-bi	SS,TM ABC_tran	4.6 4.6
45	412841	AJ751157	Hs.101395	hypothetical protein MGC11352	SS,TM	4.6
	422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Semia	4.6
	414874	D26351	Hs.77515	Inositol 1,4,5-triphosphate re	TM,RYDR_ITPR.ion_trans,MI	4.6
	418373 424487	AW750770 T08754	Hs.84344 Hs.6259	CGI-135 protein KIAA1698 protein	SS,TM,PMP22_Claudin,2OG-F SS,SS,TM,Glyco_hydro_31,G	4.6 4.6
50	426571	AA381642	. 10.0200	gb:EST94816 Activated T-cells	00,00,111,0,000,01,010,01,0	4.6
	433941	AA620612		ESTs	SS,TM,TNFR_c6	4.6
	421717	AF230924 NM_001348	Hs.107187	divalent cation tolerant prote death-associated protein kinas	-Name OTD SETTLESS OF	4.6
	450883 427361	AW732480	Hs.7678	cellular retinoic acid-binding	pkinase,GTP_EFTU,EFG_C,GT SS,TM,aminotran_1_2,LRR	4.6 4.6
55	420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	4.6
	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS,	4.6
	431498	AK001777	Hs.258551	aspartyl aminopeptidase	SS,Peptidase_M18,SS,TM,Y_	4.6
	432593 404661	AW301003	Hs.51483	ESTs, Weakly similar to hypoth C9000306*:gi[12737280[ref]XP_0	SS,TM,adh_short	4.6 4.6
60	412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	4.6
	456243	AI345001	Hs.82380	menage a trols 1 (CAK assembly	z-C3HC4	4.6
	426222 439594	BE391706 AI245026	Hs.168073 Hs.111099	DKFZP727M231 protein hypothetical protein MGC10974	GSH_synthase	4.6 4.6
	409114	AA070021	115.111055	gb:zm67h03.r1 Stratagene neuro	CLP_protease	4.6
65	429049	AW452125	Hs.119273	IGAA0296 gene product	SS,TM,trypsin	4/6
	424271	Al991887	Hs.305882	5-oxoprolinase (ATP-hydrolysin	00.714 11 4-11 1	4.6
	418741 450493	H83265 M93718	Hs.8881 Hs.166373	ESTs, Wealdy similar to S41044 nitric oxide synthase 3 (endot	SS,TM,pkinase,Activin_rec flavodoxin,FAD_binding,NO	4.6 4.6
	433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsrm,Vira	4.6
70	444893	AW249312	Hs.12109	WD40 protein Clao1	WD40	4.6
	420508	AJ270993	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	4.6
	409591 456181	AA532963 L36463	Hs.9100 Hs.1030	Homo sapiens cDNA FLJ13100 fis ras inhibitor	SS,TM,LIM,homeobox RA,SH2,VPS9,SS,TM,Nucleos	4.6 4.6
	439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.6
75	440104	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	4.5
	423279	AW959861	Hs.290943	ESTs	SS	4.5
	445087 404036	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae Target Exon	S1,SH2,Ribosomal_L23,pkin	4.5
	404036 431832	AW276866	Hs.192715	ESTs	SS,TM,cadherin,cadherin Els,SAM_PNT	4.5 4.5
80	433886	AA613598	Hs.28412	ESTs	SS	4.5
	426735	T78716	Hs.120445	ESTs	Oxysterol_BP,PH	4.5
	417825 455600	AW838994 BE061053	Hs.6363	heparan sulfate 6-0-sulfotrans gb:QV0-BT0041-271099-037-d09 B	SS,TM C4	4.5 4.5
	433600 423858	BE061053 AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	4.5 4.5

	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,mm,zf-RanBP,mm,GA	4.5
	408157	AA047685	Hs.62946	ESTs	pkinase	4.5
	434303	AW204058		transforming growth factor bet	SS,TM,SSF,FG-GAP,vwa,inte	4.5
_	440745	AW303627	Hs.143301	ESTs		4.5
5	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	enk DAGKa DAGKa DAG_PE-bi	4.5
-	447208	BE315291	Hs.237971	hypothetical protein MGC5627		4.5
	436163	R84938		gb:yt65f04.r1 Soares refina N2		4.5
	456858	AK001528	Hs.347285	Homo saplens, Similar to DiGeo		4.5
	410817	Al262789	Hs.93659	oratolo dicultato incomerces es	CC thioma	4.5
10				protein disulfide isomerase re	SS,thiored	
10	434558	AW264102	Hs.39168	EST8	SS,TM,LRRCT,LRR	4.5
	440548	AL117408	Hs.7274	DKFZP434P1750 protein		4.5
	450200	AW975625	Hs.173088	ESTs	zfUBP,zf-C3HC4	4.5
	432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	SS,pkinase	4.5
	440042	AI073387	Hs.133898	ESTs	SS	4.5
15	454328	AW372097	Hs.278429	hepatocellular carcinoma-assoc		4.5
	458196	A1802408		ubiquilin A-52 residue ribosom	SS,TM,fn3,FKBP,TPR	4.5
	433472	Al541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	4.5
	408928	AW295827	Hs.255479	hypothetical protein MGC5566	A_deaminase,A_deaminase	4.5
	448093	AW977382	Hs.15898	2,4-diencyl CoA reductasa 2, p	adh_short,NDK	4.5
20	426272	AW450671	Hs.189284	ESTs		4.5
20	453610	AW368882	Hs,33818	RecQ protein-like 5	SS,DEAD,helicase_C,SS,DEA	4.5
	441327					4.5
		AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	
	424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,7tm_	4.5
25	443443	AI344042	Hs.9347	regulator of G-protein signali	TM,Na_Pi_cotrans	4.5
23	426877	AW949856	Hs.97165	ESTs	SS	4.5
	412482	A1499930	Hs.334885	mitochondrial GTP binding prot	SS	4.4
	425236	AW067800	Hs.155223	stanniocalcin 2	Stanniocalcin,SS	4.4
	423229	AC003965	Hs.125532	protease, serine, 26	trypsin,SS	4.4
	412338	AA151527	Hs.69485	hypothetical protein FLJ 12436	SS,TM,TIG,Sema,PSI	4.4
30	419395	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide	AICARFT_IMPCHas,MGS,AICAR	4.4
	442462	AF031405		gb:AF031405 Soares fetal liver	-	4.4
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like,SS	4.4
	423876	8E502835	Hs.15463	Homo saplens, clone IMAGE:2959	SS efhand	4.4
	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	4.4
35						4.4
22	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF,SS,TM	
	448947	BE615408	Hs.337228	ESTs, Weakly similar to AXHU a	SS,TM,ig,pkinase	4.4
	407755	AJ151353	Hs.29742	Homo sapiens serine palmitoyl	SS,TM,aminotran_1_2	4.4
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase	4.4
40	458171	A1420016	Hs.192090	ESTs	SS,TM	4.4
40	424443	A1751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	4.4
	427002	AA524093	Hs.23158	ESTs	SS,xf-C2H2	4.4
	404344			C7002191*:gi[5053028]gb]AAD388	SS_ABC_tran	4.4
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	4.4
	419764	8E262524	Hs.93183	vasodilator-stimulated phospho	WH1	4.4
45	446872	X97058	Hs.16362	pyrimklinergic receptor P2Y, G	7tm_1,SS,TM	4.4
1.5	435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	4.4
		113003	110.4373		infamphold Toleme	4.3
	403945	500070	12- 4004	Target Exon	Harris HEDA OO	
	435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	4.3
50	421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	4.3
50	425245	A1751768	Hs.155314	KIAA0095 gene product	SS,TM	4.3
	423348	AA324687		gb:EST27558 Cerebellum II Homo	SS,TM	4.3
	452105	AA022838	Hs.6570	ESTs, Wealtly similar to S10889	SS,TM,TBC,rm	4.3
	431934	AB031481	Hs.272214	STG protein	SS	4.3
	429499	AA453809	Hs.99350	ESTs		4.3
55	453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	4.3
	459393	BE409283	Hs.193264	hypothetical protein MGC3234	•	4.3
	405364			ENSP00000239138*:Guanine nucle		4.3
	428345	A1242431	Hs.118282	PAP-1 binding protein	SS,TM	4.3
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	4.3
60	435327	AW963263	Hs.65377			4.3
v				ESTs, Moderately similar to KI	TM,SS,TM,EF_TS,UBA,transm	
	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	4.3
	409936	AK001691	Hs.57655	hypothetical protein FLJ10829	SS,TM	4.3
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	4.3
ce	424251	AA677466	Hs.143696	coactivator-associated erginin	SS,SNF2_N,helicase_C,brom	4.3
65	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	4.3
	432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	4.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	4.3
	456863	T16837	Hs.4241	EST&	fusion_gly,homeobox,TM	4.3
	417823	R88869	Hs.102447	TSC-22-like	PWWP	4.3
70	406621	X57809	Hs.181125	immunoglobulin lambda locus	SS	4.3
				ESTs, novel cytochrome P450	SS,p450,SS	4.3
	431493	AI791493	Hs.129873			
	412958	8E391579	Hs.75087	Fas-activated serine/threonine	SS,pkinase	4.3
	431658	BE409917	Hs.266935	tRNA selenocysteine associated	rm,SS,RCC1	4.3
75	419579	W49529	Hs.296200	hypothetical protein AF053356_	MSP_domain,SS,TM,CUB,NTR,	4.3
75	410076	T05387	Hs.7991	ESTs	SS	4.2
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	4.2
	424709	AL137589	Hs.152149	hypothetical protein DKFZp434K		4.2
	418419	X55039	Hs.85004	centromere protein B (80kD)	CENP-B,HTH_5	4.2
	447377	X77343	Hs.334334	transcription factor AP-2 alph	TF_AP-2,TF_AP-2	4.2
80	416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen,SS	4.2
	411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	4.2
			He 122010	Homo sapiens cDNA FLJ12797 fis	SS,lg,tsp_1,ZU5,SS,TM,Nuc	4.2
	419073	AW372170	Hs.183918			4.2
	406887	AA157857	Hs.182265	keratin 19	filament,bZiP,SS,filament	9.2
	432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	4.2
					266	

	418910	Z25821 AL040504	Hs.89466 Hs.25063	Homo sapiens, Similar to dodec	ECHLSS,TM.aminotran_3,ABC	4.2 4.2
	437300 426615	AA400678	Hs.6473	PRO0461 protein gb:zu70a11.r1 Soares_testis_NH	SS,TM,pkinase,cyclin,F-bo	4.2
	421453	AA234652	Hs.104555	neuropeptide FF-amide peptide	SS,bZIP,zf-C2H2,bZIP,zf-C	4.2
5	409616	AA076248	13.101333	gb:zm18c10.r1 Stratagene pancr	COURT IN COLUMN IN CO.	4.2
•	444744	BE394732	Hs.147562	ESTS	SS	4.2
	412575	AA113177		gb:zm29e05.s1 Stratagene pancr	TM,ER_lumen_recept	4.2
	429542	AF038660	Hs.206713	UDP-GatbetaGlcNAc beta 1,4- g	Galactosyl_T_2,ig,SS,TM,A	4.2
10	435995	BE260415	Hs.348198	hypothetical protein FLJ20262	00.11-1-11-1	4.2
10	451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	4.2
	456153 455340	AW972270 AW901435	Hs.144054	ESTs gb:RC0-NN1012-270300-031-a10 N	SS,TM	4.2 4.2
	457268	AW272279		ESTs, Moderately similar to AL		4.2
	432311	BE083080	Hs.274323	similar to slalytransferase 7	Glyco_transf_29	4.2
15	409656	NM_005133		RCE1, prenyl protein protease	Abl,SS,CPSase_L_chain,HMG	4.2
	424919	BE314461	Hs.153768	U3 snoRNP-essociated 55-kDa pr	WD40,SS,KH-domain	4.2
	416528	H65052	Hs.337621	ESTs		4.2
	415137	A1634834	Hs.72451	Homo saplens PAC clone RP5-108		4.2
20	417334	AA337572	Hs.157240	hypothetical protein MGC4737	SS,TM,lon_trans	4.2
20	451920	AA224483	Hs.27239	DKFZP586K0524 protein	SS,TM,SS,TM	4.2
	413049	NM_002151		hepsin (transmembrane protease	trypsin,SS,TM,ATP1G1_PLM_	4.2 4.2
	458988	AW410431	Hs.283670	CGI-119 protein FGENES predicted novel secrete		4.2
	406964 451595	M21305 AW965569	Hs.20996	ESTs	SS,WD40	4.2
25	449728	AI820751	Hs.107635	ESTs -	SS ·	4.1
	453245	T99801	Hs.339751	ESTs	TM_ABC_tran	4.1
	432238	AL133057	Hs.274135	Homo saplens mRNA; cDNA DKFZp4	WD40,LRR	4.1
	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	4.1
20	442196	AI902646	Hs.31844	hypothetical protein FLJ 12586	SS,SCAN	4.1
30	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	4.1
	415014	AW954064	Hs.24951	ESTs	00 (00) 010 000V-/D b	4.1
	440088	BE559877	Hs.183232	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-B_box	4.1
	418837	U48263	Hs.89040	prepronociceptin hypothetical protein MGC2650	Optods_neuropep,SS SS_ART,TM	4.1 4.1
35 ·	410239 446975	AI568350 BE246446	Hs.61273 Hs.16695	ubiquilin-activating enzyme E1	ThiF,UBACT	4.1
55	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	4.1
	448241	AW811064		gb:MR2-ST0131-211099-008-c06 S	SS	4.1
	441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip,SS,TM,Cytidylyltransf	4.1
4.0	450848	A1677994	Hs.428	fms-related tyrosine kinase 3	fli3_flg,SS,Ribosomal_L13	4.1
40	429218	AA225065	Hs.198269	Target CAT	SS,Nop	4.1
	425437	AK000482	Hs.181780	hypothetical protein FLJ20241		4.1
	406613			Target Exon	SS,pkinase,LRR,LRRCT,Ribo	4.1
	431239	AL039971	Hs.251216	hypothetical protein DKFZp434A	ank,WH2	4.1 4.1
45	436057	AJ004832 AL048891	Hs.5038 Hs.12185	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b SS,TM,eminotran_1_2,LRR	4.1
73	415193 424619	8E387282	Hs.207443	hypothetical protein MGC14333 hypothetical protein MGC10848	33,1Maimore:[1_2d4/	4.1
	432968	BE614192	Hs.279869	melanoma-associated enligen re	SS,TM,RGS,DIX	4.1
	428156	BE269388	Hs.182698	mitochondrial ribosomal protei	SS	4.1
	414084	AW168771	Hs.71574	hypothetical protein FLJ14926	SS,P5CR,EF1BD	4.1
50	424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	4.1
	431410	AW299534	Hs.105739	ESTs		4.1
	435968	AW161481	Hs.111577	integral membrane protein 3	TM .	4.1
	432351	AI270313	Hs.127762	hypothetical protein MGC12982	OO OO aarlandana E	4.1
55	426120	AA325243	Hs.166887	copine I	C2,SS,aminotran_5	4.1 4.1
55	416877	BE386266 AK001500	Hs.85658 Hs.165186	hypothetical protein FLJ23436 hypothetical protein FLJ13852	SS.P5CR.Enimerase.zi-C2H2	4.1
	425970 434848	BE256304	Hs.32148	AD-016 protein	SS.TM.SS.TM.LRR.P.Pepiida	4.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	IBR.zf-C3HC4,SS,TM,IRF,CK	4.1
	435851	AA700946	112.110.100	EST8		4.1
60	425538	BE270918	Hs.164026	Homo sapiens, clone IMAGE:3534	SS,SNF2_N,helicase_C,brom	4.1
	444416	AW288085	Hs.11156	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	4.0
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.0
	444596	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept	4.0
65	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	4.0
03	447402	H54520	Hs.18490	hypothetical protein FLJ20452	SS,TM	4.0 4.0
	450184	W31096	Hs.237617 Hs.166154	Homo saplens, clone IMAGE:3447 jagged 2	SS DSLEGF,wc.granulin,SS,T	4.0
	426068 4592 5 5	AF029778 Al493244	Hs.239500	hypothetical protein MGC13114	SS	4.0
	403182	WHODEAA	115.205500	Targel Exon	SS	4.0
70	432078	BE314877	Hs.24553	hypothetical protein FLJ12541	SS.TM	4.0
	459167	BE504370		ESTs, Wealty similar to CA13_H	SS	4.0
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	SS,TM,ig,HLH	4.0
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	19,SS,TM,HLH	4.0
75	434171	BE247688	Hs.347349	KIAA0948 protein	mma milita	4.0
75	422155	AW249152		sirtuin (silent mating type in	SIR2,HLH,Myc_N_term,Myo-L	4.0
	433262	A1571225	Hs.284171	KIAA1535 protein	SS,TM,cNMP_binding,ton_tr	4.0
	442599	AF078037	Hs.324051	ReiA-associated inhibitor	SH3, ank, SS, TM, HHH, ig	4.0 4.0
	452500	AW373011		hypothetical protein FLJ22222		4.0
80	437563	A1217204 AA531128	Hs.144968 Hs.115803	ESTs ESTs	SS	4.0
30	432234 433135	AA443873	Hs.110477	dolichyl-phosphate mannosyltra		4.0
	447495	AW401864		programmed cell death 8 (apopt	pyr_redox,SS,Ets	4.0
	452857	BE072814	Hs.258519	ESTs, Moderately similar to S6	SS	4.0
	427834	AA506101	Hs.285813		SS,TM	4.0
					267	
					LU /	

	418963 437340 455928	BE304571 AL353935 BE170313	Hs.89529 Hs.135917	aldo-keto reductase family 1, hypothetical protein DKFZp761D gb:QV4-HT0538-040500-193-g02 H	ablo_ket_red TBC,bZiP,WD40,WD40 SS	4.0 4.0 4.0
5	400607 424825 438143	AF207069 BE500981	Hs.153357 Hs.269652	Target Exon procellagen-lysina, 2-oxogluta ESTs	SS,homeobox 20G-Fell_Oxy,Glycos_trans	4.0 4.0 4.0
	433173 412550	Z35093 R52452	Hs.3196 Hs.26370	surfeit 1 gb:yg80g07.r1 Soares Infant br	SURF1,SS,TM,SURF1,SURF4	4.0 4.0
10	CAT number	e Eos probese : Gene cluste: Genbank acce	number			
15	Pkey	CAT Number	Assessates			
15	408215	10478_1	BE614290 A			BE221263 Al348910 Al985031 Al090078 Al359617 7250002 AA503756 Al934519 AW272086 N26520
20	408294	1050553_1		175823 BE141331 AW178416 AW178430 B		
20	409114	110088_1		A126205 AA082771 AA102169 AA083530	AA082183 AA115915 AA085147 AA1259	905 AA063336 AA079206
	409164 409616	110421_1		A064707 AL036920 Al651598		
	409938	114348_1 116091_1		A120958 AA122152 AA076249 \A652153 AA649671 AA078582		
	409960	116270_1			W04622 Al291655 AW879092 AA130776	B BE314003 AA908246 AW960808 AA385346
25			AA205977 C Al567682 AA	02043 AA 135057 AA 078870 AA 377395 A AS 32839 A1056920		AW370250 AW370244 T85930 AA759250
	410445	120374_2		J143895 AW961629 AA322482	04.C 41410207770	
	411219 411674	1236055_1 1253746_1		\W832913 AW832906 AW832788 AW8329		W856780 AW856782 AW856789 AW856772
30	411074	1200740_1		W856786 AW856776 AW85635 AW8567		10307 00 AV10307 02 AV10307 03 AV10307 72
50	412091	1276564_1		891805 AW901892 AW901895		
	412173	1280870_1		902279 AW897608		
	412575	130769_1	AA113177 A	W894515 AA113847		
25	413534	1375357_1		E146780 BE146788 BE146967 BE146774	BE146963 BE146907	
35	413564	1376722_1	BE260120 B			
	413764 413837	1387163_1		E162705 BE162732 BE162702 BE162694		77959 AIC03409 ANNOO254 A T2443C AITCCCC
	413037	139363_1				7252 Al692198 AW003514 T24436 Al765658 AW299513 AA132529 Al340991 Al912836
				650609 AA279	34030 A04000 A1120022 A11004000	
40	414413.	1443696_1	BE294877 B			
	415126	1523506_1		346 D81568 D80539		
	419120	182026_1				W504757 N51688 Al400700 AA578548 AA714130
			AA779455 A		043 AA409943 AW4/4826 AA/6/165 AA3	26817 AA593859 AW952245 AW341739 AA805093
45	422155	21235_1			14 R05553 AF083107 AF160214 NM 012	237 BE258447 BE253088 AA297721 H58948
			W39153 AA	070372 H14246 AL079367 R24561 AW40:		597 AA297787 Z42780 AA297072 T81280 T83544
	400040	007070 4		126063 AA26		
	423348 425858	227276_1 257265_1		A325155 AW962038 AW963483 BE182774 C21461		
50	426571	269283_1		A381664 AW963560 AW949848 AA38172	78 AA381608	
•	427326	277229_1		1804160 AA400787		
	428092	286920_1	AW879141	AA421182 AJ734104 AJ733923 AA430600		
	429720	308153_1		773950 AA586573 AA457225		
55	430168	313927_1		AA468507 AI478223 AW513008 AI762122	AI554512 AA862642 AA468976	
23	431424 433319	333110_1 363095_1	AA583232 A	A806560 AA504839 AA805261		
	433933	377703_1			IB63355 AW131720 AI674922 AI949042 A	AJ990060 AI623178 AW469497 AA620354
•	433941	377883_1		A994983 AA994990		
~	434303	383224_1		A1424379 A1669663 AA629077 AW613033		
60	434743	3925_1	AW505595			126 AA215407 A1633829 AA292122 N42783 4951 AW966080 M78807 N31947 AA521151
	434796	393400_1		AW974514 AA764999 AA649302		
	435851	411522_1		A702712 AA947620		
65	436163	41515_6		047151 AA310309 AW063200 Al569528 A	1307823 N49975	
	437215	43473_1	AL117488 A			
	438999 439246	467686_1 47021_3		AA829050 AA829190 Wasinga aagsaas aabsagra alagarng	AA206609 AW190187 AA555262 AF0860	057 F35814 AW516382 AA377885 N50847 F27148
	403240	41021_0		AA417728 AI003145		301 1 300 14 A 110 100 0 110 0 11 1 1 1 1 1 1 1 1 1
70	440317	49187_1		BE560615 BE562102		
	442462	543232_1	AF031405 I			
	442472	543371_1		AW806852 AF049582		7.774 (0 1 1000000 Decomo D (07 (0 1 1700000
75	445625	64558_1		A317806 Al678000 AW189953 Al986207) T57442 A1399986 R50073 R48743 A1769689 J469257 A1954604 H21954 T25141 AA856793
	445631	6457_1			957 AW193951 Al347975 AW081323 AW6	562527 Al343924 Al380749 AA938153 T66968
	*******	0101				5 AW593995 Al336927 Al336928 Al357036 R60592
			H19058 R1			
00	447128	70934_1				5259 AW973696 F25787 F35749 Al568815
80	*****			AA554539 C00201 AA961610 AW059537	R77127	
	448241	756181_1	AW811064	AW811160 AJ478413	2 DEEASTED AANESERT DE (ARENS DE 240	1514 AW956702 AI656234 AI636283 AI567265
	448993	79225_1	AW340858	BE207794 AA053085 R69173 AA292343 AA394063 AA454	AA454908 AA293504 AI659741 AI927478	3 AA399460 AI760441 AA346416 BE047245
					260	

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BE299996 BE297115 BE270415 BE295214 BE296526
AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
AW851734 AW851676 AW851693 AW851713 AW851722 AW851616 AW851731 AW851618 AW851648 AW852215
           453446
                         967533 1
                         1228976_1
           454582
           455035
                         1249762_1
           455340
                         1283604_1
                                       AW901435 BE094527
 5
                                       AW995839 AW995907
BE061053 BE008959 BE008957 BE091618
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                         1325974_1
           455600
                         1335877_1
                                       BE153524 BE153576 BE153583
                         1380385_1
           455885
                                       BE170313 BE158339 BE158290
           455928
                         1383899_1
                                       Al279811 Al301071 Al214696 Al279813 AA588460 AA287256 BE171665
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10
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448900_1
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                                       AA776638 RF439540
           457978
                                       AI802408 AA907424 AI279233 AI302762 N33153 BE045678 AI853332 AW173558 AI302328 Z20793 D25594 BE326823
                         503719_1
           458196
                                       BES04370 Al243453 Al809556 Al702878 Al702163 Al300626 AW0772219 Al369492 Al349587 AW779061 W78149 AA055693 AA974162 Al394380 AR80098 AW054857 Al870008 AW207658 AW665508 AW300695 Al192992 AW628019 Al274365 AA906922 N92547 AW054727 AW206667 AW136707 AW13761
           459167
                         92053_1
15
                                       AL045934 AL039532 H55631
           459271
                         969257_1
           TABLE 23C:
           Pkey: Unique number corresponding to an Ecs probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
20
           human chromosome 22 Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
           Ni_position: Indicates nucleotide positions of predicted exons
25
                                                      Nt position
                                       Strand
                                                      35559-36295
           400460
                         8389428
                                       Plus
           400607
                         9887666
                                       Plus
                                                      3112-4159
           400833
                         8705148
                                       Minus
                                                      187599-188138
                                                      34428-34612
           400845
                         9188605
                                       Plus
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                         7637836
                                                      94518-94659
           400923
                                       Minus
            400933
                         7651935
                                       Minus
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130810-130927,133367-133504
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                         7712287
                                       Plus
                                       Plus
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           401278
                         9799936
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                         7705041
                                                      9877-11997
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                         7689903
                                                      138788-138927,139157-139298,139440-139599,139960-140159
                                       Plus
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                         9931268
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                                        Minus
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            403055
                                        Minus
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            403128
                                        Plus
            403182
                         9838273
                                        Plus
                                                       102163-102345,102545-102725
                         7711795
                                                      48636-48822
            403938
                                        Plus
                                                      32141-32263
                                        Minus
            403945
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                         8567760
                                        Minus
            404333
                          9802821
                                                       137948-138024,138111-138300
                                        Minus
            404343
                          9838093
                                        Plus
                                                       122664-122931
                                                      127865-128384
50151-50319,50859-51098
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9964977
            404344
                                        Plus
            404365
                                        Plus
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            404661
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                         9797073
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                                                       100933-101083,101580-101782
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                          7706327
                                        Plus
            404807
                          4165210
                                        Minus
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            405334
                          3135285
                                        Plus
                                                       101982-102171
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2281075
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                                        Minus
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                                                       47657-47768,48461-48596
161628-161734,162823-163014,164439-164652
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            405594
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            405928
                          7717155
                                        Minus
                                                       2923-3209
                                                       71716-72515
                          4760409
                                        Plus
            406230
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            406244
                          7417725
                                                       39422-39595
                                        Plus
            406301
                          8575868
                                                       57291-57494
                                                      82039-82902
174661-174978
            406487
                          7711306
                                        Plus
            406495
                          7711328
                                        Minus
                          2957168
                                        Plus
                                                       5029-5147
            406613
70
```

Table 24A lists about 117 genes down-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 23A, except that the numerator was set to the 75th percentile amongst various non-malignant ovary specimens, the denominator was set to the 96th percentile value amongst various ovarian cancers, the numerator was greater than or equal to 75 units, and the ratio was greater than or equal to 2.0 (i.e., 2-fold downregulation in tumor vs. normal ovaries).

TABLE 24A:

75

Pkey: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number

UG ID: UniGene number 80 Title: UniGene gene title

Protein Dom.: Predicted protein domain

R1: Ratio of normal ovaries to tumor

	O *	F		Title	Protoin Dans	R1
	Pkey 428232	Ex. Acon BE272452	UG ID Hs.183109	Title monoamine oxidase A	Protein Dom. Amino_oxidase,pyr_redox,F	16.9
	433563	A1732637	Hs.277901	ESTs	SS S	10.8
_	444931	AV652066	15.271001	general transcription factor I	SS, Glypican	8.7
5	451573	AW130351		ESTs	SS	8.3
	429570	8E242256	Hs.2441	KIAA0022 gene product	tectin_c,SS,TM SS	7.9 7.5
	453510 410295	A1699482 AA741357	Hs.42151	ESTs nidogen (enactin)	SS,EGF,idl_recept_b,thyro	6.9
	438549	BE386801	Hs.21858	trinucleotide repeat containin	SS,serpin,SS,WD40,FYVE	6.5
10	407969	AA046217	Hs.105370	ESTs	SS,Pep_M12B_propep,Reprol	6.2
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 famil	aldedh	6.0
	448438	BE613081	Hs.24654	Homo sapiens cDNA FLJ11640 fis	SS.TM	5.7 5.1
	441422 413391	R43777 Al223328	Hs.21384 Hs.75335	ESTs glycine amidinotransferase (L- '	Amidinotransf	3.9
15	428022	Z39686	Hs.27865	ESTs	SS	3.6
13	423044	AA320829	Hs.97266	protocadherin 18		3.6
	416039	AA376989	Hs.78989	atcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
	452854	AA437061	Hs.14060	prokinetich 1 precursor	SS	3.4
20	436772	AW975688	11. 70074	metallothionein 1E (functional	SS,TM,7tm_2,HRM HLH	3.2 3.2
20	415162	AF035718	Hs.78061 Hs.99070	transcription factor 21 ESTs	SS	3.1
	427794 433072	AA709186 A1928037	Hs.158832	ESTs	SS	3.1
	418318	U47732	Hs.84072	transmembrane 4 superfamily me	transmembrane4	2.9
~ -	410059	NM_007038		a disintegrin-like and metallo	Reprolysin,tsp_1,Pep_M12B	2.9
25	431933	AI187057	Hs.132554	ESTs .	TM,SS,TM	2.9
	420303	AA258282	Hs.278436	KIAA1474 protein		2.8 2.8
	438780 427661	M64936 AA410292	Hs.104761	gb:Homo saplens retinoic acid- ESTs	SS.wnt	2.8
	437342	AW903297		hypothetical protein DKFZp761K	Sec7,PH	2.8
30	453828		Hs.293821	ESTs	SS,Pep_M12B_propep,Reprol	2.7
	418444	A1902899	Hs.85155	butyrate response factor 1 (EG	zf-CCCH,SS	2.7
	453767	AB011792	Hs.35094	extracellular matrix protein 2	vwc,LRR,SS,LRR	2.7
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevin)	kazal,SS,kazal laminin_B,laminin_EGF,lam	2.7 2.7
35	413305 414504		Hs.323511 Hs.115175	Homo sapiens cDNA: FLJ23176 fi sterile-alpha motif and leucin	SS,pkinase,SAM	2.7
22	439897	NM_015310		KIAA0942 protein	Sec7,PH	2.7
	421639		Hs.106309	Friend of GATA2	SS	2.7
	442498	U54617	Hs.8364	Homo saptens pyruvate dehydrog	HATPase_c,HATPase_c	2.6
40	410494	M36564	Hs.64016 .	protein S (alpha)	EGF,laminin_G,gla	2.6
40	452958	AA883929	Hs.40527	ESTs	SS SS	2.6 2.5
	449648 435519	AW205607 Al218950	Hs.253499 Hs.125461	ESTs hypothetical protein FLJ11539	SS	25
	433690	Al373949	Hs.279610	hypothetical protein FLJ10493	SS	2.5
	424319	AW961026		ESTs, Weakly similar to ALU8_H		2.5
45	420174	AIB24144	Hs.199749	ESTs		2.5
	421709	AA159394	Hs.107056	CED-6 protein	PID,Herpes_UL6	2.4 2.4
	417622	AW298163	Hs.82318	WAS protein family, member 3	WH2 SS,TM,zona_pellucida	2.4
	453655 408468	AW960427 AI909712	Hs.342874	transforming growth factor, be phosphatidylinositol transfer	SS,PX,PH,PLDG,PH,PLDG,PX	24
50	400829	M303712		C11000244:gi]11056030[ref]NP_0	SS,TM,SS,TFIID_30kD	2.3
50	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	ras	2.3
	437862	AW978107	Hs.5884	Homo saplens mRNA; cDNA DKFZp5	HLH	2.3
	425462	A1491852	Hs.46783	Homo saplens cDNA: FLJ22382 fi	A1 O A - A	2.3 2.3
55	417094	NM_00689	5 Hs.81182	histamine N-methyltransferase	Acyl-CoA_dh	2.3
23	403247 441916	AA993571		Targel Exon ESTs		2.3
	422746		Hs.119651	glypican 3	Glypican,SS .	2.3
	416777	AF146760	Hs.79844	OKFZP564M1416 protein	SS,GTP_CDC,SS	2.3
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fi	SS,TM	2.3
60	418956	AA234831		KIAA0788 protein	SS No to Chatharla	2.3
	410073	AW408163		catenin (cadherin-associated p	Vincutin, Stathmin hormone_rec, zf-C4, hormone	2.3 2.3
	419461 429319	A1452601 AL023754	Hs.288869 Hs.199068	nuclear receptor subfamily 2, similar to calcium/calmodulin	SS,pkinase	2.2
	452123	ALU23754 Al267615	Hs.38022	ESTs	SS	2.2
65	453305	R39224	Hs.267997	EHM2 gene		2.2
•••	416157		3 Hs.342874	transforming growth factor, be	zona_pellucida,SS,TM,zona	2.2
	405637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p	2.2
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA	p450 SS	2.2 2.2
70	408915		1 Hs.48950	heptacellular carcinoma novel programmed cell death 4	MA3,LRR	2.2
70	420929 456972	Al694143 Al054347	Hs.326248 Hs.2017	ribosomai protein L38	SS,TM	22
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	C2,PH,PI-PLC-Y,PI-PLC-X	2.2
	410209	Al583661	Hs.60548	hypothetical protein PRO1635	SS,TM,Fork_head	2.2
7.	449500	AW956345	Hs.12926	ESTs	SS,TM	2.2
75	447806	W03616	Hs.10432	ESTs, Weakly similar to 138022	•	2.1
	441712	AW391927		KIAA1288 protein	SS,BAG,UPF0001	2.1 2.1
	445025	A1768895 N52543	Hs.295727 Hs.142940	ESTs, Weakly similar to ALUB_H ESTs	SS,BAG,UPF0001 SS	2.1
	444161 427156	N52543 BE621719		KIAA0603 gene product	SS,TM,TBC	21
80	436995	Al160015	Hs.125489	ESTs	SS,TM,RasGEF,actin,RasGEF	. 2.1
	408443	N33937	Hs.10336	ESTs	SS	2.1
	448274	A1268097	Hs.67317	Homo saplens cDNA FLJ11775 fis	TT 0111141113-1 TWO 00	21
	426354		0 Hs.169470	dystrophin (muscular dystrophy	ZZ,CH,WW,spectrin,bZiP,SS	2.1 2.1
	443906	AA348031	Hs.7913	ESTs ,		4.1

	Dhou	Eu Ann	110.10	Title	Protein Dom.	R1
	Pkey 428232	Ex. Acon BE272452	UG ID Hs.183109	Title monoamine oxidase A	Amino_oxidase,pyr_redox,F	16.9
	433563	AI732637	Hs.277901	ESTs	SS SS	10.8
1	444931	AV652066	15,277501	general transcription factor I	SS,Glypican	8.7
5	451573	AW130351		ESTs	SS	8.3
	429570	BE242256	Hs.2441	KIAA0022 gene product	lectin_c,SS,TM	7.9
	453510	Al699482	Hs.42151	ESTs	SS	7.5
	410295	AA741357		nidogen (enactin)	SS,EGF,IdI_recept_b,thyro	6.9
10	438549	BE386801	Hs.21858	trinudeotide repeat containin	SS,serpin,SS,WD40,FYVE	6.5 6.2
10	407969 414541	AA046217	Hs.105370	ESTs	SS,Pep_M12B_propep,Reprol aldedh	6.0
	448438	BE293116 BE613081	Hs.76392 Hs.24654	aldehyde dehydrogenase 1 famil Homo sapiens cDNA FLJ11640 fis	aveun	5.7
	441422	R43777	Hs.21364	ESTs	SS.TM	5.1
	413391	Al223328	Hs.75335	glycine amidinotransferase (L- 1	Amidinotransf	3.9
15	428022	239686	Hs.27865	ESTs	SS	3.6
	423044	AA320829	Hs.97266	protocadherin 18		3.6
	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
	452854	AA437061	Hs.14060	prokineticin 1 precursor	SS	3.4
20	436772	AW975688		metallothionein 1E (functional	SS,TM,7tm_2,HRM	3.2
20	415162	AF035718	Hs.78061	transcription factor 21	HUH	3.2
	427794	AA709186	Hs.99070	ESTs	SS SS	3.1 3.1
	433072 418318	A1928037 U47732	Hs.158832 Hs.84072	ESTs	transmembrane4	2.9
	410059	NM_007038		transmembrane 4 superfamily me a disintegrin-like and metallo	Reprolysin,tsp_1,Pep_M12B	2.9
25	431933	Al187057	Hs.132554	ESTs	TM,SS,TM	2.9
	420303	AA258282	Hs.278436	KIAA1474 protein	,	2.8
	438780	M64936		gb:Homo saplens retinoic acid-		2.8
	427661	AA410292	Hs.104761	ESTs	SS,wnt	2.8
•	437342	AW903297	Hs.236438	hypothetical protein DKFZp761K	Sec7,PH	2.8
30	453828	AW970960	Hs.293821	ESTs	SS,Pep_M12B_propep,Reprol	2.7
	. 418444	Al902899	Hs.85155	butyrate response factor 1 (EG	zf-CCCH,SS	2.7
	453767	AB011792	Hs.35094	extracellular matrix protein 2	vwc,LRR,SS,LRR	2.7
	413624	BE177019 NM_000426	Hs.75445	SPARC-like 1 (mast9, hevin)	kazal,SS,kazal Iaminin_B,laminin_EGF,lam	2.7 2.7
35	413305 414504	AW069181		Homo sapiens cDNA: FLJ23176 fi sterile-alpha motif and leucin	SS,pkinase,SAM	2.7
55	439897	NM_015310		KIAA0942 protein	Sec7,PH	2.7
	421639	NM_012082		Friend of GATA2	SS	2.7
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrog	HATPase_c,HATPase_c	2.6
	410494	M36564	Hs.64016 .	protein S (alpha)	EGF,laminin_G,gla	2.6
40	452958	AA883929	Hs.40527	ESTs	SS	2.6
	449648	AW205607	Hs.253499	ESTs	SS	2.5
	435519	Al218950	Hs.125461	hypothetical protein FLJ11539	SS	2.5
	433690	Al373949	Hs.279610	hypothetical protein FLJ10493	SS	2.5
45	424319	AW961026	Hs.96752	ESTs, Weakly similar to ALU8_H		2.5 2.5
40	420174	AI824144	Hs.199749	ESTs CCD 6 acatain	DID Homes 18 6	2.5 2.4
	421709 417622	AA159394	Hs.107056	CED-6 protein	PID,Herpes_UL6 WH2	2.4
	453655	AW298163 AW960427	Hs.82318 Hs.342874	WAS protein family, member 3 transforming growth factor, be	SS,TM,zona_pellucida	2.4
	408468	Al909712	113.042074	phosphatidylinositol transfer	SS,PX,PH,PLDc,PH,PLDc,PX	2.4
50	400829			C11000244:gi]11056030 ref NP_0	SS,TM,SS,TFIID_30kD	2.3
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	ras	2.3
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp5	i HLH	2.3
	425462	AI491852	Hs.46783	Homo sapiens cDNA: FLJ22382 fi		2.3
55	417094	NM_006895	Hs.81182	histamine N-methyltransferase	Acyl-CoA_dh	2.3
23	403247			Target Exon		2.3 2.3
	441916 422746	AA993571 NM_004484	No 110661	ESTs glypican 3	Glypican, SS .	2.3
	416777	AF146760	Hs.79844	DKFZP564M1416 prolein	SS,GTP_CDC,SS	2.3
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fi	SS,TM	2.3
60	418956	AA234831		KIAA0788 protein	SS · ·	2.3
	410073	AW408163	Hs.58488	catenin (cadherin-associated p	Vinculin, Stathmin	2.3
	419461	AI452601	Hs.288869	nuclear receptor subfamily 2,	hormone_rec,zf-C4,hormone	2.3
	429319	AL023754	Hs.199068	similar to calcium/calmodulin	SS,pkinase	2.2
CE	452123	AI267615	Hs.38022	ESTs	SS	2.2
65	453305	R39224	Hs.267997	EHM2 gene	0.41.00.71	2.2
	416157		Hs.342874	transforming growth factor, be	zona_pellucida,SS,TM,zona	2.2
	406637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p .	2.2 2.2
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA	p450 SS	2.2
70	408915 420929	NM_016651 Al694143	Hs.326248	heptacellular carcinoma novel programmed cell death 4	MA3,LRR	2.2
, 0	456972	AI054347	Hs.2017	ribosomal protein L38	SS,TM	2.2
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	C2,PH,PI-PLC-Y,PI-PLC-X	2.2
	410209	AI583661	Hs.60548	hypothetical protein PRO1635	SS,TM,Fork_head	2.2
_ ~	449500	AW956345	Hs.12926	ESTs	SS,TM	2.2
75	447806	W03616	Hs.10432	ESTs, Weakly similar to 138022	•	2.1
	441712	AW391927	Hs.7946	KIAA1288 protein	00.00	2.1
	445025	Al768895	Hs.295727	ESTs, Weakly similar to ALUB_H	SS,BAG,UPF0001	2.1
	444161	N52543	Hs.142940	ESTs	SS SS THE TRO	2.1
80	427156	BE621719	Hs.173802	KIAA0603 gene product	SS,TM,TBC	2.1 2.1
ου	436995	AI160015	Hs.125489	ESTs ESTs	SS,TM,RasGEF,actin,RasGEF . SS	21
	408443 448274	N33937 Al268097	Hs.10336 Hs.67317	Homo sapiens cDNA FLJ11775 fis	•	2.1
	426354		Hs.169470	dystrophin (muscular dystrophy	ZZ,CH,WW,spectrin,bZIP,SS	21
	443906	AA348031	Hs.7913	ESTs ,		21
	1,10000					

	444815		Hs.1227	aminolevulinate, delta-, dehyd	SS,ALAD	2.1
	420728	AA767718	Hs.93581	hypothetical protein FLJ10512	SS,TM,Sema,PSI,ig	2.1
	404245			NM_007116*:	fibrinogen_C,fn3,SS	21
	436420	AA443966	Hs.31595	ESTs	SS,TM,PMP22_Claudin,SS,TM	21
5	410066	AL117664	Hs.58419	DKFZP586L2024 protein		2.0
-	414476	AA301867	Hs.76224	EGF-containing fibulin-like ex	EGF,TIL,SS	2.0
	424137	AA335769	Hs.16262	ESTs	Corpridos	2.0
	447659	AA017472	Hs.107260	hypothetical protein DKFZp586H	SS	2.0
	444862	AI209158	Hs.143929	ESTs	SS,TM	20
10	426086	T94907	Hs.188572	ESTs	PH,CH,spectrin	2.0
10	436080	AI684710				2.0
			Hs.201645	ESTs	SS,ATP-synt_C	
	424651	A1493206	11- 070040	ESTs	SS (COURT - LOUIS	2.0
	432939	AL038924	Hs.279849	KIAA0438 gene product	zf-C3HC4,myosin_head,DIL,	2.0
15	449088	A1654048	Hs.196556	ESTs	SS,MACPF,sushi,ktl_recept	2.0
15	428642	NM_014899		KIAA0878 protein	BTB,ras	2.0
	419577	L36531	Hs.91296	integrin, alpha 8	TM,integrin_A,FG-GAP	2.0
	450435	AI695975	Hs.201805	ESTs	taminin_B,taminin_EGF,tam	2.0
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	SS	2.0
	421255	BE326214	Hs.93813	ESTs	TM	2.0
20	432467	T03667	Hs.239388	Human DNA sequence from clone	SS	2.0
	408654	BE018882	Hs.46721	UCC1 protein	SS,Ependymin,SS	2.0
	412611	AA732036	Hs.164478	hypothetical protein FLJ21939		2.0
	453355	AW295374	Hs.31412	myopodin		2.0
	424665	AW368576		cavedin 2	SS,TM,Caveolin,Caveolin	2.0
25	458147	AW752597		gb:IL3-CT0214-161299-045-B06 C	SS,TM,PMM	2.0
	447566	N50432	Hs.102648	ESTs		2.0
	414496	W73853		ESTs	SS,TM,pkinase,F5_F8_type_	2.0
	425618	AW119112	He 9052	Homo saptens cDNA: FLJ22042 fi	SS,TM	2.0
	415166	NM_003652		carboxypeptidase Z	Zn_carbOpept,Fz,Dioxygena	2.0
30	422157	AW957295		6.2 kd protein	SS	2.0
50	450253				SH3	2.0
		AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp4		
	418919	AA232635	11. 440477	ESTs	SS,DUF25	2.0
	444846	A1871055	Hs.148477	ESTs	SS,TM	2.0
35	418781	T41160	Hs.8404	ESTs		2.0
33						
	TABLE 24B:					
			t identifier number			
	CAT number:					
40			number ssion numbers			
40	Accession: 0	Senbank acces	esion numbers			
40			esion numbers			
40	Accession: 0	Senbank acces	Sion numbers Accession	2 BE000369 AA376876 N75269 AA345398 AA34	9053 AW960062 R76169 R70638 AA05477	70 Al378587 Al338002 Al762398
40	Accession: C	Genbank acces CAT Number	ssion numbers Accession Al909712 AL03975	2 BE000369 AA376876 N75269 AA345398 AA34 NA74112 AW450880 AA668668 R76114 AW2426		
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40 45	Accession: C	CAT Number 105033_1	Accession Al909712 AL03975 N47873 Al066549 A AW297099	A1474112 AW450680 AA668668 R76114 AW2428	28 N58855 AW080313 Al378491 Al807102	2 AA417043 Al565444 AW263286
	Accession: 0 Pkey 408468	Genbank acces CAT Number	Accession AL03975: A47873 AL03975: N47873 AL066549 A AW297099 AA741357 AL87000	A1474112 AW450680 AA668668 R76114 AW2428 0 W75997 H50726 AV658709 A1498817 AL03780	128 N58855 AW080313 Al378491 Al807102 14 W67847 BE018553 Al033256 N76810 N	2 AA417043 A1565444 AW263286 31548 A1032084 N36278 AW075272
	Accession: 0 Pkey 408468	CAT Number 105033_1	ssion numbers Accession Al909712 AL03975; N47873 Al066549 AAW297099 AA741357 Al87000 Al032081 R35753 V	A1474112 AW450680 AA668668 R76114 AW2428	128 N58855 AW080313 Al378491 Al807102 14 W67847 BE018553 Al033256 N76810 N	2 AA417043 A1565444 AW263286 31548 A1032084 N36278 AW075272
	Accession: C Pkey 408468 410295	CAT Number 106033_1 11922_2	Accession numbers Accession Al909712 AL03975: N47873 Al066549 A AW297099 AA741357 Al87000 Al032081 R35753 W69374 AA15	A1474112 AW450680 AA668668 R76114 AW2426 O W75997 H50726 AV658709 A1498817 AL03780 N93372 AA700790 A1903697 N529B5 R82468 AV	128 N58855 AW080313 A1378491 A1807102 14 W67847 BE018553 A1033256 N76810 N V580252 AL036760 A1052219 R36621 W07	2 AA417043 A1565444 AW263286 31548 A1032084 N36278 AW075272 047 AA088621 A1249109 W68776
	Accession: 0 Pkey 408468	CAT Number 105033_1	Accession AI909712 AL03975; N47873 AI066549 AW297099 AA741357 AI87000 AI032081 R35753 VW59374 AA15 W73853 AA928112	A1474112 AW450680 AA668668 R76114 AW2426 O W75997 H50726 AV658709 A1498817 AL03780 N93372 AA700790 A1903697 N52985 R82468 AV W77887 AW889237 AA148524 A1749182 A1754	128 N58855 AW080313 A1378491 A1807102 14 W67847 BE018553 A1033256 N76810 N V580252 AL036760 A1052219 R36621 W07 142 A1338392 A1253102 A1079403 A137054	2 AA417043 AI565444 AW263286 31548 Al032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 Al697341 H97538 AW188021
45	Accession: C Pkey 408468 410295	CAT Number 106033_1 11922_2	Accession Al909712 AL03975: N47873 Al066549 A AW297099 AA741357 Al87000 Al032081 R35753 V W69374 AA15 W73853 AA928112 Al927669 W72716 J	A1474112 AW450680 AA668668 R76114 AW2426 O W75997 H50726 AV658709 A1498817 AL03780 N93372 AA700790 A1903697 N529B5 R82468 AV	128 N58855 AW080313 A1378491 A1807102 14 W67847 BE018553 A1033256 N76810 N V580252 AL036760 A1052219 R36621 W07 142 A1338392 A1253102 A1079403 A137054	2 AA417043 AI565444 AW263286 31548 Al032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 Al697341 H97538 AW188021
	Accession: C Pkey 408468 410295 414496	CAT Number 106033_1 11922_2 145392_1	Accession Al909712 AL03975: N47873 Al066549 A AW297099 AA741357 Al87000 Al032081 R35753 V W69374 AA15 W73853 AA928112 Al927669 W72716 A	A1474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 A1498817 AL03780 N93372 AA700790 A1903697 N52985 R82468 AV W77887 AW889237 AA148524 A1749182 A1754- AI051402 A1188071 A1335900 N21488 AW77047	128 N58855 AW080313 A1378491 A1807102 14 W67847 BE018553 A1033256 N76810 N V580252 AL036760 A1052219 R36621 W07 142 A1338392 A1253102 A1079403 A137054	2 AA417043 AI565444 AW263286 31548 Al032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 Al697341 H97538 AW188021
45	Accession: C Pkey 408468 410295 414496 418919	CAT Number 106033_1 11922_2 145392_1 180623_1	Accession AI909712 AL03975: N47873 AI066549 A AW297099 AA741357 AI87000 AI032081 R35753 V W69374 AA15 W73853 AA928112 AI927669 W77215 AI868132 H98 AA232635 AI37370	A1474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 A1498817 AL03780 N93372 AA700790 A1903697 N52985 R82468 AV W77887 AW889237 AA148524 A1749182 A1754 A1051402 A1188071 A1335900 N21488 AW77047 3 AA233330	128 N58855 AW080313 AI378491 AI807102 04 W67847 BE018553 AI033256 N76810 N V580252 AL036760 AI052219 R36621 W07 442 AI338392 AI253102 AI079403 AI37054 8 W92522 AI691028 AI913512 AI144448 W	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 AI697341 H97538 AW188021 173819 AA604358 N28900 W95221
45	Accession: C Pkey 408468 410295 414496	CAT Number 106033_1 11922_2 145392_1	Accession numbers Accession Al909712 AL03975; N47873 Al066549 AW297099 AA741357 Al87000 Al032081 R35753 W69374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 AA234831 Al70030	A1474112 AW450680 AA668668 R76114 AW2426 O W75997 H50726 AV658709 A1498817 AL03780 N93372 AA700790 A1903697 N52985 R82468 AV I W77887 AW889237 AA148524 A1749182 A1754- A1051402 A1188071 A1335900 N21488 AW77047 I3 AA233330 I2 AA906216 AA776957 R49415 A1420777 AA666	128 N58855 AW080313 AI378491 AI807102 14 W67847 BE018553 AI033256 N76810 N V580252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 8 W92522 AI691028 AI913512 AI144448 W 1394 AI830619 AA779469 AI972390 N4098	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 AI697341 H97538 AW188021 173819 AA604358 N28900 W95221
45	Accession: C Pkey 408468 410295 414496 418919 418956	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1	Accession numbers Accession Al909712 AL03975: N47873 Al066549 AW297099 AA741357 Al87000 Al032081 R35753 VW59374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232831 Al70030 Al688257 Al804295	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL03786 N93372 AA700790 Al903697 N52985 R82468 AV 2 W77887 AW889237 AA148524 Al749182 Al7544 Al051402 Al188071 Al335900 N21488 AW77047 N3 AA233330 N3 AA233330 N3 AA236216 AA776957 R49415 Al420777 AA666 N4897791 AA232893 Al348680 Al356232 AA23	128 N58855 AW080313 AI378491 AI807102 04 W67847 BE018553 AI033256 N76810 N V580252 AL036760 AI052219 R36621 W07 442 AI338392 AI253102 AI079403 AI37054 8 W92522 AI691028 AI913512 AI144448 W 3394 AI830619 AA779469 AI972390 N4098 5138 F31396 AW079977 H16405	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 11 AI697341 H97538 AW188021 773819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994
45 50	Accession: C Pkey 408468 410295 414496 418919	CAT Number 106033_1 11922_2 145392_1 180623_1	Accession numbers Accession Al909712 AL03975: N47873 Al066549 A AW297099 AA741357 Al87000 Al032081 R35753 V W69374 AA15 V73853 AA928112 Al868132 H98 AA232635 Al37370 AA234831 Al70030 AB68257 Al804295 A493205 AA73231	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL03780 N93372 AA700790 Al903697 N52985 R82468 AV W77887 AW889237 AA148524 Al749182 Al754- Al051402 Al188071 Al335900 N21488 AW77047 3 AA233330 22 AA906216 AA776957 R49415 Al420777 AA666 5 AA897791 AA232893 Al348680 Al356232 AA23 5 AA344619 AA904035 AW952967 AA488889 A	128 N58855 AW080313 AI378491 AI807102 14 W67847 BE018553 AI033256 N76810 N VS80252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 8 W92522 AI691028 AI913512 AI144448 W 15394 AI830619 AA779469 AI972390 N4098 15138 F31396 AW079977 H16405 1635644 BE245127 AA669979 AA761874 N	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 11 AI697341 H97538 AW188021 773819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994
45	Accession: C Pkey 408468 410295 414496 418919 418956 424651	CAT Number 105033_1 11922_2 145392_1 180623_1 180862_1 241981_1	Accession AI909712 AL03975: N47873 AI066549 A AW297099 AA741357 AI87000 AI032081 R35753 V W69374 AA15 W73853 AA928112 AI826669 W77217 AI8263 AI37370 AA234831 AI70303	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL03780 N93372 AA700790 Al903697 N52985 R82468 AV W77887 AW889237 AA148524 Al749182 Al754- Al051402 Al188071 Al335900 N21488 AW77047 3 AA233330 12 AA96216 AA776957 R49415 Al420777 AA666 5 AA9697791 AA232893 Al348680 Al356232 AA23 5 AA344619 AA904035 AW952987 AA488899 AV 14 AL521825 AA746092 AA743152 Al478562 H888	128 N58855 AW080313 AI378491 AI807102 14 W67847 BE018553 AI033256 N76810 N VS80252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 8 W92522 AI691028 AI913512 AI144448 W 15394 AI830619 AA779469 AI972390 N4098 15138 F31396 AW079977 H16405 1635644 BE245127 AA669979 AA761874 N	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 11 AI697341 H97538 AW188021 773819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994
45 50	Accession: C Pkey 408468 410295 414496 418919 418956 424651 436772	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1	Accession numbers Accession Al909712 AL03975: N47873 Al066549 A AW297099 AA741357 Al87000 Al032081 R35753 V W59374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 AL858257 Al804295 AL93206 AA73231 AA766495 W76175 AW975688 AA7316	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL03786 N93372 AA700790 Al903697 N52985 R82468 AV 1 W77887 AW889237 AA148524 Al749182 Al754- Al051402 Al188071 Al335900 N21488 AW77047 13 AA233330 12 AA906216 AA776957 R49415 Al420777 AA666 5 AA897791 AA232893 Al348680 Al356232 AA23 5 AA344619 AA904035 AW952967 AA488899 AI 6 AL521825 AA746092 AA743152 Al478562 H888 163 N67084	128 N58855 AW080313 AI378491 AI807102 04 W67847 BE018553 AI033256 N76810 N V580252 AL036760 AI052219 R36621 W07 442 AI338392 AI253102 AI079403 AI37054 8 W92522 AI691028 AI913512 AI144448 W 6394 AI830619 AA779469 AI972390 N4098 5138 F31396 AW079977 H16405 AG35644 BE245127 AA669979 AA761874 H	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 AI697341 H97538 AW188021 773819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 H28767 AA910081 AA837086
45 50	Accession: C Pkey 408468 410295 414496 418919 418956 424651	CAT Number 105033_1 11922_2 145392_1 180623_1 180862_1 241981_1	Accession numbers Accession Al909712 AL03975: N47873 Al066549 AW297099 AA741357 Al87000 Al032081 R35753 VW59374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 Al668257 Al804295 Al493206 AA73231 AA766496 W7675 MW975688 AA7316 M64936 Al025512 A	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL03786 N93372 AA700790 Al903697 N52985 R82468 AV W77887 AW889237 AA148524 AI749182 AI754- AI051402 AI188071 AI335900 N21488 AW77047 03 AA233330 12 AA906216 AA776957 R49415 AI420777 AA666 15 AA997791 AA232893 AI348680 AI356232 AA23 15 AA344619 AA904035 AW952967 AA488889 AV 14 AI34825 AA746092 AA743152 AI478562 H888 163 N57084 AI382987 BE061777 AA089966 BE169930 T4117	128 N58855 AW080313 AI378491 AI807102 104 W67847 BE018553 AI033256 N76810 N 1V580252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 18 W92522 AI691028 AI913512 AI144448 W 1394 AI830619 AA779469 AI972390 N4098 15138 F31396 AW079977 H16405 1633644 BE245127 AA669979 AA761874 R 153	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 AI697341 H97538 AW188021 773819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 H28767 AA910081 AA837086
45 50	Accession: C Pkey 408468 410295 414496 418919 418956 424651 436772 438780	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1	Accession numbers Accession Al909712 AL03975: N47873 Al066549 A AW297099 AA741357 Al87000 Al032081 R35753 V W69374 AA15 V73853 AA928112 Al868132 H98 AA232635 Al37370 AA234831 Al70003 Al688257 Al80429 A493206 AA73231 AA766495 W76175 AW975688 AA7321 AM975688 AA7321	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL03780 N93372 AA700790 Al903697 N52985 R82468 AV W77887 AW889237 AA148524 Al749182 Al754- Al051402 Al188071 Al335900 N21488 AW77047- 3 AA233330 2 AA233330 2 AA234519 AA236957 R49415 Al420777 AA666 5 AA897791 AA232893 Al348680 Al356232 AA23 5 AA344619 AA904035 AW952967 AA488889 AV AL352887 BA746092 AA743152 Al478562 H888 103 N67084 Al382987 BE061777 AA089966 BE169930 T4117 8 BE327710 AW975215 AW896268 AA884990 BE	128 N58855 AW080313 AI378491 AI807102 104 W67847 BE018553 AI033256 N76810 N 1V580252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 18 W92522 AI691028 AI913512 AI144448 W 1394 AI830619 AA779469 AI972390 N4098 15138 F31396 AW079977 H16405 1633644 BE245127 AA669979 AA761874 R 153	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 1 AI697341 H97538 AW188021 773819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 H28767 AA910081 AA837086
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45 50 55 60 65 70	Accession: C Pkey 408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Unique Ref: Sequer huma Strand: Indic Nt_position: Pkey 400829	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 1910_	Accession numbers Accession Al909712 AL03975: N47873 Al066549 AAV297099 AA741357 AI87300 Al032081 R35753 V W59374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 AA234831 Al70030 AI868257 AI804295 AI493205 AA73231 AG64936 AI025512 AI079277 AV241318 AV9575688 AA7310 AV652068 AA45981 AJ98671 AA9715 AV652068 AA45981 AJ98671 AU9717 AV652068 AA45981 AJ98671 AA9715 AJ98671	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 AI498817 AL0378 N93372 AA700790 AI903697 N52985 R82468 AV 1 W77887 AW889237 AA148524 AI749182 AI754 AI051402 A1188071 AI335900 N21488 AW77047 33 AA233330 12 AA306216 AA776957 R49415 AI420777 AA666 55 AA397791 AA232893 AI348680 AI356232 AA23 55 AA344619 AA904035 AW952987 AA488899 AV AI521825 AA746092 AA743152 AI478562 H888 IGS N67084 AI382987 BE061777 AA089966 BE 169930 T4117 8 BE327710 AW975215 AW896268 AA884990 Bt I8 AI937262 80 T58512 T58561 AI651255 N49838 H87921 AV 8 AI871252 AI376942 AI740496 AA452836 AI277 699 AI603973 781 AW849062 AW848490 AW752699 AW75260 probesel this column are Genbank Identifier (GI) numbers. (1999) Nature 402489-495 s were predicted redicted exons ostition 76-152616	128 N58855 AW080313 AI378491 AI807102 104 W67847 BE018553 AI033256 N76810 N 10580252 AL036760 AI052219 R36621 W07 1442 AI338392 AI253102 AI079403 AI37054 18 W92522 AI691028 AI913512 AI144448 W 16394 AI830619 AA779469 AI972390 N4098 16338 F31396 AW079977 H16405 1633 F31396 AW079977 H16405 1633 F31396 AW079977 AA761874 N633 164 AW594624 BE502415 AA121893 AI2692 165 AW594624 BE502415 AA121893 AI2692 167 AI149141 AA456147 AI784566 AI0039 165 AW752700	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 7047 AA088621 AI249109 W68776 11 AI697341 H97538 AW188021 773819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 H28767 AA910081 AA837086 283 T40311 AI684569 AA257011 D62894 AW341452 AA243652 775 AI245674 AI433703 AI200208
45 50 55 60 65	Accession: C Pkey 408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Uniqu Ref: Sequer huma Strand: India Nt_position: Pkey 400829 403247	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 190000000000000000000000000000000000	Accession numbers Accession Al909712 AL03975: N47873 Al066549 AW297099 AA741357 Al87000 Al032081 R35753 VW59374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 AA234831 Al70030 Al688257 Al804295 A493206 AA73231 AA766495 W7613 AM936680 AA73231 AA766495 W7613 AW975688 AA7310 M64936 Al025512 AM93868 AJ938571 AA9715 AW975688 AA7340 AW9752597 AW848 AW752597 AW848	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL0378(N93372 AA700790 Al903697 N52985 R82468 AV 1 W77887 AW889237 AA148524 AI749182 AI754 AI051402 AI188071 AI335900 N21488 AW77047 3 AA233330 3 AA233330 2 AA906216 AA776957 R49415 Al420777 AA666 5 AA697791 AA232893 AI348680 AI356232 AA23 5 AA344619 AA904035 AW952967 AA488899 AV I AI521825 AA746092 AA743152 AI478562 H888 AI382987 BE061777 AA089966 BE169930 T4117 8 BE327710 AW975215 AW896268 AA884990 BE 18 AI937262 80 T58512 T58561 AI651255 N49838 H87921 AV 8 AI871252 AI376942 AI740496 AA452836 AI277 699 AI803973 781 AW849062 AW848490 AW752699 AW75260 probasel this column are Genbank Identifier (GI) numbers. (1999) Nature 402489-495 I were predicted redicted exons osition 76-152616 6-77140	128 N58855 AW080313 AI378491 AI807102 124 W67847 BE018553 AI033256 N76810 N V580252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 143 AI338392 AI253102 AI079403 AI37054 154 AI830619 AA779469 AI972390 N4098 15138 F31396 AW079977 H16405 1533 F31396 AW079977 H16405 1533 164 AW594624 BE502415 AA121893 AI2692 15327514 174 AI49141 AA456147 AI784566 AI0039 175 AW752700 "Dunham I. et al." refers to the publication	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 1047 AA088621 AI249109 W68776 1 AI697341 H97538 AW188021 173819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 128767 AA910081 AA837086 1283 T40311 AI684569 AA257011 10 D62894 AW341452 AA243652 175 AI245674 AI433703 AI200208 entitled *The DNA sequence of
45 50 55 60 65 70	Accession: C Pkey 408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Unique Ref: Sequer huma Strand: Indic Nt_position: Pkey 400829	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 1910_	Accession numbers Accession Al909712 AL03975: N47873 Al066549 AW297099 AA741357 Al87000 Al032081 R35753 V W99374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 AA234831 Al70030 Al688257 Al804295 A4493206 AA73231 AA766495 W76175 AW975688 AA7310 M64936 Al025512 Al079277 Al241318 AA99351 AA971 AV65206 AA73231 AA994618 Al816803 Al268985 Al38 AW130351 AW3881 AW752597 AW8481 Besponding to an Eos to 7 digit numbers in the 22" Dunham, et al. and from which exons eolide positions of pr Strand Nt_pelss Strand Nt_pelss Flus Strand Nt_pelss Flus Strand Nt_pelss Flus Strand Nt_pelss Flus S601 Flus S601	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL0378(N93372 AA700790 Al903697 N52985 R82468 AV 1 W77887 AW889237 AA148524 AI749182 AI754- AI051402 AI188071 AI335900 N21488 AW77047 3 AA233330 2 AA906216 AA776957 R49415 Al420777 AA666- 5 AA897791 AA232893 AI348680 AI356232 AA23- 5 AA344619 AA904035 AW952967 AA488889 AV IAI521825 AA746092 AA743152 AI478562 H888- IAI521825 AA746092 AA743152 AI478562 H888- IAI521825 AI76932 AA745092 BE169930 T4117- B BE327710 AW975215 AW896268 AA884990 BE18 AI837262 BO T58512 T58561 AI651255 N49838 H87921 AV 3 AI871252 AI376942 AI740496 AA452836 AI277- 699 AI803973 781 AW849062 AW848490 AW752699 AW75260 probesel this column are Genbank Identifier (GI) numbers. (1999) Nature 402489-495 were predicted redicted redicted exons csition 76-152616 6-77140 9-36282,37073-37813,38948-39314,40355-4065	128 N58855 AW080313 AI378491 AI807102 124 W67847 BE018553 AI033256 N76810 N VS80252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 143 AI338392 AI253102 AI079403 AI37054 144 AI338392 AI253102 AI079403 AI37054 15394 AI830619 AA779469 AI972390 N4098 15139 F31396 AW079977 H16405 1633644 BE245127 AA669979 AA761874 N 163 164 AW594624 BE502415 AA121893 AI2692 16327514 175 AI149141 AA456147 AI784566 AI0039 176 AW752700 **Dunham I. et al.** refers to the publication 184 AW752700 184 AW752700 185 AI396 AI391 AI3696,45698 AI3030, 185 AI398 AI391 AI3696,45698 AI3030, 185 AI398 AI391 AI3696,45698 AI391,42738 AI3028,43391 AI3696,45698 AI3030, 185 AI398 AI398 AI399 AI3696,45698 AI398 AI3998	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 1047 AA088621 AI249109 W68776 11 AI697341 H97538 AW188021 173819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 1428767 AA910081 AA837086 1283 T40311 AI684569 AA257011 10 D62894 AW341452 AA243652 175 AI245674 AI433703 AI200208 110 The DNA sequence of
45 50 55 60 65 70	Accession: C Pkey 408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Uniqu Ref: Sequer huma Strand: India Nt_position: Pkey 400829 403247	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 190000000000000000000000000000000000	Accession numbers Accession Al909712 AL03975: N47873 Al066549 AAV297099 AA741357 AI87300 Al032081 R35753 V W59374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 AA234831 Al70030 Al868257 Al804295 Al493205 AA73231 AA766495 W76175 AW975688 AA7310 M64936 Al025512 AA AA93871 AA9715 AV652068 AA4588 AJ938618 Al816803 AJ938618 Al816803 AW130351 AW3381 AW752597 AW848* Besponding to an Eos to 7 digit numbers in the 22° Dumharn, et al. and from which exons eotide positions of pr Strand NL pt Plus 1521 Minus 7662 Plus 3601 5493	N474112 AW450680 AA68868 R76114 AW2426 0 W75997 H50726 AV658709 AI498817 AL0378 N93372 AA700790 AI903697 N52985 R82468 AV 1 W77887 AW889237 AA148524 AI749182 AI754 AI051402 A188071 AI335900 N21488 AW77047 3 AA233330 12 AA906216 AA776957 R49415 AI420777 AA668 5 AA897791 AA232893 AI348680 AI356232 AA23 5 AA344619 AA904035 AW952987 AA488899 AI AI521825 AA746092 AA743152 AI478562 H888 AIS31825 BE061777 AA089565 BE16930 T4117 BB E327710 AW9752515 AW896268 AA884990 BE BA H3937262 80 T58512 T58561 AI651255 N49838 H87921 AV 3 AI871252 AI376942 AI740496 AA452836 AI277 699 AI803973 781 AW849062 AW848490 AW752699 AW75260 probesel this column are Genbank Identifier (GI) numbers. (1999) Nature 402489-495 swere predicted redicted exons osition 76-152616 6-77140 9-38282,37073-37813,38946-39314,40355-4065 5,55201-55509,55926-56240,56355-56672,57076	128 N58855 AW080313 AI378491 AI807102 124 W67847 BE018553 AI033256 N76810 N VS80252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 143 AI338392 AI253102 AI079403 AI37054 144 AI338392 AI253102 AI079403 AI37054 15394 AI830619 AA779469 AI972390 N4098 15139 F31396 AW079977 H16405 1633644 BE245127 AA669979 AA761874 N 163 164 AW594624 BE502415 AA121893 AI2692 16327514 175 AI149141 AA456147 AI784566 AI0039 176 AW752700 **Dunham I. et al.** refers to the publication 184 AW752700 184 AW752700 185 AI396 AI391 AI3696,45698 AI3030, 185 AI398 AI391 AI3696,45698 AI3030, 185 AI398 AI391 AI3696,45698 AI391,42738 AI3028,43391 AI3696,45698 AI3030, 185 AI398 AI398 AI399 AI3696,45698 AI398 AI3998	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 1047 AA088621 AI249109 W68776 11 AI697341 H97538 AW188021 173819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 1428767 AA910081 AA837086 1283 T40311 AI684569 AA257011 10 D62894 AW341452 AA243652 175 AI245674 AI433703 AI200208 110 The DNA sequence of
45 50 55 60 65 70	Accession: C Pkey 408468 410295 414496 418919 418956 424651 436772 438780 441916 444931 . 451573 458147 TABLE 24C: Pkey: Uniqu Ref: Sequer huma Strand: India Nt_position: Pkey 400829 403247	CAT Number 106033_1 11922_2 145392_1 180623_1 180862_1 241981_1 426854_1 46501_1 528799_1 62567_1 875588_1 488021_1 190000000000000000000000000000000000	Accession numbers Accession Al909712 AL03975: N47873 Al066549 AAV297099 AA741357 AI87300 Al032081 R35753 V W59374 AA15 W73853 AA928112 Al927669 W72716 Al868132 H98 AA232635 Al37370 AA234831 Al70030 Al868257 Al804295 Al493205 AA73231 AA766495 W76175 AW975688 AA7310 M64936 Al025512 AA AA93871 AA9715 AV652068 AA4588 AJ938618 Al816803 AJ938618 Al816803 AJ938618 Al816803 AW130351 AW3388 AW752597 AW848* Besponding to an Eos to 7 digit numbers in and from which exons eotide positions of pr Strand NL pt Plus Strand NL pt Plus Strand Strand Strand NL pt Plus Strand Strand NL pt Plus S620 Plus S620 S483	N474112 AW450680 AA668668 R76114 AW2426 0 W75997 H50726 AV658709 Al498817 AL0378(N93372 AA700790 Al903697 N52985 R82468 AV 1 W77887 AW889237 AA148524 AI749182 AI754- AI051402 AI188071 AI335900 N21488 AW77047 3 AA233330 2 AA906216 AA776957 R49415 Al420777 AA666- 5 AA897791 AA232893 AI348680 AI356232 AA23- 5 AA344619 AA904035 AW952967 AA488889 AV IAI521825 AA746092 AA743152 AI478562 H888- IAI521825 AA746092 AA743152 AI478562 H888- IAI521825 AI76932 AA745092 BE169930 T4117- B BE327710 AW975215 AW896268 AA884990 BE18 AI837262 BO T58512 T58561 AI651255 N49838 H87921 AV 3 AI871252 AI376942 AI740496 AA452836 AI277- 699 AI803973 781 AW849062 AW848490 AW752699 AW75260 probesel this column are Genbank Identifier (GI) numbers. (1999) Nature 402489-495 were predicted redicted redicted exons csition 76-152616 6-77140 9-36282,37073-37813,38948-39314,40355-4065	128 N58855 AW080313 AI378491 AI807102 124 W67847 BE018553 AI033256 N76810 N VS80252 AL036760 AI052219 R36621 W07 142 AI338392 AI253102 AI079403 AI37054 143 AI338392 AI253102 AI079403 AI37054 144 AI338392 AI253102 AI079403 AI37054 15394 AI830619 AA779469 AI972390 N4098 15139 F31396 AW079977 H16405 1633644 BE245127 AA669979 AA761874 N 163 164 AW594624 BE502415 AA121893 AI2692 16327514 175 AI149141 AA456147 AI784566 AI0039 176 AW752700 **Dunham I. et al.** refers to the publication 184 AW752700 184 AW752700 185 AI396 AI391 AI3696,45698 AI3030, 185 AI398 AI391 AI3696,45698 AI3030, 185 AI398 AI391 AI3696,45698 AI391,42738 AI3028,43391 AI3696,45698 AI3030, 185 AI398 AI398 AI399 AI3696,45698 AI398 AI3998	2 AA417043 AI565444 AW263286 31548 AI032084 N36278 AW075272 1047 AA088621 AI249109 W68776 11 AI697341 H97538 AW188021 173819 AA604358 N28900 W95221 10 AI094453 AA826397 AA535994 1428767 AA910081 AA837086 1283 T40311 AI684569 AA257011 10 D62894 AW341452 AA243652 175 AI245674 AI433703 AI200208 110 The DNA sequence of

Table 25A provides Unigene ID, Unigene Title, Picey, and Exemplar Accession for sequences in Table 26. The Information in Table 25A is linked by SEQ ID NO: to Table 26.

80

Table 25A: Pkey: Unique Eos probeset identifier number

Ex. Acon: Exemplar Accession number, Genbank accession number UG ID: UniGene number Title: UniGene title

sequences in Table 2	6
×	equences in Table 2

2					
	Pkey	Ex. Acon	UGID	Title ·	SEQ ID NO
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	SEQ ID NO: 1-2
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	SEQ ID NO: 3-4
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	SEQ ID NO: 5-6
10	458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	SEQ ID NO: 7-8
	422956	BE545072	Hs.122579	ECT2 protein (Epithelia) cell transformi	SEQ ID NO: 9-10
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	SEQ ID NO: 11-12
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	SEQ ID NO: 13-22
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	SEQ ID NO: 23-24
15	451110	AI955040	Hs.265398	PAR-6 beta (partitioning defective 6 h	SEQ ID NO: 25-26
10					SEQ ID NO: 27-28
	428187	Al687303	Hs.285529	G protein-coupled receptor 49	
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	SEQ ID NO: 29-30
	433159	AB035898	Hs.150587	kinesin-like protein 2	SEQ ID NO: 31-32
	426427	MB6699	Hs.169840	TTK protein kinase	SEQ ID NO: 33-34
20	425371	D49441	Hs.155981		SEQ ID NO: 35-38
20				mesothelin	
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	SEQ ID NO: 39-40
	456546	AI690321	Hs.203845	KCNK15 potasstum channel, subfamily K, m	SEQ ID NO: 41-42
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	SEQ ID NO: 43-44
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	SEQ ID NO: 45-46
25	424520	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	SEQ ID NO: 47-48
20	412078	X69699			SEQ ID NO: 49-52
			Hs.73149	paired box gene 8	
	409178	BE393948	Hs.50915	kallikrein 5	SEQ ID NO: 53-54
	448243	AW369771		integrin, beta 8	SEQ ID NO: 55-56
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	SEQ ID NO: 57-58
30	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	SEQ ID NO: 59-60
-	431130		Hs.2719		SEQ ID NO: 61-62
		NM_006103		HE4; epididymis-specific, whey-acidic pr	
	415539	AI733881	Hs.72472	BMP-R1B	SEQ ID NO: 63-64
	423961	D13666	Hs.136348	periostin (OSF-2os)	SEQ ID NO: 65-66
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	SEQ ID NO: 67-68
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	SEQ ID NO: 69-70
-	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	SEQ ID NO: 71-72
	444381	BE387335	Hs.283713	ESTs. Wealdy similar to S64054 hypotheti	SEQ ID NO: 73-74
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	SEQ ID NO: 75-76
	450375	AA009647		a disintegrin and metalloproteinase doma	SEQ ID NO: 77-78
40	426215	AW963419	Hs.155223	stanniocalcin 2	SEQ 1D NO: 79-80
	430044	AA464510	Hs.152812	ESTs	SEQ ID NO: 81
	447033	AJ357412	Hs.157601	ESTs	SEQ ID NO: 82-87
	410418	D31382	Hs.63325	transmembrane protease, serine 4	SEQ ID NO: 88-89
4.5	411274	NM_002776	Hs.69423	kallikrein 10	SEQ ID NO: 90-91
45	422260	AA315993	Hs.105484	regenerating gene type IV	SEQ ID NO: 92-93
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	SEQ ID NO: 94-95
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	SEQ ID NO: 96-97
	404977	M1001000	115.105055		SEQ ID NO: 98-99
		*****		Insulin-like growth factor 2 (somatomedi	
5 0	427747	AW411425	Hs.180655	serine/threonine kinase 12	SEQ ID NO: 100-101
50	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	SEQ ID NO: 102-103
	431846	BE019924	Hs.271580	uroplakin 1B	SEQ ID NO: 104-105
	425465	L18964	Hs.1904	protein kinase C, lota	SEQ ID NO: 106-107
	432938	T27013	Hs.3132		SEQ ID NO: 108-109
				steroidogenic acute regulatory protein	
E E	421451	AA291377	Hs.50831	ESTs	SEQ ID NO: 110-117
55	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	SEQ ID NO: 118-119
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	SEQ ID NO: 120-121
	424078	AB006625	Hs.139033	paternally expressed 3	SEQ ID NO: 122-123
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	SEQ ID NO: 124-125
		AUX 044704	11- 404220		
60	428450	NM_014791	Hs.184339	KIAA0175 gene product	SEQ ID NO: 126-127
60	438167	R28363	Hs.24286	chemoldne binding protein 2 (CCBP2), mRN	SEQ ID NO: 128-129
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SEQ ID NO: 130-131
	430691	C14187	Hs.157208	aristaless-related homeobox protein ARX	SEQ ID NO: 132-133
	408081	AW451597	Hs.167409	intron of basic-helix-loop-helix-PAS pro	SEQ ID NO: 134
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SEQ ID NO: 135-138
65					SEQ ID NO: 139-140
UJ	407792	A1077715	Hs.39384	putative secreted ligand homologous to f	
	428093	AW594506	Hs.104830	ESTs	SEQ ID NO: 141 -144
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	SEQ ID NO: 145-148
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	SEQ ID NO: 149-150
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	SEQ ID NO: 151-152
70	431369			secretory teukocyte protease Inhibitor (SEQ ID NO: 153-154
, 0		BE184455	Hs.251754		
	436972	AA284679	Hs.25640	claudin 3	SEQ ID NO: 155-156
	429504	X99133	Hs.204238	tipocalin 2 (oncogene 24p3) (NGAL)	SEQ ID NO: 157-158
	410001	AB041036	Hs.57771	kallikrein 11	SEQ ID NO: 159-160

75

TABLE 258: Pkay: Unique Eos probeset identifier number CAT number: Gene duster number Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	448243	75629 1	AW359771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 AI480343 AA044582 AW956159 AA373451 AA127965 AL134913
			AW994956 BE622314 BE006298 BE006312 BE006305 BE006317 BE006303 AA043906 AA234175 AA479726
	450375	83327 1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
			AA190993 H03231 H59605 H01642 AA652876 AA113758 AA626915 AA746952 AL161014 AA099554 R69067

```
TABLE 25C:
        Pkey: Unique number corresponding to an Eos probeset
        Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
             human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
        Strand: Indicates DNA strand from which exons were predicted
        Ni_position: Indicates nucleotide positions of predicted exons
                             Strand
10
        404977
                   3738341
                             Minus
                                        43081-43229
        406400
                                        1553-1712,1878-2140,4252-4385,5922-6077
                   9256298
                             Plus
        Table 26
15
        Sec ID NO: 1 DNA sequence
        Nucleic Acid Accession #: NM_006115.1
        Coding sequence: 236..1765
                                   21
                     11
20
        GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCCT GCAGCCCCTC AGCACCGCTC
                                                                                              60
        CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA
        ACTOTOTGAG GAAAAACCAT TTTGATTATT ACTOTCAGAC GTGCGTGGCA ACAAGTGACT
                                                                                             180
        GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA
                                                                                             240
25
        ACGAAGGCGT TTGTGGGGTT CCATTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG
                                                                                             300
        CCCACGAGA CTTGTGGAGC TGGCAGGCA GĂGCCTGCTG AAGGATGAGG CCCTGGCCAT
TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA
                                                                                             360
                                                                                             420
        CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC
        TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA
                                                                                              540
30
        TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAAC TTCAAGTGCT
                                                                                             600
        GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG
TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA
                                                                                             660
        TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT
                                                                                             780
        CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA
GAAAAATGTA CTACGCCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA
                                                                                              840
35
                                                                                             900
        TATCAGATG ATCCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTTGG AAGTGACTTG
TACCTGGAAG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT
                                                                                              960
                                                                                            1020
        GCGTAGACTC CTCCTCCCC ACATCCATGC ATCTTCCTAC ATTTCCCCGG AGAAGGAAGA
                                                                                            1080
        GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA
TGTGGACTCT TTATTTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGATGAA
                                                                                            1140
40
                                                                                            1200
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        GTCCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCCTGAGT CTAAGTGGGG TCATGCTGAC
                                                                                            1320
         CGATGTAAGT CCCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA
                                                                                            1380
         CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTTGCCCTCC TGCCTTCCCT
                                                                                            1440
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                                                                                            1500
         CTTGCAGAGT CTCCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC
         TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCCTA
                                                                                            1620
         TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCCAGCA TGGTCTGGCT
                                                                                            1680
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GTGCCCCTGT TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC
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50
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                                                                                            1860
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                                                                                            1920
         GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTTGACTTG AGGAGTTAAT
                                                                                            1980
        GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA
GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC
                                                                                            2040
55
         TOTTGAAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAA AAAAAAAA
         Seg ID NO: 2 Protein seguence
         Protein Accession #: NP 006106.1
60
                      11
                                    21
                                                                41
         MERRRLWGSI QSRYISMSVW TSPRRLVELA GQSLLKDEAL AIAALELLPR ELFPPLFMAA
FDGRHSQTLK AMVQAWPFTC LPLGVLMKGQ HLHLETFKAV LDGLDVLLAQ EVRPRRWKLQ
VLDLRKNSHQ DFWTVWSGNR ASLYSFPEPE AAQPMTKKRK VDGLSTEAEQ PFIPVEVLVD
                                                                                               60
                                                                                              120
                                                                                              180
65
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         TCTWKLPTLA KFSPYLGOMI NLRRLLLSHI HASSYISPEK EEQYIAQFTS QFLSLQCLQA
                                                                                              300
         LYVDSLFFLR GRLDQLLRHV MNPLETLSIT NCRLSEGDVM HLSQSPSVSQ LSVLSLSGVM
                                                                                              360
         LTDVSPEPLQ ALLERASATL QDLVFDECGI TDDQLLALLP SLSHCSQLTT LSFYGNSISI
                                                                                              420
         SALQSLLQHL IGLSNLTHVL YPVPLESYED IHGTLHLERL AYLHARLREL LCELGRPSMV
70
         WLSANPCPHC GDRTFYDPEP ILCPCFMPN
         Seg ID NO: 3 DNA seguence
         Nucleic Acid Accession #: Eos seguence
         Coding sequence: 264..782
75
                      11
                                    21
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         TCATCGCGGG ACTAATTTTC CTTAAAATTT AGACTTGCAC AGTAAGGACT TCAACTGACC
         TTCCTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC
                                                                                              180
80
         TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC
AACTTATCAG CAAGGAGCTC ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG
                                                                                              240
                                                                                              300
         TGATCGCGGT GGTGTCCCTC TTCCTGCAGG CCTGCTTCCT CACCGCCATC AACTACCTGC
                                                                                              360
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TCAGCAGGCA CATGGCCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCCAGGTTC

CCAGGCCCAG CCCTGGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA

CAGAGAGAGA CATCCCAATG TCTGATTCCC TTTACAGGCA TGACAGCGAC ACACCCTCAG

85

420

		TAGCTCCTGC					600
		CGTCTTTTCT GGAAATCACA					660 720
_	TCTGGTATTT	TGTCAACCCT	GCTCTGTCTG	AGCCAGCGGA	ATATGATCAA	GTGGCCATGT	780
5		TATTTTTAAT					840
		TTTTTCCCCC GTGGAGAAGA					900 960
	CCTGGTCTGT	ACCCAAAAAA	GCTGTTCGTT	CCTCAAAAAC	AAAAACAAGG	CTTGGCTGGG	1020
10		AATGCCCCGG GAACTATGGA					1080 1140
		AAGGTTGAAT					1200
	TGACTTCCCT	TTGAGCTCTT					1260
	AAAATAGCAA	CCACCACCA					
15		4 Protein s	-				
	Protein Acc	ession #: I 11	Sos sequence 21	9 31	41	51	
	Ī	Ī	ī	Ĭ	Ĩ	Ī	
20		GLVIAVVSLF					60
20		TQTERDIPMS DYENIKEITD					120
	0 TD NO	5 DW					
		5 DNA seque d Accession		90.			
25	Coding sequ	lence: 342	2457				
	1	11	21 	37: 1	41 1	51 	
	AGCGGCCGCG	GCACAAAGTT	GGGGCCGCG	AAGATGAGGC	TGTCCCCGGC	GCCCCTGAAG	60
30		CTCCGGCACT					120
30		CCCTGGACAA					180 240
	GACTTCTACA	AGCCGGGAAC	CAGCTACCGC	GTAACACTTT	CAGCTGCTCC	TCCCTCCTAC	300
		TCACATTAAT					360
35		CCTTCCAGAT					420 480
-	CCACCAGCGG	GAACAGGCTG	CGTGATTCTG	AAGGCCAGCA	TCGTACAAAA	ACGCATTATT	540
		ATGAGGGCTC					600
		ACAAACCCAT GGAATTGGTC					660 720
40	CACTGGTCTG	CGATCATCGG	AGGATCCCAC	TCCAAGAATT	ATGTACTGTG	GGAATATGGA	780
		GCGAAGGCGT					840 900
		GACAACAGAG AGCCTCTCAA					960
15	ACGCGCCATT	TAATGTCCTT	CCTGACCATG	ATGGGCCCTA	GTCCCGACTG	GAACGTAGGC	1020
45		AAGATCTGTG GGGACGCTGG					1080 1140
		AGGAGAAAAT					1200
		AGGGTGGGTC					1260
50		AACAATGCAA AGAAAGATGA					1320 1380
• •		CCTGCAGCTC					1440
		AGCTGGACCT					1500 1560
		GCTGCAGTGA GCAGCATCTC					1620
55	CAGTTCCCGG	AGGACGGCTC	OGTGTGCACG	CTGCCCACTG	AGGAAACGGA	GAAGTGCACG	1680
		AGTGCTCTCC CCTGCGGCAT					1740 1800
		CCATGTGCAA					1860
60		TCCCATGCTT					1920
00		GCATGCGAAC ATCTGGAGCA					1980 2040
						AGGCCACGTG	2100
						CCCAGAGACT	
65						CCAAAAGCTA GTCTGAAGGG	2220 2280
	GAGCAGTTCC	CAGGTTGTAG	GATGCGCCCA	TGGACGGCCT	GGTCAGAATG	CACCAAACTG	2340
						AAGCTCCCAG TTGTTAGCAA	
						TGGATTATTT	2520
70	GCTTGTTTAA	GACAATTTAA	ATTGTGTACG	CTAGTTTTCA	TTTTTGCAGT	GTGGTTCGCC	2580
						GTACAGGCTG CAGCCACCTT	
		GAAACATGTC					2760
75	GACCTACTCC	ACATGGAGAG	GCAACCATGT	CTGGAAGTGA	CTATGCCTGA	GTCCCAGGGT	2820
75						TCATCTTTGG GTCTCTTTTC	
						TTGAAGAGGA	
						TTTGTCTCAC	
80						ATGGCTGCTT TAGAGTGTAT	
- •	TTTTCCCTTG	CTTTTGGGGG	TTCAGAGGAG	TATGTACAAT	TCTTCTGGGA	AGCCAGCCTT	3240
						AATTGGTCTC	
	TGCAAATCAG	TTTTTAGCAA	GAAAACATTT	TTGCTATACA	AACATTTTGC	CGTTCAAGTT	3420
85	CAAAGCCCCC	CCAATGCATT	CCTTCAACAA	AATACAATCT	CTGTACTTTA	AAGTTATTTT	3480

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	TGCTCCACAC	CAGGGCTGTG	GTCCTCCCAG	ACATGCATAG	GAATGGCCAC	AGGTTTACAC	3660
							3720
5 .	TGCCTTCCCA						-
Э.	TAAAAGGACA	TTTTCTCAGT	TGGGTCCATC	AGCAGTTTTT	CTTCCTGCAT	TTATTGTTGA	3780
	AAACTATTGT						3840
	ATTGGTGAGA	CACATACAAT	GCTCTGAATA	CACTACGAAT	TTGTATTAAA	CACATCAGAA	3900
	TATTTCCAAA	TACANCATAC	TATACTOCTC	TOATSTATE	TTTDACACAA	GAGAGACTAT	3960
• ^	TCAATAAAA						4020
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	TTCTTGGAGG						4140
	CTTAAATGAA	TTGCTTTCTC	CCAAAAAAAG	CACAATATAA	AGAAACACAA	GATTTAATTA	4200
	TTTTTCTACT						4260
	CTAAGCTATC	TATCTAACTC	TCAGCCCATG	ATAAAGTTCC	TTAAGCTGGT	GATTCCTAAT	4320
15	CANCCACAAC	CCACCCTACT	ביתירים מעייתים	תיבובו התיתונו ביותו	CCCACTTCCC	TACATTTTAA	4380 .
1.5							
	AATCCTGATT	TTGGAGACTT	AAAACCAGGT	TAATGGCTAA	GAATGGGTAA	CATGACTCTT	4440
	GTTGGATTGT	And Andread of the Wall	TTCCAATCCC	CAATTTATAA	AACCATCAA	CACALCALA LANCE	4500
	TACCAAAGTC	TIGITAGGIG	GTTTATAGTT	CTTTTGGCTA	AÇAAATCATT	TTGGAAATAA	4560
	AGATTTTTTA	CTACAAAAAT	G				
20			-				
20							
	Seg ID NO:	6 Protein s	eovence				
	-		-				
		ession #: E					
	1	11	21	31	41	51	
	1	1	1	1.	1	1	
35	1	1	1		1		
25	MRLSPAPLKL	SRTPALLALA	LPLAAALAFS	DETLDKVPKS	EGYCSRILRA	QGTRREGYTE	60
				RGFTLIALRE			120
				PAGTGCVILK			180
	LCEODSTEDG	VTDKPTI.DCC	ACGTAKVRIT	FYGNWSEKTH	PKDYPRRAMH	WSALIGGSHS	240
20				EIRQQSDEVL			300
30	PSAEFSVORT	RHLMSFLTMM	GPSPDWNVGT.	SAEDLCTKEC	GWVOKVVODT.	IPWDAGTDSG	360
-							
				DPEGGSITQV			420
	NVDDIVADLA	PEEKDEDDTP	ETCIYSNWSP	WSACSSSTCD	KGKRMRORML	KAQLDLSVPC	480
				SPCSISCGMG			540
	PTEETEKCTV	NEECSPSSCL	MTEWGEWDEC	SATCGMGMKK	RHRMIKMNPA	DGSMCKAETS	600
35				GKGMRTRORM			660
55							
	MLPECPIDCE	LTEWSOWSEC	NKSCGKGHVI	RTRMIQMEPQ	FGGAPCPETV	QRKKCRIRKC	720
				QFPGCRMRPW			780
				Qr FGCKrken	IMMSECTACE	GOGTOWINI	
	VKKRFKSSQF	TSCKOKKEIR	ACNVHPC				
40							
+ 0	sed in no:	7 DNA seque	ence				
	Nucleic Aci	d Accession	1 #: NM 0224	154			
			_				
	courne sed	ience: 205.	. 1449				
	1	11	21	31	41	51	
	1	11	21		41	51 1	
15	1	1	1 '	1	1	}	
45	1	1	1 '		1	}	60
45	 GCAGTGTCAC	 TAGGCCGGCT	GGGGGCCCTG	 GGTACGCTGT] AGACCAGACC] GCGACAGGCC	
45	 GCAGTGTCAC AGAACACGGG	TAGGCCGGCT CGGCGGCTTC	GGGGGCCCTG GGGCCGGGAG	 GGTACGCTGT ACCCGCGCAG) AGACCAGACC CCCTCGGGGC	 GCGACAGGCC ATCTCAGTGC	120
45	 GCAGTGTCAC AGAACACGGG	TAGGCCGGCT CGGCGGCTTC	GGGGGCCCTG GGGCCGGGAG	 GGTACGCTGT) AGACCAGACC CCCTCGGGGC	 GCGACAGGCC ATCTCAGTGC	
45	GCAGTGTCAC AGAACACGGG CTCATTCCCC	TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG	120 180
45	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC	TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC AGGCCTGGAG	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC	120 180 240
	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA	TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC AGGCCTGGAG CCCAGAGCGC	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC GCTGCCCGCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG	120 180
	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA	TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC AGGCCTGGAG CCCAGAGCGC	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC GCTGCCCGCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG	120 180 240 300
45 50	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC TGAGCCCCAT	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC GCTGCCCGCG CGGGGACATG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC GCGAGGCGCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC	120 180 240 300 360
	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGA GCCAGAGTCGC GGAGCACCGG	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC GCTGCCCGCG CGGGGACATG GGGCCGAGCC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGGCGAGT	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC GCGAGGCGCC CCCGTATCCG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG	120 180 240 300 360 420
	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGA GCCAGAGTCGC GGAGCACCGG	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC GCTGCCCGCG CGGGGACATG GGGCCGAGCC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC GCGAGGCGCC CCCGTATCCG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG	120 180 240 300 360
	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCCAGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA	TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC AGGCCTGAGCCCCAT CCAGAGCACCAT CCAGGGCCCCAT CCAGGGCCGC TGGTGTGGGC	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC GCTCCCCGGG CGGGGACATG GGGCCGAGCC TAAGGACGAG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCGAGT CGCAAGCGGC	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACG GGCTGGGCCC GCGAGGCGCC CCCGTATCCG TGGCGCAGCA	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGGCCGATG GAATCCAGAC	120 180 240 300 360 420 480
	GCAGTGTCAC AGAACACGG CTCATTCCCC GGACCGGGGC CAGACCCAGA GCCAAGTCGC GAGCACCGC AACGCTTTCA CTGCACAACG	TAGGCCGGCT CGGCGGCTTC AGGCCTGGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC TGGTGTGGGC CCGAGTTGAG	GGGGCCCTG GGGCCGGGA CCGCGTCGGG CGCCATGAGC GCTGCCCGCG CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGGCGAGT CGCAAGCGGC GGCAAGTCGT	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC CCCGTATCCG TGGCGCAGCA GGAAGGCGCC CGAAGGCGCC	GCGACAGGCC ATCTCAGTGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGCCGATG GAATCCAGAC GACGCTGGCCG	120 180 240 300 360 420 480 540
50	GCAGTGTCAC AGAACACGG CTCATTCCCC GGACCGGGGC CAGACCCAGA GCCAAGTCGC GAGCACCGC AACGCTTTCA CTGCACAACG	TAGGCCGGCT CGGCGGCTTC AGGCCTGGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC TGGTGTGGGC CCGAGTTGAG	GGGGCCCTG GGGCCGGGA CCGCGTCGGG CGCCATGAGC GCTGCCCGCG CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCGAGT CGCAAGCGGC	AGACCAGACC CCCTCGGGGC CGTCCGGCGG CGGGATACGC GGCTGGGCCC CCCGTATCCG TGGCGCAGCA GGAAGGCGCC CGAAGGCGCC	GCGACAGGCC ATCTCAGTGC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGCCGATG GAATCCAGAC GACGCTGGCCG	120 180 240 300 360 420 480
50	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTCA CTGCACAACG GAGAAGCGGC	TAGGCCGGCT CGGCGGCTTC CGGCGCTCCC AGGCCTGGAG CCCAGAGCGC TGAGCCCAT CCGGGGCCGC TGGTGTGGGC CCGAGTTGAG CCTTCGTGGA	GGGGCCCTG GGGCCGGGA CCGGGTCGGG GCTGCCCGCG GGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGCAGAG	GGTACGCTGT ACCCGCGAG GGAGGCGGC AGCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCGAGT CGCAAGCTGCCGC CGCTGCCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCTGGGCCC GCGAGGCGCC CCCGTATCCG TGGCGCAGCA TGGCGCAGCA TGCAGCACAT TGCAGCACAT	GCGACAGGCC ATCTCAGTGC ATCTCAGTGG AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGAACAGC GCGCCCAGT GAATCCAGAC GACGCCGAC GACGCTGGCG	120 180 240 300 360 420 480 540
	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCCGGGC CAGAGCCAGG GCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACCG GGAGAGCGGC CCCAACTACA	TAGGCCGGCT CGGCGGCTTC ACCCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC TGGTGTGGG CCTTCGTGGA AGTACCGCC	GGGGCCCTG GGGCCGGGAG CCGGGTCGGG CGCCATGAGC GCTGCCCGGG CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCCGGCGG	GGTACGCTGT ACCCGCGCAG ACCCGGATG GGAGGCGGCG AGCCCGGATG AAGGTGAAGG AAGGTGAAGG CGCAAGCGGC GGCAAGTCGT CGGCTGCGCG AAGCAGGTGA	AGACCAGACC CCCTCGGGGG CGTCCGGCGG CGGGATACGC GGCAGGCGC CCCGTATCCG TGGCGCAGCA GGAAGGCGCT TGCAGCACAT AGCGCTGAA	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GACGCTGGCG GCAGGACCAC GCGGGTCGAG	120 180 240 300 360 420 480 540 600 660
50	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCCGGGC CAGAGCCAGG GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACG GAGAGCGG CCCAACTACA GGCGGCTTCC	TAGGCCGGCTTC CGGCGCTTCC AGCCCTCCCA AGGCCTCAT CCCAGAGCGCC TGAGCCCCAT CCGGGCCGC TGGTTGGGC CCTTCGTGGA AGTACCGGCC TGCACGCCCT TGCACGCCCT	GGGGCCCTG GGGCCGGGAG CCGCGTGGG CGCCATGAGC GCTGCCCGGG CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGGCGGGG GCGTGAGCCG	GGTACGCTGT ACCCGCGCAG ACCCGGATG GTGATGGCCG AAGGTGAAGG AAGGTGAAGG GGCAAGTCGT CGCAAGTCGT CGCAAGTGAT CGCAAGTGAT CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTCCC	AGACCAGACC CCCTCGGGGC CGTCGGGGG CGGGATACGC GGCAGGGGCCC CCCGTATCCG TGGCGCAGCA TGCAGGCACT TGCAGCACAT TGCAGCACAT TGCAGCACAT CGCTGGCCCACACACACACACACACACACACACACACACA	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGGACAGG GCGGCCGATG GAATCCAGAC GACGCTGGCG GCAGGACCAC GCGGGTGGAG CGAGGGCGGC	120 180 240 300 360 420 480 540 600 660 720
50	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCCGGGC CAGAGCCAGG GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACG GAGAGCGG CCCAACTACA GGCGGCTTCC	TAGGCCGGCTTC CGGCGCTTCC AGCCCTCCCA AGGCCTCAT CCCAGAGCGCC TGAGCCCCAT CCGGGCCGC TGGTTGGGC CCTTCGTGGA AGTACCGGCC TGCACGCCCT TGCACGCCCT	GGGGCCCTG GGGCCGGGAG CCGCGTGGG CGCCATGAGC GCTGCCCGGG CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGGCGGGG GCGTGAGCCG	GGTACGCTGT ACCCGCGCAG ACCCGGATG GTGATGGCCG AAGGTGAAGG AAGGTGAAGG GGCAAGTCGT CGCAAGTCGT CGCAAGTGAT CGCAAGTGAT CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTGAC CAGCAGGTCCC	AGACCAGACC CCCTCGGGGC CGTCGGGGG CGGGATACGC GGCAGGGGCCC CCCGTATCCG TGGCGCAGCA TGCAGGCACT TGCAGCACAT TGCAGCACAT TGCAGCACAT CGCTGGCCCACACACACACACACACACACACACACACACA	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGGACAGG GCGGCCGATG GAATCCAGAC GACGCTGGCG GCAGGACCAC GCGGGTGGAG CGAGGGCGGC	120 180 240 300 360 420 480 540 600 660
50	GCAGTGTCAC GGAGCGGGG CTGATTCCCC GGAGCCAGA GCCGAGTCGG GGAGCACAGA ACGCTTTCA CTGCACAACG GAGAAGCGG CCCAACTACA GGCGGCTTCC CGCGTGGCCA	TAGGCCGGCT CGGCGGCTTCC AGCCCTCCC AGGCCTGGAG CCCAGAGCGC TGGGCCCAT CCGGGCCGC TGGTGTGAG CCTTCGTGA AGTACCGCCT TGGACGCCT TGGACGCCT	GGGGCCCTG GGGCGGGAG CGGGTCGGG GCCATGAGC GCTGCCGGG CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGCAGAG GGGCGGGGGG GGCTGAGCCG GGGCTCAACCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCGAGT CGCAAGCGGC CGCAAGCTGC CGCAGCGCG AAGCAGGTGA ACAGCAGGTGA CAGGCGCCG TTCCCCCAGC	AGACCAGACC CCCTCGGGGC CGTCCGGGGG CGGGATACGC GGCAGGGGCC CCCGTATCGG TGGGGAGCGCT TGCAGCACAT AGCGGCTGAA GGGGCTGAA AGGGCTTCCC AGGGCTCCA	GCGACAGGCC ATCTCAGTGC ACGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGTTGAGG GCAGGACCAC GCAGGTTGAGG CCAGGCCGCCCG	120 180 240 300 360 420 480 540 660 720 780
50	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CACAGTCGC GGAGCACGG AACGCTTTCA CTGCACAACG GGAGAGCGGC CCCAACTACA GGCGGCTTCC CGCGTGCCA CCGCTGCCGC	TAGGCCGGCTTC CGGCGGCTTCC AGCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGCACGCCT TGCACGCCT CCCCACACAC CTCCCCACACA	GGGGCCCTG GGGCGGGAG CCGGGTCGGG GCCATGAGC GCCATGAGC CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCGCGCG GGCTGAGCCG GGGCCTCCAG GGGCCTCCAG	GGTACGCTGT ACCCGCACG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGGCGAGT CGCAAGTCGT CGGCTGCGGCG AAGCAGGTGA CAGGCGGCCG TTCCCGAGC TACCCGCACC	AGACCAGACC CCCTCGGGGC CGTCCGGGGG GGGATACGC GGCTGGGCCC CCCGTATCCG TGGGCACA TGCAGCACA AGGGCTT AGCGCTGAA AGGGCTTGAA AGGGCTTGAA AGGGCTTGAA AGGGCTTCCC GCCAGAGTCT	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GAGGCTGGAC GCAGGACCAC GCGGGTGGAAG CGAGGACCAC GCGGGCCCG GGGCGCCCC GGGCCCCC	120 180 240 300 360 420 480 540 600 660 720 780
50 55	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CACAGTCGC GGAGCACGG AACGCTTTCA CTGCACAACG GGAGAGCGGC CCCAACTACA GGCGGCTTCC CGCGTGCCA CCGCTGCCGC	TAGGCCGGCTTC CGGCGGCTTCC AGCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGCACGCCT TGCACGCCT CCCCACACAC CTCCCCACACA	GGGGCCCTG GGGCGGGAG CCGGGTCGGG GCCATGAGC GCCATGAGC CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCGCGCG GGCTGAGCCG GGGCCTCCAG GGGCCTCCAG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGG AAGGCGAGT CGCAAGCGGC CGCAAGCTGC CGCAGCGCG AAGCAGGTGA ACAGCAGGTGA CAGGCGCCG TTCCCCCAGC	AGACCAGACC CCCTCGGGGC CGTCCGGGGG GGGATACGC GGCTGGGCCC CCCGTATCCG TGGGCACA TGCAGCACA AGGGCTT AGCGCTGAA AGGGCTTGAA AGGGCTTGAA AGGGCTTGAA AGGGCTTCCC GCCAGAGTCT	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GAGGCTGGAC GCAGGACCAC GCGGGTGGAAG CGAGGACCAC GCGGGCCCG GGGCGCCCC GGGCCCCC	120 180 240 300 360 420 480 540 660 720 780
50 55	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCCGGGC CAGAGCCAGG GGACCACGG AACGCTTTCA CTGCACAACG CAACTACA GGCGGCTTCC CGCTGGCCA CCGCTGCCGC CCCACTACCACCG	TAGGCCGGCTTC CGGCGGCTTC ACCCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCCAT CCGGGGCCGC TGGTTGGG CCTTCGTGGA AGTACCGGCC TGGACGCCT TGGACGCCT TGGACGCCT CTCCCGCACAT GCTACCGCT	GGGGGCCCTG GGGCCGGGAG CCGGGTCGGG GCCATGAGC GCTGCCCGGG CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCGGCGGC GGCTCAAGCCG GGGCGGCCAC GGCCCCCACGCCC	GTACGCTGT ACCCGCGCAG ACCCGGATG GTGATGGCCG AAGGTGAAGGCGAGT CGCAAGCGGC GGCAAGTGGT CGCAGGGGC AAGCAGGTGA CAGGGGGCG TTCCCCCAGGC TACCCGGACT GACACGTCCC GACACGTCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCAGGGCCC CCCGTATCCG GGCAGGCCC CCCGTATCCG TGGCGCAGCA GGAAGGCCC TGCAGCACA AGCGCTTAA GGCGCTGAA GGCGCTGAA CGCTGGCCC CCCTGGACCC CCCGGACTCCC CCCTGGACCC CCCGGACCC CCCGGACCC CCCGGACCC CCCGGACCC	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGACAGG GCGGCCCATG GAATOCAGAC GACGCTGGCG GCAGGACCAC GCGGGTGGAG CGAGGGCGCC CGCCCGGCCCC CGGCCCCC CGGGCGCCCT CGTGGACCCC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	GCAGTGTCAC GGAGCGGGG CTCATTCCCC GGAGCCAGA GCCAGAGCCAGA GCCAGATCGC GGAGCACGG AACGCTTTCA GAGAAGCGGC CCCAACTACA GGCGGCTTCC CGCGTGGCCA CCGCTGGCCA CCGCTCGCGCT	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCAGAGCGC TGGGGCCCAT CCGGGGCCGC TGGTTGGAG CCTTCGTGGA AGTACCGCCT TGGACGGCCT TGGACGGCCT TTCGCCGACAT TCTTCGCCGC	GGGGGCCTG GGGCGGGAG CGGGTCGGG GCCATGAGC GCCATGAGC CTGCCGGG CTGCCGGG CGGGACATG GGGCCGAGCC GAGGCAGAG GGGCGGGGGG GGCTGAGCCG GGGCTCCAG GGGCGCCACGCC CCCCATGCC	GTACGCTGT ACCCGCACA GCAGGCCGCACA GCACGCCGATG GTGATGACGC AAGGCGAGT CGCAAGCGGC AAGGCGAGT CGCAAGCGGC AAGCAGGTGA AAGCAGGCGC TTCCCCGAGC TACCGCGACT GACACGTGCC GACACGTGCC GACACGTCCC GACACGTCCC GACACGTCCC	AGACCAGACC CCCTCGGGGG CGCGATACGC GGCAGGGGCC GCGGAGGGCC CCCGTATCGG GGAAGGGCCT TGCAGCACAT AGGGGCTGAA GGGGCTGAA GGGGCTGAA GGGGCTGCAG GCAGGCCCG GCAGAGTTCCC GCAGAGTTCCC GCAGAGTCC	GCGACAGGCC ACGTTGAGG CAGTGACGAC GCGGTGACGAC GCGGCCGATG GAACAGC GCAGGACAC GCAGGACAC GCAGGACCAC CACCTACAGC	120 180 240 300 360 420 480 540 660 720 780 780 900 960
50 55	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG GCCAGTCGC GGAGCACGG AACGCTTTCA CTGCACAACG GGAGAACGGC CCCAACTACA GGCGGCTTC CGCGTGGCCA CCGCTGCTGC GACCCGCTTTCACG CCCCTCCTGC CCCCTGCACA	TAGGCCGGCT TAGGCCGCTTCC AGGCCTCCC AGGCCTGGAG CCAGAGCGC TGAGCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGGACGCCT TCGCACAT TCTCGCCACAT TCTTCGCCC TCTCGGACTA	GGGGCCCTG GGGCGGGAG CCGGGTCGGG CGCCATGAGC CGCGAGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCGCGGC GGCTGAGCCG GGGCCTCCAG GGGCCTCCAG GGGCCTCCAG CCCACGCCC CCCCATGCCC CCCGATGCCC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGAGT CGCAAGTCGT CGCAAGTCGT CAGCAGGCGAAGTCAAGCAGGCGCCG AAGCAGGTGA TTCCCCCGAGC TACCGCGACT GACACGTCCC GGGGACTGCC	AGACCAGACC CCCTCGGGGG CGCTCGGGGG GGCTGGGCCG GGCTGGGCCC CCCGTATCCG TGGGCCC TGGGCCC TGGAGCACA AGCGCTGAA AGCGCTGAA AGCGCTGAA AGCGCTGAA AGCGCTTCC GCCAGAGTCT GCCAGAGCCCG CGGCCGGCCGG CGGCCGGTCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACTACAGC CACCTACAGC CATGCACCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG GCCAGTCGC GGAGCACGG AACGCTTTCA CTGCACAACG GGAGAACGGC CCCAACTACA GGCGGCTTC CGCGTGGCCA CCGCTGCTGC GACCCGCTTTCACG CCCCTCCTGC CCCCTGCACA	TAGGCCGGCT TAGGCCGCTTCC AGGCCTCCC AGGCCTGGAG CCAGAGCGC TGAGCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGGACGCCT TCGCACAT TCTCGCCACAT TCTTCGCCC TCTCGGACTA	GGGGCCCTG GGGCGGGAG CCGGGTCGGG CGCCATGAGC CGCGAGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCGCGGC GGCTGAGCCG GGGCCTCCAG GGGCCTCCAG GGGCCTCCAG CCCACGCCC CCCCATGCCC CCCGATGCCC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGAGT CGCAAGTCGT CGCAAGTCGT CAGCAGGCGAAGTCAAGCAGGCGCCG AAGCAGGTGA TTCCCCCGAGC TACCGCGACT GACACGTCCC GGGGACTGCC	AGACCAGACC CCCTCGGGGG CGCTCGGGGG GGCTGGGCCG GGCTGGGCCC CCCGTATCCG TGGGCCC TGGGCCC TGGAGCACA AGCGCTGAA AGCGCTGAA AGCGCTGAA AGCGCTGAA AGCGCTTCC GCCAGAGTCT GCCAGAGCCCG CGGCCGGCCGG CGGCCGGTCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACTACAGC CACCTACAGC CATGCACCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG ACGCTTTCA CTGCACAAC CTGCACAAC GAGAGCGGC CCCAACTACA GGCGGTTCC CGCTGGCGC CCGCTGCTGC CAGCCAGCT TACGCGCAGC CCGCTCGACG	TAGGCCGGCT TAGGCCGCCC AGGCCTCCC AGGCCTGAG CCCAGAGGGC TGAGCCCCAT CCGGGCCGC TGGTGTGAG CCTTCGTGAG AGTACCGGCC TGGACGCCT TCGACGGCCT TCTCGCACAT CTTCGCACAT CTTCGCACAT CCTTCGCACAT CCTTCGCACAT CCTACCGCCT TCTCGCACAT CAGAGCCCT TCTCGCACAT CAGAGCCCGC	GGGGCCCTG GGGCCGGAG CCGGGTCGGG GCCATGAGC GCCATGAGC GCGCGAGACATG GGGCCGAGC TAAGGACGAG GAGGCAGAG GCGCGCGCG GGCTGAGCCG GGCTGAGCCG GGCCTCCAG GGGCGGCCAC GCCACGCCC CCCGATGCCC CGCTGCCCC GGGTCCCCCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGGCGAGT CGCAAGCGGC GGCAAGTCGT CGGCTGCGGCG AAGCAGGTGA CAGGGGGCTG TTCCCCGAGC TACCGCGACT GACACGTGCC CCGGAGCTCC ATTCCGGGCCTC ATTCCGGGCCC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGGGATACGC GGGGCAGC GGGAGGGCC CCCGTATCCG GGAGGGCCC GGAGGGCCC GGAGGCCC GGAGGCCC GGCAGAGC GGCAGAGC GCCAGAGTC CGCCGGCCGG CGCGGGCCG CCGCGGGCCC CCGCGGGCCC CCCGCGCCC CCCGCGCCC CCCCGCGCCC CCCCGCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCGGTGGAG CCAGGGCCGG GGGCGCCCG GGGCGGCCCT CGTGGACCCC CACCTACAGC CATGCACCC ACCCAGCGCCC	120 180 240 300 360 420 480 660 720 840 900 960 1020 1080
50 55	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCCGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACT GCGTGGCCA CCGCTGGCCA CCGCTGCTGC CAGCTGCCC GACCACGGCTT TACGCGCAGC CGACTCGCC CGCTCGACG CGACTCGCC CCCTTCGACG CGACTCGCC CTTCACGTGCC CTTCACGTGCC CTTCACGTGTGC CTTCACGTGTGC	TAGGCCGGCTTC CGGCGCTTCC AGCCTCCCAGAGCGC TGAGCCCCAT CCGGGGCGCC TGGTTGGGC CCTAGTTGAG ACTACCGGCCT TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGCACAT CTCCGCACAT CTTCCGCACAT CCTTCGGACT TCTTCGCGCCACT TCTCGCACAT CCTACCGCCCT TCTCGGACTA CAGAGCCCGC ACTACGGCCGC	GGGGCCCTG GGGCCGGGAG CCGGGTCGGG GCCATGAGC GCTGCCCGGG CGGGGACATG GGGCCGAGGC TAAGGACGAG GGAGGCAGAG GGGCGGCGG GGCCTCCAG GGGCCTCCAG GGCCACGCCC CCCGATGCCC CCCGATGCCC CGGTCCCTCG GGTCCCTCG	GGTACGCTGT ACCCGCGCAG ACCCGGATG GGAGGCGGCG AAGGTGAAGG AAGGTGAAGGCGAAGTCGT CGCAAGTCGT CGCAAGTGAT CAGCTGCGCG AAGCAGGTGAC CAGCGCACT CCCCGAGC TCCCCGAGC TACCGCACT CGCAACTCCC CGGGACTCCC CCGGAGCTCC CCCGGGCCGCC CCCCGGGCCGC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGGGATACGC GGGGATACGC GGCAGGGCCC CCCTATATCCG TGGGGCAGCA TGCAGGCACC TGCAGGCACC AGGGCTTCCC GCCAGAGTCT CGCTGACCG CGCCGGTCC CCCGGTCCC CCCGGTCC CCCGGCCGG	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGGGACAGC GAGCCGATG GAATCCAGAC GAGGCCGAC GCAGGACCAC GCAGGACCAC CGCCGGCCCG CCTGGACCCC CACCTACAGC CACCAGCCCC CCGCCCCC CCGCCCCC CCGCCCCC CCGCCCCC CCCGCCCCC CCCGCCCCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
50 55 60	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCCGGGC CAGAGCCAGA GCCGAGTCGC GGAGCACCGG AACGCTTTCA CTGCACAACT GCGTGGCCA CCGCTGGCCA CCGCTGCTGC CAGCTGCCC GACCACGGCTT TACGCGCAGC CGACTCGCC CGCTCGACG CGACTCGCC CCCTTCGACG CGACTCGCC CTTCACGTGCC CTTCACGTGCC CTTCACGTGTGC CTTCACGTGTGC	TAGGCCGGCTTC CGGCGCTTCC AGCCTCCCAGAGCGC TGAGCCCCAT CCGGGGCGCC TGGTTGGGC CCTAGTTGAG ACTACCGGCCT TGCACGGCCT TGCACGGCCT TGCACGGCCT TCTCGCACAT CTCCGCACAT CTTCCGCACAT CCTTCGGACT TCTTCGCGCCACT TCTCGCACAT CCTACCGCCCT TCTCGGACTA CAGAGCCCGC ACTACGGCCGC	GGGGCCCTG GGGCCGGGAG CCGGGTCGGG GCCATGAGC GCTGCCCGGG CGGGGACATG GGGCCGAGGC TAAGGACGAG GGAGGCAGAG GGGCGGCGG GGCCTCCAG GGGCCTCCAG GGCCACGCCC CCCGATGCCC CCCGATGCCC CGGTCCCTCG GGTCCCTCG	GGTACGCTGT ACCCGCGCAG ACCCGGATG GGAGGCGGCG AAGGTGAAGG AAGGTGAAGGCGAAGTCGT CGCAAGTCGT CGCAAGTGAT CAGCTGCGCG AAGCAGGTGAC CAGCGCACT CCCCGAGC TCCCCGAGC TACCGCACT CGCAACTCCC CGGGACTCCC CCGGAGCTCC CCCGGGCCGCC CCCCGGGCCGC	AGACCAGACC CCCTCGGGGC CGGGATACGC GGGGATACGC GGGGATACGC GGCAGGGCCC CCCTATATCCG TGGGGCAGCA TGCAGGCACC TGCAGGCACC AGGGCTTCCC GCCAGAGTCT CGCTGACCG CGCCGGTCC CCCGGTCCC CCCGGTCC CCCGGCCGG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCGGTGGAG CCAGGGCCGG GGGCGCCCG GGGCGGCCCT CGTGGACCCC CACCTACAGC CATGCACCC ACCCAGCGCCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
50 55 60	GCAGTGTCAC GGAGCGGGG CTCATTCCCC GGAGCCAGA GCCAGATCGC GGAGCAGGGGC GGAGCACAGG GAGAACCGG AACGCTTTCA GGCGGCTTCC CCGCTGGCCA CCGCTGCCAC TACGCGCTTCC CCCTTCACGC CGACTGGCCA CGCTGCCC CTTCACGTGT ATGCAGCGC TTACGGCCC CTTCACGTGT	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGCGC TGGGCCCAT CCGGGCCCAT CCGGGCCCC TGGTTGGAG ACTACCGCC TGCACGCCT TTCGCGCC TTCGCGCCT TCTCGCGCC TCTCGCGCACAT TCTTCGCCC TCTCGGACTA ACACCCGC ACACCAGC	GGGGCCCTG GGGCGGGAG CCGGGTCGGG CCCATGAGC CTCCCCGG CGGGACATG GGCCGAGCC TAAGGACAG GAGGCAGAG GGGCGGGGCG	GGTACGCTGT ACCCGCGCGG GGAGGCGGGGGGGGGGGG	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGCC CCCGTATCGG GGAAGGGCC TGCAGCACAT AGGGGCTC TGCAGCACAT AGGGGCTGAA GGGGTTCCC GCAGAGTTCC GCCAGAGTTCC TGCAGCCC TGCAGCCC AGGGCTTCCC CGCAGAGTTCC TGCAGCCC CGCCGGCCG CGCCGGCCG CCCCCGGGCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CCCGGACAG	120 180 240 300 360 420 660 660 660 720 780 840 900 1020 1020 1140 1200
50 55	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CACAGTCGC GGAGCACGG GGAGCACGG AACGCTTTCA CTGCACAACG GGAGGAGCGGC CCCAACTACA CGCGGGCTTCC CGCGTGGCCA CCGCTTGACG GACCCGGCTT TACGGCACGGC	TAGGCCGGCT TAGGCCGCTCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC TGGTTGAG CCTTCGTGGA AGTACCGCC TGCACGGCCT TGCACGCCT TCTCGCACAT TCTTCGCCGC TCTCCGCACAT TCTTCGCCGC ACTACCGCCC ACTACGGCCG ACACCAGCA ACCAGCAC TCCGGAGCACA CTCCGGAGCAC CTCCGGACACA CAGAGCCCGC ACACCAGCA CTCCGGAGGCC ACCACGCA CTCCGGAGGCC ACCACGCA CTCCGGAGGCC CTCCGGAGGGC	GGGGCCCTG GGGCGGGGG GGCCATGAGC GCCATGAGC GCCATGAGC GCGCGACATG GGGCCGAGCC TAAGGACGAG GAGACAGGC GAGACAGAG GCGCGCGCCC GGGCCCCACGCCC CCCGATGCCC GGGTCCCCG GGTCCCTCG GATGGCCC GATGGCCC GATGGCCC GATGGCCC GATGGCCCACAC ACTGCCCCACA	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGAGT CGCAAGTCGT CGCAAGTCGT CAGCTGCGCG AAGCAGGTCA AAGCAGGTCAC CAGCAGCCGCCG GACACGTCCC CCCGGGGCCG CCCCGGGCCCC CCCCGGGCCCC CCCCGGCCCC CCCCGGCCCC CCCCGGCCCC	AGACCAGACC CCCTTCGGGGC CGTCCGGGGG CGGGATACGC GGCTGGGCCC CCCGTATCCG TGGGCACACA AGCGCTGAACA AGCGCTGAA AGCGCCGGGCCGG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGGCCGATG GCAGGACCAC GCGGGCCCG GGCGGCCCC GGGCCCCC CCTGGACCCC CACCTACAGC CACCTACAGC CACCTACAGC CCCGGCCCC ACCCAGCGCC CCGCCTCCAC TCAGCCCC CCCGCCCCC CCGCCTCCAC TCAGCCCCC	120 180 240 300 360 420 480 600 660 720 780 980 1020 1080 1140 1200 1260
50 55 60	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CACAGTCGC GGAGCACGG GGAGCACGG AACGCTTTCA CTGCACAACG GGAGGAGCGGC CCCAACTACA CGCGGGCTTCC CGCGTGGCCA CCGCTTGACG GACCCGGCTT TACGGCACGGC	TAGGCCGGCT TAGGCCGCTCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC TGGTTGAG CCTTCGTGGA AGTACCGCC TGCACGGCCT TGCACGCCT TCTCGCACAT TCTTCGCCGC TCTCCGCACAT TCTTCGCCGC ACTACCGCCC ACTACGGCCG ACACCAGCA ACCAGCAC TCCGGAGCACA CTCCGGAGCAC CTCCGGACACA CAGAGCCCGC ACACCAGCA CTCCGGAGGCC ACCACGCA CTCCGGAGGCC ACCACGCA CTCCGGAGGCC CTCCGGAGGGC	GGGGCCCTG GGGCGGGGG GGCCATGAGC GCCATGAGC GCCATGAGC GCGCGACATG GGGCCGAGCC TAAGGACGAG GAGACAGGC GAGACAGAG GCGCGCGCCC GGGCCCCACGCCC CCCGATGCCC GGGTCCCCG GGTCCCTCG GATGGCCC GATGGCCC GATGGCCC GATGGCCC GATGGCCCACAC ACTGCCCCACA	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGAGT CGCAAGTCGT CGCAAGTCGT CAGCTGCGCG AAGCAGGTCA AAGCAGGTCAC CAGCAGCCGCCG GACACGTCCC CCCGGGGCCG CCCCGGGCCCC CCCCGGGCCCC CCCCGGCCCC CCCCGGCCCC CCCCGGCCCC	AGACCAGACC CCCTTCGGGGC CGTCCGGGGG CGGGATACGC GGCTGGGCCC CCCGTATCCG TGGGCACACA AGCGCTGAACA AGCGCTGAA AGCGCCGGGCCGG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CCCGGACAG	120 180 240 300 360 420 480 600 660 720 780 980 1020 1080 1140 1200 1260
50 55 60	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG GGAGCACCGG AACGCTTCA CTGCACAACC GGAGCACCGG CCCAACTACA GGCGGTTCC CCGCTGGCC CCGCTGGCC CAGCTGCCC CGACTACAC GACCAGGCT TACGCGCAG CGACTCGCC CTTCACGTGC CGACTCGCC CGTCGCCC CGTCCCCC GACCTCCCC	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTCAAGGCGC TGAGCCCCAT CCGGGGCCGC TGGTGTGGA ACTACCGGCC TGGCCCT TGGACGCCT TGGACGCCT TGGACGCCT TCTCCGCACAT CTTCGCGACT TCTTCGCGC ACTACCGCT TCTCGGACT CTCCGACT TCTCGGACT CTCCGACT ACACACCAGCA ACACCAGCA ACTACCGGCCT ACACAGCA ACTACGGCGC ACTACGGCGC ACTACGGCGC ACTACGGAGC GCGAGGTGGA	GGGGCCCTG GGGCCGGAG CCGGGTCGGG CGCCATGAGC GGTCCGAGC TAAGGACGAG CAAGATGCTG GGGCCGAGAG GCGCGGCGCG	GTACGCTGT ACCCGCGCAG GCAGGCGGCG AGCCCGGATG GTGATGGCCG AGCCGGAGC AAGGCGAGC CGCAAGCGGC CGCAAGCGGC TCCCCCGAGC TTCCCCGAGC TACCCGGACT GACACGTCC CCCGGAGCCTC ATTCCGGGCCC CCCGGGCGCG CACCCAGCAGC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCG	AGACCAGACC CCCTCGGGG CGGGATACGC GGGGATACGC GGGGATACGC GGCGGCGGGCGCCCCCCGTATCCG GGAAGGGCCT TGCAGCACAT AGCGCTGAA AGCGCTTAA AGCGCTTCAC GCCAGAGTTCC GCCAGAGTCC CCCCGGG CCGCCGGCCGG CCGCCGGCCGAA ACCCCCCGGG ACCCCCCAGA ATCTGCACTT	J GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGGCAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGACCAC GCGGCCGGCCCC GGGCGGCCCC CACCTACAGC CACCTACAGC CACCTACAGC CACCCAGCCCC CACCCAGCCCC CGGCTCCAGCCCC CGGCCCCC CGGCCCCC CGGCCCCC CGGCCCCC CGGCCCCC CGGCCCCC CGGCCCCC CGGCCCCC CGGCTTCCAG	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1200 1260 1320
50 55 60	GCAGTGTCAC GGAGCGGGG CTCATTCCC GGAGCGGGG CAGAGCCAGA GCCAGATOGC GGAGCACAGG GAGACCAGG AACGCTTTCA GAGAAGCGG CCCAACTACA CGCGTGGCCA CGCTGGCCA CGCTCGAC GACCCGGCTT TACGCGCAG CGTCAGCC CTTCAGTGT ATGCAGCCG CCTCCAGCC CTTCAGTGT CTGCCCCC CGGCTCCCCCC CGGCTCCCCCC CGGCTCCCCCC CGAGCTCCTCG	TAGGCCGGCT CGGCGGCTTCC AGGCCTGCA AGGCCCATGGAG CCAGAGGCC TGGGGCCGC TGGTGTGAG CCTTCGTGAA AGTACCGCCT TGGACGCCT TCGCGACAT TCTTCGCGC TCTCGGACTA CAGACCCGG ACACCAGCA ACACCAGCA CTCCCGGAGGC ACACCAGCA CTCCCGGAGGC ACACCAGCA CTCCCGGAGGC CGGGAGGTGGA GCCTCCCCTA	GGGGCCCTG GGGCGGGGG GCCATGAGC GCCATGAGC GCCATGAGC GCGCGACGC GGGCCAGGC TAAGGACAA GAGGCAGGC GGGCGAGCC GGGCCAGGC GGGCCTCAGG GGCCTCAG GGGCCTCAG GGCCTCAG GGCCTCAG GGCCAGCC CCCAATGCC CCCATGCC CGGTCCCTCG GATGGCCC GGTCCCTCG GATGGCCC CGACCACA ACTGCCCTGA ACTGCCCTGA	GTTACGCTGT GTTACGCTGT ACCCGCACA GCAGGCCGCAC GCAGGCCCGATG GTGATGGCCG AAGGTGAAGCGC GGCAAGTGCC CGCCAGCTCCCCGAGC TTCCCCGAGC TACCCGACCTCCCCGAGCCTCCCCGGAGCCTCCCCGAGCCTCCCCGAGCCTCCCCGGGCGCGCCCCCCGGGCGCCCCCGGGCGCCCCCGGGCGC	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGCC CCCGTATCGG GGAGGGCC CCGTATCGG GGAGGGCCT TGCAGCACAT AGGGGCTCAC AGGGCTTCCC GCAGAGTTCCC GCAGAGTTCCC GCAGAGTCC CGCCGGGCGC ACCCCCGGG CGGCGGCGCACCCAC ACCCCCGGG ACCCCCAGAGTCC TGAGCCCAG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CCCGGACAG CCCGGACAG CCCGGACAG CCCGGACAG CCCGGACAG CCAGCCCC CGGTTGCAAC CCAGCCCC CGGTTGCAAC CCAGCCCC	120 180 240 300 360 420 660 660 660 720 780 960 1020 1140 1200 1320 1380
50 55 60	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCAGATCGC GGAGCACGG AACGCTTTCA GCGACACG GAGAACGCGC CCCAACTACA CGCGGTGGCCA CGCGTGGCCA CGCTGCTGACG GACACGGCTTTCACGTGT ATGCAGCGC CCGTCAGCGC CTTCACGTGC CCGTCGCCCC GAGCTCCTCC CCGTGGCCCC CTTCACGTGC CCGTCGCCCC CGAGCTCCTCC CCGTGGCCCC CTCGAGATGG	TAGGCCGGCT TAGGCCGCTTCC AGGCCTCCCAGAGCGC TGAGCCCAT CCGGGGCCGC TGATTGGGC CCTAGTGGA AGTACCGCCT TGGACGCCT TGGACGCCT TCTCGCACAT TCTCGCACAT TCTTCGCGC TCTCGGACTA CAGAGCCGC ACTACCGGCC ACTACCGGCC ACTACGGCCT ACACCAGCA CTCCGGAGGC	GGGGCCCTG GGGCGGGGG GCCATGAGC GCCATGAGC GCCATGAGC GCGCGAGCC TAAGGACGAG GCAGGCGAGCC TAAGGACGAG GCGCGGGCGGGGCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGC GGCAAGTCGT CGCAAGTCGT CAGCAGCCGCCG TTCCCCGAGC TACCGCGACT CCCGGAGCCTC ATTCCGGGCC CCCGGGCCGC CACCGGCCCC TTTCCCGGCCC CCCGGGCCCC CCCGGGCCCC TTTCAACAGT TTTCAACAGT TACCGCGGCCAGCCCC CGGGACGCCACACCCCCGGGCCCACACCACCACCACCACC	AGACCAGACC CCCTTCGGGGC CGCGGATACGC GGCTGGGCCG GCGGGCAGCACACACACACACACACACACACAC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GCGACAGG GCGACAGG GCAGACAG GCAGGACCAC GCGGCTGGAG CCACGGCCCG GGCGCCCC GGCCGCCCC GGCCGCCCC CACCTACACC CACCTACAGC CACCGACCCC CCGGCCCCC CCGCCCCC CCGCCCCC CCCCGCCCCC CCCTCCACCCC CCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 900 1020 1140 1200 1260 1380 1380 1440
50 55 60	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCAGATCGC GGAGCACGG AACGCTTTCA GCGACACG GAGAACGCGC CCCAACTACA CGCGGTGGCCA CGCGTGGCCA CGCTGCTGACG GACACGGCTTTCACGTGT ATGCAGCGC CCGTCAGCGC CTTCACGTGC CCGTCGCCCC GAGCTCCTCC CCGTGGCCCC CTTCACGTGC CCGTCGCCCC CGAGCTCCTCC CCGTGGCCCC CTCGAGATGG	TAGGCCGGCT TAGGCCGCTTCC AGGCCTCCCAGAGCGC TGAGCCCAT CCGGGGCCGC TGATTGGGC CCTAGTGGA AGTACCGCCT TGGACGCCT TGGACGCCT TCTCGCACAT TCTCGCACAT TCTTCGCGC TCTCGGACTA CAGAGCCGC ACTACCGGCC ACTACCGGCC ACTACGGCCT ACACCAGCA CTCCGGAGGC	GGGGCCCTG GGGCGGGGG GCCATGAGC GCCATGAGC GCCATGAGC GCGCGAGCC TAAGGACGAG GCAGGCGAGCC TAAGGACGAG GCGCGGGCGGGGCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGC GGCAAGTCGT CGCAAGTCGT CAGCAGCCGCCG TTCCCCGAGC TACCGCGACT CCCGGAGCCTC ATTCCGGGCC CCCGGGCCGC CACCGGCCCC TTTCCCGGCCC CCCGGGCCCC CCCGGGCCCC TTTCAACAGT TTTCAACAGT TACCGCGGCCAGCCCC CGGGACGCCACACCCCCGGGCCCACACCACCACCACCACC	AGACCAGACC CCCTTCGGGGC CGCGGATACGC GGCTGGGCCG GCGGGCAGCACACACACACACACACACACACAC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GCGACAGG GCGACAGG GCAGACAG GCAGGACCAC GCGGCTGGAG CCACGGCCCG GGCGCCCC GGCCGCCCC GGCCGCCCC CACCTACACC CACCTACAGC CACCGACCCC CCGGCCCCC CCGCCCCC CCGCCCCC CCCCGCCCCC CCCTCCACCCC CCCCCCCCCC	120 180 240 300 360 420 480 600 660 720 780 840 900 1020 1140 1200 1260 1380 1380 1440
50556065	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG GGAGCACCGG AACGCTTCA CTGCACAAC GGAGCACACG CCCAACTACA GGCGGTTCC CGCTGGCCA CGCTGGCCC CGCTGGCCC CTTCACGGCC CTTCACGGCC CTTCACGGCC CTTCACGGCC CTTCACGGCC CTTCACGGCC CTTCACGTGT CCGCTCGCCC CGGCCCCTCGCCCC GAGCTCCTCG GGCGCATTT GACGTGTACA	TAGGCCGGCT TAGGCCGCTCCC AGGCCTCCCC AGGCCTCGAGGCGC TGAGCCCAT CCGGGGCCGC TGAGTTGAG CCTTCGTGGA AGTACCGGCCT TGGACGCCT TCTCGCACAT CTTCGCGACAT CTTCGCGACAT CTTCGCGACAT CTTCGCGACAT CTTCGCGACAT CTTCGCGCCT ACTACGGGCCT ACTACGGGGC ACTACCGGTGGAGC ACTACGGGGC ACTACCGGGGC ACTACCGGGGC ACTACGGGGC ACTACCGGGGC ACTACCGGGCC ACTACCGGGCC ACTACCGGGCC ACTACCGGCC ACTACCGGCC ACTACCGGCC ACTACCGGCC ACTACCGGCC ACTACCGGCC ACTACCGCCC ACTACCGCCCCCCAACAC ACTACCGGCCC ACTACCGCCCCCCAACAC ACCACCCCCCCCCAACAC ACCACCCCCC	GGGGCCCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCCAGGCCCCCAGGCCCCCAGGCCCCCC	GTACGCTGT GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGGCGAGT CGCAAGTCGT CGCAAGTCGT CAGCAGCGCG TTCCCCGAGC TTCCCCGAGC TACCGCGACCT CCCGGGGCGC CCCCGGGGCGC CCCCGGGCGCC CCCCGGGCGCC CCCGGGCCC CCCGGGCCC CCCGGGCCC CCCGGGCCC CCCGGGCCC CCCGGGCCC CCCGGGCCC CCCGGGCCC CCCGGGCCC CCCGGCCCC CCCGGCCCC CCCGGCCCC CCCGGCCCC CCCGGCCCC CCCCGCCCCC CCCCGCCCCC CCCCGCCCCC CCCCGCCCCC CCCCCC	AGACCAGACC CCCTTCGGGGC CGGGATACGC GGGGATACGC GGGGAGGGCCC CCCGTATCCG TGGGCACC GGAGGGCCC TGGGCACC GGAGGCCCC GCCAGAGTC GGCAGGCCCC GCCAGAGTC TCCTGGCCC GCCAGAGTC TCCTGGCCC ACCCCCGGC ACCCCCGGC ACCCCCGGC ACCCCCAGA ATCTGCACTT TGAATTCCC TGAATCTCC ACACACTT TGAATTCCACTT TGAATTCCCC ATCTGCACTT TGAATTCCCC ATCTGCACTT TGAATTCCCC AGAAGCAGTG AGAAGCAGTG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGATG GAATCCAGAC GCGGCCGCC GCGGCCCC GCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCAGCCC CCGGACAGC CCACCAGCCC CCGGACAG TCAGCCCCC CCGTGTGCAAG CCAACAGCCAC CAACTATCCT TTACACACTT	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500
50 55 60	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG ACGCACTCCA CTGCACAACC GGAGCGGC CCCAACTACA GGCGGTTCC CGCTGGCC CCGCTGCCC CGACTGGCC CGACTGGCC CGACTGGCC CGACTGGCC CGACTGGCC CGACTCGACGC CGACTCGACGC CGACTCGACGC CGACTCGCCC CTCACGCC CTCACGCC CTCACGCC CTCACGCC CTCACGCC CCTGAGATGC CCTGAGATGG CCCTGAGATGG	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTCAAGGCCC TGAGCCCCAT CCGGGCGCC TGGTTGAGC CCTTCGTGA AGTACCGCC TGGAGTTGAG AGTACCGCC TGGACGCCT TGGACGCCT TCTCGCACAT CCTCGCACAT CCTCGCACAT CCTCGACTA CCTCGGACTA CCTCGGACTA CCTCGGACTA CCTCGGACTA CTCCGACTA CTCCGACTGCT CCTCGGTGGT CCTCGCTGAC CCTCAGTGGT CCTAAGGAAAT	GGGGGCCTG GGGCGGGAG CCGGGTCGGG CGCATGAGC CAGGGCATGAGC TAAGGACGAG GCAGGACATG GGGCCGAGGC TAAGGACGAG GCGCGGCGAGAG GCGCGGCGCG	GTACGCTGT ACCCGCGCAG ACCCGGATG GGAGGCGGCG AAGGTGAAGGCGG AAGGTGAAGGCGG AAGGTGAAGGCGG GGCAAGCGGC GGCAAGCGGC TTCCCCGAGC TACCCGGAGCTC GACACGTCCC CCGGGGCCTC ATTCCGGGCC CCCGGGACGCA TTTGAACAGT GACTCCGCGG CCTCCGCGCCC CCGGGACGCC CCGCGCCCC CCGCGCCC CCGCGCCC CCGCGGCCC CCGCGGCCC CCGGGGCCC CCGGGGCCC CCGGGGCCC CCGGGCCC CCGGGGCTTTTTT	AGACCAGACC CCCTCGGGG CGGGATACGC GGCGGGGATACGC GGCGGGGCGCGC CCCCTATCCG TGGGCCACACA TGCGCCACACA AGCGCTTCA AGCGCTTGAC GCAGAGTTCCG GCAGAGTTCCC GCCAGAGTCC CCCCGGGCCGCCC CCCCGGGCCGCCC TCCTGGCCCACACACC TCCTGGCCCCACACC TCCTGCGCCC TCCTGCACCT TGAATCTCCC TATATTACTG GTTGTTGCTG GTTGTTGCTG GTTGTTGCTG	GCGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGACCG GCGGGCCCC CGCGCCCC CACCTACAGC CACCTACCAC CACCTACT CTTACACCTT CTTGTTGTTTT	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1140 1260 1320 1380 1440 1500
50556065	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG ACGCACTCCA CTGCACAACC GGAGCGGC CCCAACTACA GGCGGTTCC CGCTGGCC CCGCTGCCC CGACTGGCC CGACTGGCC CGACTGGCC CGACTGGCC CGACTGGCC CGACTCGACGC CGACTCGACGC CGACTCGACGC CGACTCGCCC CTCACGCC CTCACGCC CTCACGCC CTCACGCC CTCACGCC CCTGAGATGC CCTGAGATGG CCCTGAGATGG	TAGGCCGGCT CGGCGGCTTC ACCCCTCCC AGGCCTCAAGGCCC TGAGCCCCAT CCGGGCGCC TGGTTGAGC CCTTCGTGA AGTACCGCC TGGAGTTGAG AGTACCGCC TGGACGCCT TGGACGCCT TCTCGCACAT CCTCGCACAT CCTCGCACAT CCTCGACTA CCTCGGACTA CCTCGGACTA CCTCGGACTA CCTCGGACTA CTCCGACTA CTCCGACTGCT CCTCGGTGGT CCTCGCTGAC CCTCAGTGGT CCTAAGGAAAT	GGGGGCCTG GGGCGGGAG CCGGGTCGGG CGCATGAGC CAGGGCATGAGC TAAGGACGAG GCAGGACATG GGGCCGAGGC TAAGGACGAG GCGCGGCGAGAG GCGCGGCGCG	GTACGCTGT ACCCGCGCAG ACCCGGATG GGAGGCGGCG AAGGTGAAGGCGG AAGGTGAAGGCGG AAGGTGAAGGCGG GGCAAGCGGC GGCAAGCGGC TTCCCCGAGC TACCCGGAGCTC GACACGTCCC CCGGGGCCTC ATTCCGGGCC CCCGGGACGCA TTTGAACAGT GACTCCGCGG CCTCCGCGCCC CCGGGACGCC CCGCGCCCC CCGCGCCC CCGCGCCC CCGCGGCCC CCGCGGCCC CCGGGGCCC CCGGGGCCC CCGGGGCCC CCGGGCCC CCGGGGCTTTTTT	AGACCAGACC CCCTCGGGG CGGGATACGC GGCGGGGATACGC GGCGGGGCGCGC CCCCTATCCG TGGGCCACACA TGCGCCACACA AGCGCTTCA AGCGCTTGAC GCAGAGTTCCG GCAGAGTTCCC GCCAGAGTCC CCCCGGGCCGCCC CCCCGGGCCGCCC TCCTGGCCCACACACC TCCTGGCCCCACACC TCCTGCGCCC TCCTGCACCT TGAATCTCCC TATATTACTG GTTGTTGCTG GTTGTTGCTG GTTGTTGCTG	GCGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGACCG GCGGGCCCC CGCGCCCC CACCTACAGC CACCTACCAC CACCTACT CTTACACCTT CTTGTTGTTTT	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1140 1260 1320 1380 1440 1500
50556065	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCAGATCGC GGAGCACGG AACGCTTCA CTGCACAACG GAGAACGC CCCAACTACA GGCGGTTGCC CCGCTGGCCA CGCTGGCCA CTTCACGTT TACGCGCAGG CACTCCC CTTCACGTGT ATGCAGCCC CTTCACGTGT CCTGACGG CGAGTCCTCC GAGCTCCTCG CGAGTGGCCC CTTCACGTTT CCTGACGGC CCTGACGGC CCTGACGGC CCTGACGGC CCTGACGGC CCTGACGGC CCTGGACGG CCTGGACGG CCTGGACGG CCTGGAGGG CCTGGAGGGG CCTGGAGGAG CCTGGAGGAG CCTGGAGGAG CTTAAAGGTG	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGCA AGGCCCATGAGC CCAGAGCGC TGGTGTGGG CCTAGTGGA AGTACCGGCC TGCACGGCCT TGGACGCCT TCTCGGACAT CCTCGGACTA CAGAGCCGC ACTACGGCC ACTACGGCC ACTACGGCC ACTACGGCA CTCCGGAGGC ACTACGGCA CTCAGGAGAT CTCGGAGGA CTAAGGAAT TGTTGGCATA	GGGGCCCTG GGGCGGGGG GCCATGAGC GCCATGAGC GCCATGAGC GCGGGACATG GGGCCGAGCC TAAGGACGAG GCAGGCGGGGCGG	GTACGCTGT ACCCGCGCAG GCAGGCCGGATG GTGATGGCCG AAGCTGAGCGGATG CGCAAGCGGC AAGCAGGCGC AAGCAGGTGA CAGCAGCGCC TTCCCCGAGC TACCGCGACT CCCGGAGCCT CCCGGAGCCT CCCGGAGCCT CCCGGAGCCT CCCGGAGCCT CCCGGAGCCT CCCGGAGCCT CCCGGGGCGC TTTCAACAGT TTTAAACAGT TACTCCGCGG CCTGCAGGCCC CTGCAGGCCC CTGCAGGCCC CTGCAGGCCC CTGCAGGCCC CTGCAGGCCC CTGCAGGCTTTT TAATTTATTT	AGACCAGACC CCCTCGGGGC CGCGGATACGC GGCTGGGCCC GCCGTATCCG TGCGGCAGC TGCGGCAGC TGCAGCACAT AGCGGCTTCAC AGCGCTTCAC AGCGCTTCAC CGCTGGACCCA AGCGCTTCCC GCCAGAGTCT TCTGGCCC CCCCGGGCCC CCCCCGGGCCC CCCCCGGCCCC TCTGCACCC TCTTGCACCT TCTTGCACT TGAATCTCC TATATTACTG AGAAGCAGTG TGTTTGCCACT TGTTTGCCACT	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GCGACAGG GCGACAGG GCGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CACTATCCT TTACACACTT TTGTGTTTTT TTGTAGTCTT	120 180 240 300 360 420 660 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560 1560
50556065	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG GGAGCACGG GGAGCACGG AACGCTTTCA CTGCACAAC GGCGGCTTCC CCGCTGGCCA CCGCTGGCCA CCGCTGCTGC CGACTGCCC CTTCACGTGC CAGCTGCCC CTTCACGTGC CTGACACGGCT ATGCAGCAC CCGTTGCCCC CTGAGATGC CCGTTGCCCC GAGCTCCTCG CCTGAGATGC CCTGAGATGC CCTGAGATGG CCTGAGATGG CCTGAGATGG CCTGAGATGG CCTGAGATGG CTTGAGATGT GACGTGGCC CTTGAGATGT GACGTGGCC CTTGAGATGT GACGTGGCC CTTGAGATGT GACGTGGCC CTTGAGATGT CCTGGAGGAGG TTAAAAGGTG TTGAGGGGGT TGGGGGGGTG	TAGGCCGGCT TAGGCCGCTCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC TGGTGGGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGCACGCCT TCGCACACT TCTTCGCCGC TCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGACAT TCTTCGCCG ACTACCGGC ACTACGGCG ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC GGGAGGTGGA CCTCCCTA CCTCGGTGGT AGGTCCCTGA CTAAGGAAAT TGTTGGCATA	GGGGCCCTG GGGCGGGAG CCGGGTCGGG CGCCATGAGC CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCGCGCCC GGCTGAGCCG GGCCTCCAG GGCCCCCCC CCGATGCCC CCGCTGGCCCC GGTCCCTCG GATGGCCCC GGTCCCTCG GATGGCCCC CCGCACGAGCC CCGCACGGACCAG ACTGCCCTGC CCGCACGGAA CCACGGGCCCT TCCGCCCCAG CCTCAGACTCC TCCGCCCCAG	GTACGCTGT ACCCGCGCAG GCAGGCCGCGAGCCGAGCC	AGACCAGACC CCCTTCGGGGC CGGGATACGC GGCTGGGCGC GGGGATACGC GGCGGGCACACA GGGGCACACA AGGGCTT TGCAGCACA AGGGCTT CGCTGGACC CCCGTATCGC CCCGTATCCG TGCAGCACA AGGGCTTA AGGGCTGAA AGGGCTTCC GCCAGAGTCT CGCTGGACGG CGGCGGGGCG CGGCGGGCG ACCCCCGGG ACCCCCGGG ATTTCACTT TGAATTACTG AGAAGCAGTG TTTTTGCACT TTTTTGCACT TTTTTGCACT TGTTTGCACT TTTTTGCACT AGAAGCAGTG GTTTTCCACAC GTTTCCACAC GTTTCCACAC GTTTCCACAC	GCGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGGCCGAC GCGGGCCCC GCGGCCCC CGCGGCCCC CACCTACAGC CACCTACAGC CCCGGCCCC CCTGCACG CCCGGCCCC CCTGCACG CCCGCCCC CCTGCACC CCTGTGCACC CCTGTGCACC CCACTTACCCT TTACACACTT TTGTTGTTTT TTGAACAGTT GTTGGATTGT	120 180 240 300 360 420 480 600 660 720 780 ; 840 900 1020 1140 1200 1260 1320 1380 1440 1500 1620 1680
50556065	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGC CAGAGCCAGG GGAGCACGG GGAGCACGG AACGCTTTCA CTGCACAAC GGCGGCTTCC CCGCTGGCCA CCGCTGGCCA CCGCTGCTGC CGACTGCCC CTTCACGTGC CAGCTGCCC CTTCACGTGC CTGACACGGCT ATGCAGCAC CCGTTGCCCC CTGAGATGC CCGTTGCCCC GAGCTCCTCG CCTGAGATGC CCTGAGATGC CCTGAGATGG CCTGAGATGG CCTGAGATGG CCTGAGATGG CCTGAGATGG CTTGAGATGT GACGTGGCC CTTGAGATGT GACGTGGCC CTTGAGATGT GACGTGGCC CTTGAGATGT GACGTGGCC CTTGAGATGT CCTGGAGGAGG TTAAAAGGTG TTGAGGGGGT TGGGGGGGTG	TAGGCCGGCT TAGGCCGCTCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC TGGTGGGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGCACGCCT TCGCACACT TCTTCGCCGC TCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGACAT CCTCGGACAT TCTTCGCCG ACTACCGGC ACTACGGCG ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC ACCACGCA CTCCGGAGGGC GGGAGGTGGA CCTCCCTA CCTCGGTGGT AGGTCCCTGA CTAAGGAAAT TGTTGGCATA	GGGGCCCTG GGGCGGGAG CCGGGTCGGG CGCCATGAGC CGGGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGAGGCAGAG GCGCGCGCCC GGCTGAGCCG GGCCTCCAG GGCCCCCCC CCGATGCCC CCGCTGGCCCC GGTCCCTCG GATGGCCCC GGTCCCTCG GATGGCCCC CCGCACGAGCC CCGCACGGACCAG ACTGCCCTGC CCGCACGGAA CCACGGGCCCT TCCGCCCCAG CCTCAGACTCC TCCGCCCCAG	GTACGCTGT ACCCGCGCAG GCAGGCCGCGAGCCGAGCC	AGACCAGACC CCCTTCGGGGC CGGGATACGC GGCTGGGCGC GGGGATACGC GGCGGGCACACA GGGGCACACA AGGGCTT TGCAGCACA AGGGCTT CGCTGGACC CCCGTATCGC CCCGTATCCG TGCAGCACA AGGGCTTA AGGGCTGAA AGGGCTTCC GCCAGAGTCT CGCTGGACGG CGGCGGGGCG CGGCGGGCG ACCCCCGGG ACCCCCGGG ATTTCACTT TGAATTACTG AGAAGCAGTG TTTTTGCACT TTTTTGCACT TTTTTGCACT TGTTTGCACT TTTTTGCACT AGAAGCAGTG GTTTTCCACAC GTTTCCACAC GTTTCCACAC GTTTCCACAC	GCGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGGCCGAC GCGGGCCCC GCGGCCCC CGCGGCCCC CACCTACAGC CACCTACAGC CCCGGCCCC CCTGCACG CCCGGCCCC CCTGCACG CCCGCCCC CCTGCACC CCTGTGCACC CCTGTGCACC CCACTTACCCT TTACACACTT TTGTTGTTTT TTGAACAGTT GTTGGATTGT	120 180 240 300 360 420 480 600 660 720 780 ; 840 900 1020 1140 1200 1260 1320 1380 1440 1500 1620 1680
50556065	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGCC CAGAGCCAGG ACGCTTCA CTGCACAACC GGAGCACCGG AACGCTTCA CGCGGCTTCC CGCGGCTCC CGCTGGCAC CGCTGCTGC CGACCACGG ATCACACGGCTT TACCGCAGG CTTCACGATGC CGACTGGCC CTTCACGTGT ATCAGCAGG CGGCTCTCG CCTGAGATGG CCGTCGCCC CGGGCCATT GACGTGCCCC CTGAGATGG CCTGGAGGAG TTAAAAGGTG TGGGGGGTT CGAGGGGGTT CGAGGGGGTG CCAAACCCTA	TAGGCCGGCT CGGGGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGGGC TGAGCCCCAT CCGGGGCCGC TGGTGTGGA AGTACCGGCC TGGACGGCCT TGGACGCCT TGGACGCCT TCTCGCACAT CCTCGCACAT CCTCGACAGT CCTCGGACGC ACTACCGGC ACTACCGGC ACTACCGGC ACTACCGGC ACTACCGGC ACTACCGGC ACTACCGGC ACTACCGGC ACTACCGGACG CTCCCCTA CCTCCGTAGG CCTCCCTAA CCTCCGAAGA CTCCGGAGGC GCGCTCCCTAA AGGTTCCAT TGTTGCATT TTTCCAAGTT	GGGGCCCTG GGGCCGGGG CGCATGAGC CGCGGACATG GGGCCGAGCC TAAGGACGAG CAAGATGCTG GGGCCGAGCG GCGTGAGCG GGCTGAGCG GGCCTCAG GGGCGCCCCAG GGCCCCCAG GCCACGCCC CCGATGCCC CCGATGCCC CCGATGCCC CCGCACCCAG CCACGCAC CCCCAGCCC CCCCAGCCC CCCCAGCCCC CCCCCAGCCCC CCCCCAGCCCC CCCCCCCC	GTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GGAGGCGGATG GTGATGGCCG AAGGCGAGT CGCAAGTCGT CGCTGCGCG AAGCAGTCGT CGCTGCGCG TTCCCCGAGC TTCCCCGAGC TACCCGGACTC CCCGGGGCTC ATTCCGGGCCT CCCGGGCCCC CCGGGCCGC CCCGGGCCCC CCGGGCCCC CCGGGCCC CCGGGCCCC CCGGGCCCC CCGGGCCC CCGCGCCC CCGGGCCC CCGGCCC CCGGCCC CCGGCCC CCCGCGCC CCCC CCCGCGCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	AGACCAGACC CCCTCGGGG CGGGATACGC GGCGGGGATACGC GGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGC	GCGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACAGC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCCGACCAC GCGGCCCGCCCC GCGGCCCC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCAGCCC CCGGACAG CCACCGCCC CGTGTGCAAG CCACCGCCC CTTCCAGCCC CTTCCAGCCCC CTTCCAGCCCC CTTCCAGCCCC CTTCCAGCCCC CTTCCAGCCCC CTTCCAGCCCC CTTCCAGCCCC CTTTCCAGCCCC CTTTCCATCTT CTTTCTTTTT CTTGAACAGTT TTGAACAGTTT TTGTTGGATTGT ACAGCTTCCT	120 180 240 300 360 420 660 720 780 980 960 1020 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCCAGA GCCAGATCGC GGAGCAGGGGC GGAGCACGG GAGACACGG AACGCTTTCA GAGAAGCGGC CCCAACTACA CGCGTGGCCA CGCGTGGCCA CGCGTGGCCA CTCCAGC CTCCAGC CTTCAGTGT TACGCGCAGC CTTCAGTGT CCTCAGATGG CCTGAGATGG CTGAGAGGAG TTAAAAGGTG TGGGGGGGTT CGAGGGGGT CCAACCCTA CCATTTCCTG	TAGGCCGGCT TAGGCCGGCTTC AGCCCTCCC AGGCCTGGAG CCAGAGCGC TGGGGCCGC TGGTGTGGAG CCTTCGTGGA AGTACCGGCC TGCACGGCCT TCTCGGCACAT TCTTCGCGC TCTCGGACTA CCTCGGACTA CCTCCGGACTA CCTCCGGACTA CCTCCGGACTA ACACCAGCA CTCCGGAGGC ACACCAGCA CTCCGGAGGC ACACCAGCA CTCCGGAGGT AGGCCCTA CCTCGGTGGA CCTCCCCTA CCTCGGTGGA CTTCCGTAGT AGGTTCCTTA AGGTTTCATT TTTCCAAGTT AAAGTTTATT	GGGGCCCTG GGGCGGGGG GCCATGAGC GCCATGAGC GCCATGAGC GTCCCGGG GCCAGGCC TAAGGACAG GGGCGAGCC TAAGGACAG GGGCGAGCC GGGCAGGCC GGGCTGAGCC GGGCTGAGCC GGGCTGAGCC GGCTAGGCC GGCTAGGCC GGCTAGGCC CCCATGCC CCCATGCC CCCATGCC CCCACGCC CCCACGCC CCCACGCC CCACGCC CCCC CCACGCC CCACGCC CCCC CCCC CCACGC CCCCC	GTTACGCTGT ACCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGGCAGCT CGCAAGCAGC CGCAAGTCGC CAGCCGCGCATC CAGCCGCCGCACC CACCGCACC CACCGCCCCCGGAGCCTC CCCGGAGCCTC CCCGGGCGCCC CCCGGGCGCCC CCCGGGCGCCCCCC	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGGCC GCGAGGGCC CCGTATCGG GGAGGGCC TGCAGCACAT AGGGGCTCAA AGGGGCTTCCC GCCAGAGTTCC GCCAGAGGCCCG CGGCGGCCG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCGCCCCCGGG CGGCGCCGCCCCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGGC GCAGGACCAC GCGGCCGG GCAGGACCAC CCACCTACAGC CACCTACAGC CCACCTACAGC CCGGCCCG CCGGCCCG CCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACTTCCAG CCCCGGACAG TCAGCCCCC CACTTACAGC CTACAGCCCC CTTTACACCT TTACACACTT TTGATCTT TTGAACAGTT TTGAACAGTT ACAGCTTCCT TTTCAATCTT	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCCAGA GCCAGATCGC GGAGCAGGGGC GGAGCACGG GAGACACGG AACGCTTTCA GAGAAGCGGC CCCAACTACA CGCGTGGCCA CGCGTGGCCA CGCGTGGCCA CTCCAGC CTCCAGC CTTCAGTGT TACGCGCAGC CTTCAGTGT CCTCAGATGG CCTGAGATGG CTGAGAGGAG TTAAAAGGTG TGGGGGGGTT CGAGGGGGT CCAACCCTA CCATTTCCTG	TAGGCCGGCT TAGGCCGGCTTC AGCCCTCCC AGGCCTGGAG CCAGAGCGC TGGGGCCGC TGGTGTGGAG CCTTCGTGGA AGTACCGGCC TGCACGGCCT TCTCGGCACAT TCTTCGCGC TCTCGGACTA CCTCGGACTA CCTCCGGACTA CCTCCGGACTA CCTCCGGACTA ACACCAGCA CTCCGGAGGC ACACCAGCA CTCCGGAGGC ACACCAGCA CTCCGGAGGT AGGCCCTA CCTCGGTGGA CCTCCCCTA CCTCGGTGGA CTTCCGTAGT AGGTTCCTTA AGGTTTCATT TTTCCAAGTT AAAGTTTATT	GGGGCCCTG GGGCGGGGG GCCATGAGC GCCATGAGC GCCATGAGC GTCCCGGG GCCAGGCC TAAGGACAG GGGCGAGCC TAAGGACAG GGGCGAGCC GGGCAGGCC GGGCTGAGCC GGGCTGAGCC GGGCTGAGCC GGCTAGGCC GGCTAGGCC GGCTAGGCC CCCATGCC CCCATGCC CCCATGCC CCCACGCC CCCACGCC CCCACGCC CCACGCC CCCC CCACGCC CCACGCC CCCC CCCC CCACGC CCCCC	GTTACGCTGT ACCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGGCAGCT CGCAAGCAGC CGCAAGTCGC CAGCCGCGCATC CAGCCGCCGCACC CACCGCACC CACCGCCCCCGGAGCCTC CCCGGAGCCTC CCCGGGCGCCC CCCGGGCGCCC CCCGGGCGCCCCCC	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGGCC GCGAGGGCC CCGTATCGG GGAGGGCC TGCAGCACAT AGGGGCTCAA AGGGGCTTCCC GCCAGAGTTCC GCCAGAGGCCCG CGGCGGCCG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCGCCCCCGGG CGGCGCCGCCCCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGGC GCAGGACCAC GCGGCCGG GCAGGACCAC CCACCTACAGC CACCTACAGC CCACCTACAGC CCGGCCCG CCGGCCCG CCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACTTCCAG CCCCGGACAG TCAGCCCCC CACTTACAGC CTACAGCCCC CTTTACACCT TTACACACTT TTGATCTT TTGAACAGTT TTGAACAGTT ACAGCTTCCT TTTCAATCTT	120 180 240 300 360 420 660 720 780 980 960 1020 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
50556065	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCCAGA GCCAGATCGC GGAGCAGGGGC GGAGCACGG GAGACACGG AACGCTTTCA GAGAAGCGGC CCCAACTACA CGCGTGGCCA CGCGTGGCCA CGCGTGGCCA CTCCAGC CTCCAGC CTTCAGTGT TACGCGCAGC CTTCAGTGT CCTCAGATGG CCTGAGATGG CTGAGAGGAG TTAAAAGGTG TGGGGGGGTT CGAGGGGGT CCAACCCTA CCATTTCCTG	TAGGCCGGCT TAGGCCGGCTTC AGCCCTCCC AGGCCTGGAG CCAGAGCGC TGGGGCCGC TGGTGTGGAG CCTTCGTGGA AGTACCGGCC TGCACGGCCT TCTCGGCACAT TCTTCGCGC TCTCGGACTA CCTCGGACTA CCTCCGGACTA CCTCCGGACTA CCTCCGGACTA ACACCAGCA CTCCGGAGGC ACACCAGCA CTCCGGAGGC ACACCAGCA CTCCGGAGGT AGGCCCTA CCTCGGTGGA CCTCCCCTA CCTCGGTGGA CTTCCGTAGT AGGTTCCTTA AGGTTTCATT TTTCCAAGTT AAAGTTTATT	GGGGCCCTG GGGCGGGGG GCCATGAGC GCCATGAGC GCCATGAGC GTCCCGGG GCCAGGCC TAAGGACAG GGGCGAGCC TAAGGACAG GGGCGAGCC GGGCAGGCC GGGCTGAGCC GGGCTGAGCC GGGCTGAGCC GGCTAGGCC GGCTAGGCC GGCTAGGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCACGCC CCCACGCC CCACGCC CCA	GTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GGAGGCGGATG GTGATGGCCG AAGGCGAGT CGCAAGTCGT CGCTGCGCG AAGCAGTCGT CGCTGCGCG TTCCCCGAGC TTCCCCGAGC TACCCGGACTC CCCGGGGCTC ATTCCGGGCCT CCCGGGCCCC CCGGGCCGC CCCGGGCCCC CCGGGCCCC CCGGGCCC CCGGGCCCC CCGGGCCCC CCGGGCCC CCGCGCCC CCGGGCCC CCGGCCC CCGGCCC CCGGCCC CCCGCGCC CCCC CCCGCGCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGGCC GCGAGGGCC CCGTATCGG GGAGGGCC TGCAGCACAT AGGGGCTCAA AGGGGCTTCCC GCCAGAGTTCC GCCAGAGGCCCG CGGCGGCCG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCGCCCCCGGG CGGCGCCGCCCCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGGC GCAGGACCAC GCGGCCGG GCAGGACCAC CCACCTACAGC CACCTACAGC CCACCTACAGC CCGGCCCG CCGGCCCG CCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACTTCCAG CCCCGGACAG TCAGCCCCC CACTTACAGC CTACAGCCCC CTTTACACCT TTACACACTT TTGATCTT TTGAACAGTT TTGAACAGTT ACAGCTTCCT TTTCAATCTT	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CACAGTCACG GGAGCACGG GGAGCACGG AACGCTTTCA CTGCACAACG GGAGCACTGC CCCAACTACA CGCGGGGTTGC CCGCTGGCAC CGCTGGCAC CGCTGCTGC CGACTGCCC CTTCACGTGT ATGCAGCAGG CCGTTCTCG CCGTTGCCCC GAGCTCCTCG CCTGAGATG CCTGAGATG CCTGAGATG CCTGAGATG CCTGAGATG CCTGAGATG TTAAAAGGTG TTAAAAGGTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CTAAAAAAAAAA	TAGGCCGGCT TAGGCCGCTCC AGGCCTGAG ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGCACGGCC TCTCGCACAT TCTTCGCCGC TCTCGGACTT TCTTCGCGC ACTACGGCCT ACACCAGCA TCTCGGAGTGAG CCTCCCTA CGGAGTGGA ACCACGGA TCCGGAGTGGA ACCACGGA TCCGGAGTGGA ACCACGGA TCTCGGATTACGCGC TCTCGGACTA AACCTCCCTA CCTCGGAGTGGA ACCACGGA TCTCGGATGA AGGTTCCATA TGTTGGCATA AAGTTTCATT TAAATCTGGAA	GGGGCCCTG GGGCGGGGC GGCATGAGC GGCCATGAGC GGGCGAGCC TAAGGACGAG GCAGCCAGGCC TAAGGACGAG GCGCGGCCAGGCC GGGCCTCAG GGGCCTCAG GGGCCTCAG GGGCCTCAG GGCCCACGCC CCGATGCCC CCGATGCCC CCGCACGCC CCGCACGCC CCGCACGCC CCGCACGCC CCGCACGCC CCGCACGCA	GTTACGCTGT ACCGCGCAG GGAGGCGGATG GTGATGGCG AAGGCGAGT GGCAAGCGGC GGCAAGCGGC CGCCAGCT CAGCCGGATG CAGCCGGATG CAGCCGGATG CAGCCGGAGCT CAGCAGCAGC TACCGGAACT CACCGGACT CCGGAGCTC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCCGGGCGGCGC CACCAGCACC CCGGGACTGCC CCGGGACTGCC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGCC CCCGGGCGCGCC CCTGCAGCCC CCTGCAGCCC CCTGCAGCT TTAATTATTT TCAGAGATTT AGCTTTGACAT	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGGCC GCGAGGGCC CCGTATCGG GGAGGGCC TGCAGCACAT AGGGGCTCAA AGGGGCTTCCC GCCAGAGTTCC GCCAGAGGCCCG CGGCGGCCG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCGCCCCCGGG CGGCGCCGCCCCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGGC GCAGGACCAC GCGGCCGG GCAGGACCAC CCACCTACAGC CACCTACAGC CCACCTACAGC CCGGCCCG CCGGCCCG CCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACTTCCAG CCCCGGACAG TCAGCCCCC CACTTACAGC CTACAGCCCC CTTTACACCT TTACACACTT TTGATCTT TTGAACAGTT TTGAACAGTT ACAGCTTCCT TTTCAATCTT	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CACAGTCACG GGAGCACGG GGAGCACGG AACGCTTTCA CTGCACAACG GGAGCACTGC CCCAACTACA CGCGGGGTTGC CCGCTGGCAC CGCTGGCAC CGCTGCTGC CGACTGCCC CTTCACGTGT ATGCAGCAGG CCGTTCTCG CCGTTGCCCC GAGCTCCTCG CCTGAGATG CCTGAGATG CCTGAGATG CCTGAGATG CCTGAGATG CCTGAGATG TTAAAAGGTG TTAAAAGGTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CCATTTCCTG CTAAAAAAAAAA	TAGGCCGGCT TAGGCCGCTCC AGGCCTGAG ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC CCGAGTTGAG CCTTCGTGGA AGTACCGCC TGCACGGCC TCTCGCACAT TCTTCGCCGC TCTCGGACTT TCTTCGCGC ACTACGGCCT ACACCAGCA TCTCGGAGTGAG CCTCCCTA CGGAGTGGA ACCACGGA TCCGGAGTGGA ACCACGGA TCCGGAGTGGA ACCACGGA TCTCGGATTACGCGC TCTCGGACTA AACCTCCCTA CCTCGGAGTGGA ACCACGGA TCTCGGATGA AGGTTCCATA TGTTGGCATA AAGTTTCATT TAAATCTGGAA	GGGGCCCTG GGGCGGGGC GGCATGAGC GGCCATGAGC GGGCGAGCC TAAGGACGAG GCAGCCAGGCC TAAGGACGAG GCGCGGCCAGGCC GGGCCTCAG GGGCCTCAG GGGCCTCAG GGGCCTCAG GGCCCACGCC CCGATGCCC CCGATGCCC CCGCACGCC CCGCACGCC CCGCACGCC CCGCACGCC CCGCACGCC CCGCACGCA	GTTACGCTGT ACCGCGCAG GGAGGCGGATG GTGATGGCG AAGGCGAGT GGCAAGCGGC GGCAAGCGGC CGCCAGCT CAGCCGGATG CAGCCGGATG CAGCCGGATG CAGCCGGAGCT CAGCAGCAGC TACCGGAACT CACCGGACT CCGGAGCTC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCCGGGCGGCGC CACCAGCACC CCGGGACTGCC CCGGGACTGCC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGCC CCCGGGCGCGCC CCTGCAGCCC CCTGCAGCCC CCTGCAGCT TTAATTATTT TCAGAGATTT AGCTTTGACAT	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGGCC GCGAGGGCC CCGTATCGG GGAGGGCC TGCAGCACAT AGGGGCTCAA AGGGGCTTCCC GCCAGAGTTCC GCCAGAGGCCCG CGGCGGCCG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCGCCCCCGGG CGGCGCCGCCCCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGGC GCAGGACCAC GCGGCCGG GCAGGACCAC CCACCTACAGC CACCTACAGC CCACCTACAGC CCGGCCCG CCGGCCCG CCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACTTCCAG CCCCGGACAG TCAGCCCCC CACTTACAGC CTACAGCCCC CTTTACACCT TTACACACTT TTGATCTT TTGAACAGTT TTGAACAGTT ACAGCTTCCT TTTCAATCTT	120 180 240 300 360 420 660 720 780 980 960 1020 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGCC CAGAGCCAGG ACGCTTCA CTGCACAACC GGAGCACCGG AACGCTTCA CTGCACAACC CGCAGCTCC CCGCTGGCCC CCGCTGCTGC CCGCTGCCCC CAGCTCCCC CCGTCGCCC CAGCTCCTCG CCGTCGCCC CCTTAAAAAGGTT CCAAAAACCCTA CCATTTCCTG CTAAAAAAATA Seq ID NO:	TAGGCCGGCT TAGGCCGCTCC AGGCCTCCC AGGCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCCAT CCGGGCCGC TGGTGTGAG AGTACCGGCC TGGACGCCT TGGACGCCT TGGACGCCT TCTCGCACAT CCTCGCACAT CCTCGACAGT CCTCGGACTA TCTTCGCGC ACTACCGGC ACTACCGGACT ACTCCCCTA ACTCCCCTA CCTCCGTAGGC CTAAGGAAAT TGTTGCATA AGGTTTCATT TAAAGTTTATT AAATCTGAAA 8 Protein	GGGGGCCCGGGCCGGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCCAGGCCCCCAGGCCCCCAGGCCCCCC	GTTACGCTGT ACCGCGCAG GGAGGCGGATG GTGATGGCG AAGGCGAGT GGCAAGCGGC GGCAAGCGGC CGCCAGCT CAGCCGGATG CAGCCGGATG CAGCCGGATG CAGCCGGAGCT CAGCAGCAGC TACCGGAACT CACCGGACT CCGGAGCTC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCCGGGCGGCGC CACCAGCACC CCGGGACTGCC CCGGGACTGCC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGCC CCCGGGCGCGCC CCTGCAGCCC CCTGCAGCCC CCTGCAGCT TTAATTATTT TCAGAGATTT AGCTTTGACAT	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGGCC GCGAGGGCC CCGTATCGG GGAGGGCC TGCAGCACAT AGGGGCTCAA AGGGGCTTCCC GCCAGAGTTCC GCCAGAGGCCCG CGGCGGCCG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCGCCCCCGGG CGGCGCCGCCCCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGGC GCAGGACCAC GCGGCCGG GCAGGACCAC CCACCTACAGC CACCTACAGC CCACCTACAGC CCGGCCCG CCGGCCCG CCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACTTCCAG CCCCGGACAG TCAGCCCCC CACTTACAGC CTACAGCCCC CTTTACACCT TTACACACTT TTGATCTT TTGAACAGTT TTGAACAGTT ACAGCTTCCT TTTCAATCTT	120 180 240 300 360 420 660 720 780 980 960 1020 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGA GCCAGATCGC GGAGCACGG GAGCACGG AACCCTTTCA GGAGCAACG GAGAAGCGGC CCCAACTACA CGCGTGGCCA CGCTGGCCA CGCTGGCCC CTTCACGTGT TACGCGCACG CAGTCGCCC CTTCACGTGT CCTGAGATG GGGGCTTTC CCTGAGATG GGGGCTCTTC CCTGAGATG CCTGAAAACACT CCATTTCCTG CTAAAAAATA	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGGGCCCTTCTCGGGCCT TGGTGGAA AGTACCGCCT TGCACGGCCT TCTCGGACAT TCTTCGGCCT TCTCGGACTA CAGGCCCT TCTCGGACTA CAGGCCGACAT CAGGCCGACAT CTCCGGACAT CACGGCC ACTACGGCC ACTACGGCG ACACCAGCA CTCCGGAGGC GGGAGGTGGG AGGCCCTCA CCTCGGTGGT AGGTCCCTA AGGTTCCATA TGTTGGCATA AGGTTTCATT TAAAGTTTATT AAATTTGGAA	GGGGCCCTG GGGCGGGGC GCCATGAGC GCCATGAGC GCCATGAGC GCGGGACATG GGGCCGAGCC TAAGGACGAG GCAGGCCGAGCC GAGGCAGGC GGGCCTCAGG GGCCTCAGGC GGGCTGAGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCACGCA ACTGCCCTGG CCACGCAC ACTGCCCCAG CCTCAGCACT TAATTTATGG TAAAATTTGT CAACTTAAACAA TCCTGAAAAA Bequence NP_071899	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGCGCG AAGGTGAAGGCGCGCAGCACCCCCGGAGCCT CCCCGAGCCTTCCCCGAGCTTCCCCGAGCCTCCCCGGAGCCTCCCCCGGAGCCTCCCCCGGAGCCTCCCCGGGACGCCCCCCGGACGCCCCCCGGAGCCTCCCCGGGACGCCCCCCGGAGCCTCCAGCACCCCGGACGCCCCCGGAGCCTCCAGCACCCCGGACCCCCGGACCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCCCCTGCAGCTCTCAAAAAAAA	AGACCAGACC CCCTCGGGGC CGCGGATACGC GGCAGGGGCC GCGGAGGGCC GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACAC CTGCCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GCAGGACCAC GCAGGACCAC GCAGGACCAC GCAGGACCAC CCACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGGACCAC CAGCTACAGC CAGGACCAC CAGCTACAGC CAGCTTCCAG CCAGGCCC CGGCTTCCAG CCAGCTCCAG CCAGCTTCCAG CCAGCTTCCAG CCACCTACAGCT TTACACACTT TTGTATTCT TTGTAATCTT AAA	120 180 240 300 360 420 660 720 780 980 960 1020 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
505560657075	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGCC CAGAGCCAGG ACGCTTCA CTGCACAACC GGAGCACCGG AACGCTTCA CTGCACAACC CGCAGCTCC CCGCTGGCCC CCGCTGCTGC CCGCTGCCCC CAGCTCCCC CCGTCGCCC CAGCTCCTCG CCGTCGCCC CCTTAAAAAGGTT CCAAAAACCCTA CCATTTCCTG CTAAAAAAATA Seq ID NO:	TAGGCCGGCT TAGGCCGCTCC AGGCCTCCC AGGCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCCAT CCGGGCCGC TGGTGTGAG AGTACCGGCC TGGACGCCT TGGACGCCT TGGACGCCT TCTCGCACAT CCTCGCACAT CCTCGACAGT CCTCGGACTA TCTTCGCGC ACTACCGGC ACTACCGGACT ACTCCCCTA ACTCCCCTA CCTCCGTAGGC CTAAGGAAAT TGTTGCATA AGGTTTCATT TAAAGTTTATT AAATCTGAAA 8 Protein	GGGGGCCCGGGCCGGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCCAGGCCCCCAGGCCCCCAGGCCCCCC	GTTACGCTGT ACCGCGCAG GGAGGCGGATG GTGATGGCG AAGGCGAGT GGCAAGCGGC GGCAAGCGGC CGCCAGCT CAGCCGGATG CAGCCGGATG CAGCCGGATG CAGCCGGAGCT CAGCAGCAGC TACCGGAACT CACCGGACT CCGGAGCTC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCGGGACTGCC CCCGGGCGGCGC CACCAGCACC CCGGGACTGCC CCGGGACTGCC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGC CCCGGGCGCGCC CCCGGGCGCGCC CCTGCAGCCC CCTGCAGCCC CCTGCAGCT TTAATTATTT TCAGAGATTT AGCTTTGACAT	AGACCAGACC CCCTCGGGGC CGCGATACGC GGCAGGGGCC GCGAGGGCC CCGTATCGG GGAGGGCC TGCAGCACAT AGGGGCTCAA AGGGGCTTCCC GCCAGAGTTCC GCCAGAGGCCCG CGGCGGCCG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCG ACCCCCGGG CGGCGCCGCCCCCGGG CGGCGCCGCCCCCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGGC GCAGGACCAC GCGGCCGG GCAGGACCAC CCACCTACAGC CACCTACAGC CCACCTACAGC CCGGCCCG CCGGCCCG CCGGCCCC CACCTACAGC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACTTCCAG CCCCGGACAG TCAGCCCCC CACTTACAGC CTACAGCCCC CTTTACACCT TTACACACTT TTGATCTT TTGAACAGTT TTGAACAGTT ACAGCTTCCT TTTCAATCTT	120 180 240 300 360 420 660 720 780 980 960 1020 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
505560657075	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCCGGGC CAGAGCCAGA GCCAGATCGC GGAGCACGG GAGCACGG AACCCTTTCA GGAGCAACG GAGAAGCGGC CCCAACTACA CGCGTGGCCA CGCTGGCCA CGCTGGCCC CTTCACGTGT TACGCGCACG CAGTCGCCC CTTCACGTGT CCTGAGATG GGGGCTTTC CCTGAGATG GGGGCTCTTC CCTGAGATG CCTGAAAACACT CCATTTCCTG CTAAAAAATA	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGGGCCCTTCTCGGGCCT TGGTGGAA AGTACCGCCT TGCACGGCCT TCTCGGACAT TCTTCGGCCT TCTCGGACTA CAGGCCCT TCTCGGACTA CAGGCCGACAT CAGGCCGACAT CTCCGGACAT CACGGCC ACTACGGCC ACTACGGCG ACACCAGCA CTCCGGAGGC GGGAGGTGGG AGGCCCTCA CCTCGGTGGT AGGTCCCTA AGGTTCCATA TGTTGGCATA AGGTTTCATT TAAAGTTTATT AAATTTGGAA	GGGGCCCTG GGGCGGGGGC GCCATGAGC GCCATGAGC GCGGGACATG GGGCCGAGGC TAAGGACGAG GCAGGCGAGCC TAAGGACGAG GCGCGGCGCG	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGTCGC GGCAAGTCGT CGCAAGTGGA CAGCAGGCGC TTCCCCGAGC TACCGCGACT GACACGTCCC CGGGACTGCC CCCGGGCGCC CATTCCAGCC CCCGGGCGCC CATTCCAGCC CCCGGGCCGCCCC CCGGGCCGCCCC CCGGGCCGCC	AGACCAGACC CCCTCGGGGC CGCGGATACGC GGCAGGGGCC GCGGAGGGCC GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	GCGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCTGGAC GCAGGACCAC GCGGGCCCC GCGGCCCC GCGCCCC CACCTACAGC CATGCACCC CACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CCACCTACAGC CATGCACCC ACCTACAGC CCACTTCCAGC CCACTTCCAGC CCACTTCCAGC CCACTTCCACC CTTTTGCAACC CTACTTTTTTTTTT	120 180 240 300 360 420 660 720 780 980 960 1020 1140 1200 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGCC CAGAGCCAGG ACGCTTCAC CTGCACAAC CTGCACAAC GGAGCGGGC CCCAACTACA GGCGGTTCC CCGCTGGCC CCGCTGCCC CACTTCACAC GACACGCTTCC CCGCTGCCC CCGCTGCCC CCGCTCGCC CTTCACGTGT ATGCAGCCC CTTCACGTGT CCCTTCACGTGT CCCTTCACGTGT CCTGACATGC CCTGAGATGG GGGCCATTT GACGTCTCC CCTGAGAGGG TTAAAAGGTG TGAGAGCG CAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO: Protein Ac 1	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGGGC TGAGCCCCT TGAGCCCCT TGGAGGCGC TGTTTGGGA AGTACCGGCC TGCACGGCCT TGGACGCCT TGGACGCCT TCTCGCACAT GCTACCGGACTA CAGAGCCGC ACTACGGACT ACTACGGGC ACTACGGACT ACTACGGGC ACTACGGACT ACTACGGGC ACTACGGGGC ACTACGGGGC ACTACGGGGC ACTACGGGGC ACTACGGAGA TGTTGCCTGA CTCCGTAGGA CTCCGGAGGC ACTACGGAGAAT TGTTGCATA AGGTTTCATT TTTCCAAGTT AAAGTTTATT AAATCTGGAA 8 Protein cession #: 11	GGGGGCCCTG GGGCGGGAG CCGGGACATGAGC GGCCATGAGC GCCATGAGC GCCATGAGC GCGGGACATG GGGCCGAGC TAAGGACGAG GCAGCCAGGAG GCGCGGACAG GCGCGCCCCAG GGCCACGCC CCGATGCCC CCGATGCCC CGGTCCCCC GGTCCCCC GGTCCCCC CCGCAGCCC CCGCAGCCC CCGCAGCCC CCGCAGCCC CCGCAGCCCC CCGCAGCCCC CCGCAGCCCC CCGCAGCCCC CCGCAGCCCC CCGCAGCCCC CCGCAGCCCC CCGCAGCCCC CCGCCCCAG CCTCAGACAC CCTCAGACTC TAATTTATGG CTAAAAAAA TCCTGAAAAAA Sequence NP_071899 21	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGGCGAGT CGCAAGTCGT CGCAGCGGCG AAGCAGGCGC AAGCAGGCGC TTCCCCGAGC TTCCCCGAGC TACCCGGACT CCCGGAGCTC ATTCCCGGCC CCCGGGGCGCAGCCC CCCGGGCGCAGCCC CCCGGGCCGCCCCCCCC	AGACCAGACC CCCTCGGGG CGGGATACGC GGCGGGGATACGC GGCGGGCGGCGGGCGGCGGCGCGGC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACAC CTGCCCCTGG GGCGACAGC GCGGCCGATG GAATCCAGAC GCGGCCGACC GCGGCCCGCCC GCGGCCCC CGTGGACCC CACCTACAGC CCACCTACAGC CCACTACAGC CCACCTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAT CTTCAACACT CTTCCATCT CTTCATCT CTTCCATCT CTTCT CTTCCATCT CTTCT CTTTCT CTTCT CTTCT CTTCT CTTCT CTTTCT CTTTCT CTTTC	120 180 240 300 360 420 660 720 780 960 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1800
505560657075	GCAGTGTCAC AGAACACGG GCTCATTCCCC GGAGCCGGG CAGAGCCAGA GCCAGATCGC GGAGCACGG GAGCACGG AACGCTTTCA GGAGCACACG GAGAACGCGC CCAACTACA GGCGGTTGCCA CCGCTGGCCA CCGCTGGCCA CCGCTGGCCC CTTCACGTGT ATGCAGCCC CTTCACGTGT CCTGAGATG GGGGCTTTG CCTGAGATG GGGGCATTT GAAGTTGAC CCTGGAGGG TTAAAAGGTG TGGGGGGGT TAAGGGGGGT TAAGGGGGGT TAAGGAGAG CCTGGAGGAG TGAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO: Protein AC 1 MSSPPAGYAS	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGGGCCCAT CCGGGGCCGC TGGTGTGGA ACTACCGGCC TGCACGGCCT TCTCGGACAT TCTTCGGCCT TCTCGGACTA CAGAGCCCGA ACTACCGGCC ACTACGGCC ACTACGGCG ACTACGGCG ACTACGGCG ACTACGGCG ACTACGGCG ACTACGGCG ACTACGGCG ACTACGGCG TCTCCGGAGGC CCTCGGTGGT AGGTCCCTTA CCTCGGTGGT AGGTTCCATA AGGTTCCATA AGGTTCATT TTTCCAAGTT TTTCCAAGTT TTTCCAAGTT AAAGTTTATT AAAATTTGAA	GGGGCCCTG GGGCCGGGAG CCCATGAGC CTTCCCGGG GGCCATGAGC CTTAAGACAAG GGGCCGAGCC TAAGGACAG GGGCCAGGC GGGCCTGAGCC GGGCTGAGCC GGGCTGAGCC GGGCTGAGCC GGGCTGAGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCACGCA ACTGCCCTGG CCACGCAC CCACGCACTC CCACGCACTC TAATTTATGG TAAAATTTGT CAAGTTAAAC TCATAAAGAA TCCTGAAAAAA sequence NP_071899 21 PAVMAGLGPC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAG AAGGCGGATG CGCAAGCGGC AAGGCGGCG TCCCCGAGC TCCCCGAGC TTCCCCGAGC TACCGCGACT CCCGGAGCTCC CCGGAGCCTC CCCGGAGCCTC CCCGGAGCCTC CCCGGAGCCTC CCCGGGCGCGC CCCCGGGGCGC CCCCGGGGCGC CCCCGGGGCGC CCTGCAGCCC CTGCAGCCC CTGCAGCCT TAATTATTT TCAGAGATTT AAGTTTGAACAGT TAATTTATTT TCAGAGATTT AGCTTTGAACAGT ATGTTGTCCT AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGCTCCGGGGC CGCGATACCG GGCAGGGCCC GCCGTATCCG TGCAGCACAT AGCGGCTCCC GCAGAGTCT GCAGCACAT AGCGGCTCCC GCCAGAGTCT TCCTGCAGCCC TCTTGGCGCC TCTTGGCGCC TCTTGGCCC TCTTGGCCC TCTTGCACT TCTTGCACT TCTTGCACT TGAATCTCC TATATTACTG AGAAGCACTT TGAATCTCCCAAA GTTTCCCACA GTTTCCCACA GTTTCCCACA TTTCCACACT TGATTTCCACACT TGATTTCCACACT TGTGTTGCCC TATATTACTG AGAAGCAGTTG TGTTTGCCAC TTTTCCACAC TTTCCACACT TTCCACACT TTCCACACT TTCACACT TTCACACT TTCACACT TTCACACT TTCACACT TTCACACA TTTCCCACA TTTCCCACA TTTCCACAC TTTTCCACA TTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTCCACAC TTTCACAC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GCGGCCGATG GCAGGACCAC GCGGCCCG GGGGGGCCCC GGGCGCCCC CACCTACAGC CATGCACCC CACCTACAGC CAGCTGCCC CGGCTCCAG CCAGCTCCAG CCAGCTCCAG CCAGCTCCAG CCAGCTCCAG CCACCTACAGC CAACTATCCT TTACACACTT TTGTAGTTTT TTGTACACTT AAA 51 NSGAPAGAAG	120 180 240 300 360 420 660 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1620 1620 1620 1620 1620 1620 1620
505560657075	GCAGTGTCAC AGAACACGG GCTCATTCCCC GGAGCCGGG CAGAGCCAGA GCCAGATCGC GGAGCACGG GAGCACGG AACGCTTTCA GGAGCACACG GAGAACGCGC CCAACTACA GGCGGTTGCCA CCGCTGGCCA CCGCTGGCCA CCGCTGGCCC CTTCACGTGT ATGCAGCCC CTTCACGTGT CCTGAGATG GGGGCTTTG CCTGAGATG GGGGCATTT GAAGTTGAC CCTGGAGGG TTAAAAGGTG TGGGGGGGT TAAGGGGGGT TAAGGGGGGT TAAGGAGAG CCTGGAGGAG TGAAACCCTA CCATTTCCTG CTAAAAAATA Seq ID NO: Protein AC 1 MSSPPAGYAS	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGGAG CCCAGAGGCC TGGGCCCAT CCGGGGCCGC TGGTGTGGA ACTACCGGCC TGCACGGCCT TCTCGGACAT TCTTCGGCCT TCTCGGACTA CAGGCCCT TCTCGGACTA CAGGCCGACTACGGCC ACTACGGCC ACTACGGCC ACTACGGCG ACACCAGCA CTCCGGAGGC GGGAGGTGGA CTCCGGAGGC ACACCAGCA CTCCGGAGGC ACTACGGCA TTCTCGAACT ACTCCGTAG CTTCGGACTA CCTCGGTGGT AGGTTCCATA AGGTTCCATA AGGTTCATT TTTCCAAGTT TTTCCAAGTT TAAAGTTTATT AAAATTTGAA	GGGGCCCTG GGGCCGGGAG CCCATGAGC CTACCCGGG CGCGAGACC TAAGGACAGAG CAGGCCAGAGC TAAGGACAGAG GGGCCGAGGCC GGGCCTCAGAG GGCCTAGAGC GGCCTCAGAGCC CCCATGCCC CCCATGCCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCATGCC CCCACGCAC ACTGCCCTGG CCACGCAC CCACGCAC CCACGCACTCA CTCCCCCCAG CTCCCCCAG CTCCCCCAG CTCCCCCAG CTCCCCCAG CTCCCCCAG CTCCCCAGACTC TAATTTATGG TAAAATTTGT CAAGTTAAAC TCAGAAAAA Sequence NP_071899 21 PAVMAGLGPC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAG AAGGCGGATG CGCAAGCGGC AAGGCGGCG TCCCCGAGC TCCCCGAGC TTCCCCGAGC TACCGCGACT CCCGGAGCTCC CCGGAGCCTC CCCGGAGCCTC CCCGGAGCCTC CCCGGAGCCTC CCCGGGCGCGC CCCCGGGGCGC CCCCGGGGCGC CCCCGGGGCGC CCTGCAGCCC CTGCAGCCC CTGCAGCCT TAATTATTT TCAGAGATTT AAGTTTGAACAGT TAATTTATTT TCAGAGATTT AGCTTTGAACAGT ATGTTGTCCT AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGCTCCGGGGC CGCGATACCG GGCAGGGCCC GCCGTATCCG TGCAGCACAT AGCGGCTCCC GCAGAGTCT GCAGCACAT AGCGGCTCCC GCCAGAGTCT TCCTGCAGCCC TCTTGGCGCC TCTTGGCGCC TCTTGGCCC TCTTGGCCC TCTTGCACT TCTTGCACT TCTTGCACT TGAATCTCC TATATTACTG AGAAGCACTT TGAATCTCCCAAA GTTTCCCACA GTTTCCCACA GTTTCCCACA TTTCCACACT TGATTTCCACACT TGATTTCCACACT TGTGTTGCCC TATATTACTG AGAAGCAGTTG TGTTTGCCAC TTTTCCACAC TTTCCACACT TTCCACACT TTCCACACT TTCACACT TTCACACT TTCACACT TTCACACT TTCACACT TTCACACA TTTCCCACA TTTCCCACA TTTCCACAC TTTTCCACA TTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTTCCACAC TTTCCACAC TTTCACAC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACGAC CTGCCCCTGG GCGACAGC GCGGCCGATG GAATCCAGAC GCGGCCGATG GCAGGACCAC GCGGCCCG GGGGGGCCCC GGGCGCCCC CACCTACAGC CATGCACCC CACCTACAGC CAGCTGCCC CGGCTCCAG CCAGCTCCAG CCAGCTCCAG CCAGCTCCAG CCAGCTCCAG CCACCTACAGC CAACTATCCT TTACACACTT TTGTAGTTTT TTGTACACTT AAA 51 NSGAPAGAAG	120 180 240 300 360 420 660 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1620 1620 1620 1620 1620 1620 1620
505560657075	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGGC CAGAGCCAGG GGAGCACGG AACCCTTCCA CTGCACAACG GGAGCACGG CCCAACTACA CGCGTGGCCA CCGCTGGCCA CCGCTGGCCA CGCTCGCCC GAGCTCTCCC CCTCAGACG CCACTTCACACG CCACTGCCCC CTCACACG CCACTCACACG CCACTCACACG CCACTCACACG CCACTCACACG CCACTCACACG CCACTCACACG CCACTCACACG CCACTCACACG CCTCACACGC CCTCACACG CCTCACACGC CCTCACACGC CCTCACACGC CCTCGACGATG CCATACACCCTA CCATTCCTC CTAAAAACATA Seq ID NO: Protein Ac L MSSPDAGYAS RAKGESRIRR	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGCAG ACCCCAGAGCGC TGAGCCCAT CCGGGGCCGC TGAGTTGGGC CCGAGTTGAG ACTACCGGCC TGCACAGCCCT TCGCACACT TCTCGCACAT TCTTCGCCGC TCTCGGACTA CAGAGCCCG ACTACCGGCT ACACCAGCA CTCCGGAGGGC GGGAGGTGGA CTCCCCTA CCTCGGAGGC ACTACGGGCT AGGCCCTA AGGTTCCCTA AGGTTCCATA AGGTTCATT TTTCCAAGTT TAAGGAAAT TTTCCAAGTT AAAGTTTATT AAAGTTTATT AAAGTTTATT AAAGTTTATT AAAGTTAGAA 8 Protein ccssion #: 11	GGGGGCCCTG GGGCGGGGGC GCCATGAGC CGGGACATG GGCCGAGGC TAAGGACGAG CAGGACATG GGGCCGAGGC GAGGCCTCCAG GGGCCTCCAG GGGCCTCCAG GGGCCTCCAG GGCCACCCC CGCTGGCCCC GGTCCCTCG GATGGCC CCACAGGAC ACTGCCCCAGGCC TCAGACTC TAATTTATGG TAAAATTTGT CAAGTTAACT GATCAAAAAA SEQUENCE NP_071899 21 PAVMAGLGPC DERKRLAQQN	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAG AAGGCGGATG CGCAAGTCGT CGCAAGTCGT CAGCAGCTGCAGCC GACACGTCCC GGGACTGCC CCCGCGCGCG CACCCCCCGCGCCGC CACCCCCCCC	AGACCAGACC CCCTTCGGGGC CGCGGTTCCGGGGG GGCTGGGCCC CCCGTATCCG TGGGCCAC TGGGCACAC AGCGGTTGACACA AGCGCTTCAC GCCAGAGTCT CGCTGGCCGC CGCCGGTTCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGGCCCC TCCTGCCCCAC ACCCCCGGGCCG CGCACTCC TCCTGCCCCAC ATCTACACTT TCAATCTCC TATATTACTG AGAAGCAGTG TTGTTGCCAC GTTTCCCACA GGTTCCCAAA GGGTGTTTT AAAAAAAAAA	GCGACAGGCC ATCTCAGTIGC AGGGTTGAGG CAGTGACCAC CTGCCCCTGG GGCGAACAGC GCGGCCGATG GAATCCAGAC GCGGCTGGAC GCGGGCCCAC GCGGGCCCC GGGCGCCC CCTGGACCCC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC TCAGCCCC CGGCTTCCAC TTACACACT TTACACACT TTGTGTTT TTGTATTT TTGTATTT TTTCAATCT TTTCAATCT AAA 51	120 180 240 300 360 420 660 660 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800
505560657075	GCAGTGTCAC AGAACACGGG CTCATTCCCC GGAGCGGGCC CAGAGCCAGGA ACACGCTTCAC GGAGCACGGG AACGCTTTCA CTGCACAACG GGAGGAGCACGG CCCAACTACA CGCGTGGTGC CCGCTGGACG GACCCGGCTT TACGGCACGGC	TAGGCCGGCT TAGGCCGGCTTC ACCCCTCCC AGGCCTGAG CCCAGAGCGC TGAGCCCAT CCGGGCCGC TGGTGAGG CCTCGTGAA AGTACCGGCC TGCACGCCT TGGACGCCT TCTCGCACAT TCTTCGCACAT CAGACCCGC ACTACCGGC ACTACCGGC ACTACCGGC ACTACGGGC ACTACGGGC ACTACGGGC ACTACGGGC ACTACGGGC ACTACGGGC TCTCGACTA CCTCGGACTA ACCTCCCTA AGGAGTCCCTA TGTTGCAT TTTCCAAGTT TATTCCAAGTT TAAAGTTTATT AAATCTGGAA B Protein CCSSION #: 11 DDQSGTQSAL PMNAPMVWAK DHPNYKYRPF	GGGGGCCCTG GGGCGGGAG CCGGGACATGAGC GGCCATGAGC GGGCCGAGACC TAAGGACGAG GCAGCAGAGC GCAGCCAGCC GGGCGGGC	GGTACGCTGT ACCCGCGCAG GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAGGCG AAGGTGAGGCG GGCAAGTCGT CGCTGCGGCG AAGCAGGTCGT CAGCCGGACTC GACACGTCCC GGGACTCC CCCGGGGCCG CATCCCGGGCCC CCCGGGGCCT ATTCCCGGGC CACCACCAC CCCGGGGCCT CATTCCAGCC CCGGGTTTT AATTTATTT TCAGAGATTT AGCTTTGAAT ATGTTGTCCT AAAAAAAAAA	AGACCAGACC CCCTCGGGGC CGGGATACGC GGCAGGGCGG GGGATACGC GGCAGGCGC CCCGTATCCG TGGGCACC TGGGCACC TGGAGCACA AGCGCTTCC GCCAGAGTTC GCCAGAGTTC GCCAGAGTTC TCCTGGCCC CCCGGGCGGC CGCCGGGCGG CGCCGGGCGG ATCTGACCCACA ATCTCACT TGAATTCCC TTATATTACTG AGAACCACT TGTTGCCACA GTTTCCCACA GTTTCCACA GTTCCACA GTTTCCACA GTTTCACA GTTTCCACA GTT	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACAC CTGCCCCTGG GGGCACAGG GCGGCCGATG GAATCCAGAC GCGGCCCAC GCGGCCCC GCGGCCCC CGGGCCCC CGGGCCCC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CATGCACCC CACCTACAGC CATGCACCC TCAGCACCC CTGGACCC CTGGACAC TCAGCCCGC CTGTGCACAC TCAGCCCT TTTCAACACTT TTGTTGTTTT TTGAACACTT TTGTTGTTTT TTGAACACTT TTTTCAATCTT AAA S1 I NSGAPAGAAG LAEKRPFVEE GGRVAMDGLG GGGTTAGAGACAC LAEKRPFVEE	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800
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505560657075	GCAGTGTCAC AGAACACGG CTCATTCCCC GGAGCCAGA GCCAGACCAGA	TAGGCCGGCT TAGGCCGGCTTC AGCCCTCCC AGGCCTGAGG CCCAGAGCGC TGAGCCCAT CCGGGGCCGC TGGTGTGGG CCTACGGCC TGGACGCCT TGCACGCCT TCTCGGCACAT GCTACCGCT TCTTCGCGC TCTCGGACTA CCTCGGACTA CCTCCGGACTA AGGTCCCCTA CCTCCGGAGGC ACACCAGCA CTCCGGAGGC ACACCAGCA CTCCGGAGGC TGGAGGAGTTGAA CCTCCCTA CCTCGGTGGT TTTCCCAGAGT AGGTTCCTTA CTTCGGAGT AGGTTCCTTA CTACGGACT TGGCATA AGGTTCCTTA CTACGGAGT TGTTGCCATA TGTTGCATA AAGTTTCATT AAATCTGGAA 8 Protein CCSGAGTTGA CTAAGGTT AAATTTATT AAATCTGGAA 11 DDQSQTQSAL PMNAPMVMAR DHPNYKYRPR GPPLLPPHMG	GGGGCCCTG GGGCCATGAGC CGCGAGACC GGGCCAGAGC CTAAGACCAG GGGCCAGAGC TAAGGACAG GGGCGAGCC GGGCAGAGC GGGCCAGAGC GGGCCAGAGC GGGCCAGAGC GGCCAGAGC GGCCAGACCA GCCCACGCC CCCCATGCCC CGCTGCCCCC GGTCCCTGG CCCCCAGACCAG ACTGCCCTGG CCACGCAC CCACGCACTGC TAATTTATGG TAAATTTGT CAAGTTAACT GATCAAAGAA TCCTGAAAAAA SEQUENCE NP_071899 21 PAVMAGLGPC DERKRLAQQN CRCGCCCCAG CRCCCCCAGC CCCCCAGACCC CAGCACTCC CAGCACTCC TAATTTATGG TAAATTTGT CAAGTTAACT GATCAAAGAA TCCTGAAAAAA CCTGAAAAAA CCTGAAAAAAA CCTGAAAAAAA CCTGAAAAAAA CCTGAAAAAAA CCTGAAAAAAAA CCTGAAAAAAAA CCTGAAAAAAAA CCTGAAAAAAAAAA	GGTACGCTGT ACCCGCAGA GGAGGCGGCG AGCCCGGATG GTGATGGCCG AAGGTGAAGGCGCGCG AAGGTGAAGCGCGCGCAGCCCCGGGACTCCCCGAGCCTCCCGGGCCCCCCGGGCGCCCCCCGGGCCCCCCGGGCCCCC	AGACCAGACC CCCTCGGGGC CGCGGGATACGC GGCAGGGCC GCGAGGCCC GCGAGGCCC GCAGGCCCA AGCGCTCCC GCAGAGTTCCC GCAGAGTTCCC GCCAGAGTTCCC GCCAGAGTTCCC GCCAGAGTTCCC TCTGGCCCC AGGGCTCCC TCTGGCCCC TCTTGGCCCC TCTTGGCCCC TCTTGGCCCC TCTTGCCCCC TCTTGCCCCC TCTTGCCCCC TCTTGCCCCC TCTTGCCCCC TGTATTACTG AGAGCCTTAC TGTTTCCCACAT TGAATCTCCC TTTTCCCACA GGTTTCCCACAT TGATTCCCCC TTTTCCCACACT TTCCCACACT TTCCCACACT TGAATCTCCC TTTTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCCACACT TTCCACACT TTCCCACACT TTCCACACT TTCCCACACT TTCCACACT TTCCCACACT TTCCACACT TTCCCACACT TTCCCACT TTCC	GCGACAGGCC ATCTCAGTGC AGGGTTGAGG CAGTGACAC CTGCCCCTGG GGCGACAGG GCGGCCGATG GAATCCAGAC GCGGCCCAC GCGGCCCC GCGGCCCC CGGGCCCC CGGGCCCC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CACCTACAGC CATGCACCC CACCTACAGC CATGCACCC CTGGACCC CTGGACCC CTGGACCC CTGGACAGC CCACCTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CCACTACAGC CTTCCAGC CTTTCCAGC CTTTCCAGC CTTTCCATCTT TTGTTGTTTT TTGAACAGTT TTGTTGTTTT TTGAACAGTT TTTCAATCTT AAA S1 INSGAPAGAAG LAEKRPFVEE GGRVAMDGLG GGRVAMDGLG	120 180 240 300 360 420 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800

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10	GTGGAACTCC	TAGGGCTTTT	TTGAGAGTGC	TGATTTAGAA	GAATACAAAT	CATGGCTGAA	120
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15		AAGCCTTAAA CTGGAAAATC					360 420
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		GAGTTATTGG CATGTCGCCC					600 660
20		GGAAAAAAGA					720
		GAAAAGACTT					780
		TCAGGGTTGC					840 900
25	AATGAATTTA	AAGTTCCTCC	ATTTCAAGAT	TGTATTTTAA	GTTTCCTGGG	ATTTTCAGAT	960
25		CCAATATGGA GATGCACTCA					1020 1080
		AGAAACTTTA					1140
		CTGGAGAAAC					1200
30		CAATGCTTTC					1260 1320
		CTGAGCATTC					1380
		TTAACTATGG					1440 1500
		ATGTTAATAT					1560
35	GAGGAAGGAC	AACGTGGTGG	ACCTATCCTT	GCACCAGAGG	AGATTAAGAC	TATTTTTGGT	1620
		ATATCTTTGA ATGAGAGCAA					1680 1740
	GTAAAAACCT	ACCCTCCCTT	TGTAAACTTC	TTTGAAATGA	GCAAGGAAAC	AATTATTAAA	1800
40		AGAAACCAAG AGAGCCTTGT					1860 1920
40		TARATGATCT					1980
		CTATTGGATC					2040
		CTCAAAAGCA CTTCTCACCG					2100 2160
45	CACCCCTGTG	ACAGAGGAGA	ACAAGTAACT	CTCTTCCTCT	TCAATGATTG	CCTAGAGATA	2220
		GGCACAAGGT TTAAGCATAT					2280 2340
		CAGAAGATTG					2400
50		TGCTACTCAG					2460
30		TGTGTCGACA CTGATCCAGA					2520 2580
	AGTAGAGCAT	CAAGAGCAAT	AAAAAAGACT	TCAAAAAAGG	TTACAAGAGC	ATTCTCTTTC	2640
		CAAAAAGAGC CTTCCAGCAA					2700 2760
55		TCCCTTCTCC					2820
		GTAGATCTAC					2880
		AGACACCTCA AAAGCTGGAA					2940 3000
60	TCTTGAAAGA	GTAAGGTTTA	CCTGTTACAT	TTTCAAGTTA	ATTCATGTAA	AAAATGATAG	3060
00		GTAATTTATC TGATATTAGT					3120 3180
		ACTGCTGTGA					3240
		CAGCTCAATT					3300 3360
65						AAGTATTTAA AGCATGTGGA	3420
	ADAAAATTT	TTTGCCCTCA	TTAACAAGAA	TAACATTTAA	AGGAGATTGT	TTCAAAATAT	3480
						GCAAAAACAA TCCACTAGCA	3540 3600
70						CCATGGGAAA	3660
70						ATCAGTTTTA	3720
						GGTCTTATAA CACAATAGCC	3780 3840
	TTTTTTATAGT	CAGTAATTCA	GAATAATCAA	GTTCATATGG	ATAAATGCAT	TTTTATTTCC	3900
75						TGTTTTAATA AGTAGTAAAT	3960 4020
						TAAATACCTA	
		AAAAAAAA					
	Seg ID NO:	10 Protein	sequence				
80	Protein Ac	cession #:	Q9H8V3				
	1	11	21 	31 	41	51 1	
						TRVILVQEAG	60
85						YKADCRVIGP	120 180
00	- A A THAC SÓNG	PEDELOCKEN	TOTOMMENTAL	CEIGLKKEE	TANDAIDAUN	MGGVIRKDFN	100

	SKVTHLVANC	TOGEKFRVAV	SLGTPINKPE	WIYKAWERRN	EQDFYAAVDD	PRNEFKVPPF	240
			MTEMQGGKYL				300
			YLYEKANTPE				360
5			SIGSLLDISN				420 480
,			ATIIQLFQVP IGDIFLKYSK				540
			LLIRPVORLP				600
			FDVVYEVDGC				660
10			GTFRSPHGQT				720
10			QMTSDELPKE				780
			KTSKKVTRAF LVSLPSPFER			VEGRSPSSND	840
	KHVMSKLSSI	SSUMGIFSFS	LVSDPSFFER	KSHILISKSII	uni		
	Seq ID NO:	11 DNA sequ	ience				
15			1 #: XM_0443	.66			
		ence: 115			43	51	
	1	11	21	31 	41	1	
	CTTTTGTTTC	GCCATGCCTA	GTCTAGTGGT	ATCTGGAATA	ATGGAAAGAA	ATGGGGGCTT	60
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			ATCAACTCTG				180
	· CAGGGCGGGC						240
			CCCCCACCGC				300 360
25	CCCAGCGCAG	AAGAGGCCG	AGCTGCGCCT	GAAGGGCAGC	AGCAACGACG	CGGAGTGTGT	420
			ACGTGGCCGA				480
			ACACCTACAT				540
			GGGAGGACGT				600
30			TCCGTGCCTC				660
30			AGGTGACCAT GGGCAACCAT				720 780
			ACCGCGACCC				840
			AGATOGAGAC				900
25			ACTTCCTGGC				960
35			TGCACCAGCC				1020
			GCGAGTGCGG				1080
			TTGGCTACGG GCGTGGCCGA				1140 1200
			TGCTCTTCTC				1260
40			CGGGCGCACA				1320
			GCCCCCCGGG				1380
			CCGGCGGCGG				1440
			CCTGCGGACA				1500
45			CAGAGTGTCC CGTGCCCCAT				1560 1620
			AGCCTTTTGG				1680
			AAGGGGGGAG				1740
			CTGTCCTGGA				1800
50			TACCTCAACA				1860
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			GCTCTTTGCA				2040
			CCTTGTCTTT				2100
			ACACCATCCT				2160
55			TCAGGCATCT				2220
			AATGTATCCC				2280
			AACCCCCACC CTGGTTGTGG				2340 2400
			GCGTGAGGCA				2460
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			TTATTAGCTT				2580
						CTGGGGCAAA	2640
						TGTTACAGGC	2700 2760
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						CCTTCCTCCT	
						GGAGGGGTGG	
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70						TCGGTTGCCG	3120 3180
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						AGTGAGAGAC	
						CACAGAGGAG	
75						AATATTCTAT	3420
	TTTAATAAAG	GOGTTTATTA	CCATATAAAT	GTAGCAAAGA	ACCTGGGCTA	ATATGAA	
	Can In Mo	12 Protein	60M16755				
		cession #:					
80	1	11	21	31	41	51	
	1	1	1	1	1	1	
•						LLGLGEPPAP	60
						PKGASDAKLC	120
85						KTPVRGEEPV	180 240
0.5	tun trukkenn	MINKKBIISA		VDIAMEGNIN	WEWNEGGA 1 1	RVRVPYRVVG	440

	EYNNENDFLA GEQGGDFGYG	GSPDAAIDSR GYLFPGYGVG	YSDAWRVHQP KQDVYYGVAE	VFEITGAPGN GCKPLSTFRQ TSPPLWAGQE	NSLGCIGECG NATPTSVLPS	VDSGFEAPRL SASSSSSSSA	300 360 420
5				eplogfskig Vchitatqai		RDCMVCFESE	480
		13 DNA sequent		nuence			
		ence: 129					
10	1	11	21	31	41	51	
	1			1	1		
				GTTGGCAGAA			60
				CATGTCGTTC			120
15				CCTGATGTTA			180
15	AACGAAACAG	AAAAAACTAA	AATCACTATA	GTAAAAACCT	TCAATGCTTC	AGGCGTCAAA	240
				ATTTGCAATG			300
				ACTGTTCCCC			360
				GAATTAAAAC ATGTGTGCTA			420 480
20				AATACAATGA			540
20	COTTOGRA	CATTCACAAT	TOCACCAAT	GAACACTGCT	COTOTOTO	CAGGATACCC	600
				CTTCAGTGTG			660
				TTTTCTTCCA			720
				AAAGCTACCT			780
25				CCAATAGGGG			840
				GCCATTGACA			900
				TCCGGCACCC			960
				AATGTCAACA			1020
20				TCTGATCTTG			1080
30				CCTAACCTCG			1140
				ATGCTGGCCC			1200
				AACTTTTCAA			1260
				GTGAATGCCA			1320
35				GTTTCTCTGG			1380 1440
33	AGTATTGGCA	CAATTACTCT	CTTCATCG	CTGATGAATA TTTGAAACAC	ATTIACCAGC	TCAGGACATG	1500
				GTCATATCAT			1560
				ACATTAAAGC			1620
				TTGGGCAGAA			1680
40				AGATTGAATG			1740
	CATCTAACAA	GCTTCGGCGT	TCTGCTGGAC	CTATCTAGGA	CATCTGTGCT	GCCTGCTCAA	1800
	ATGATGGCTC	TGACGTTCAT	TACATATATT	GGTTGTGGGC	TTTCATCAAT	TTTTCTGTCA	1860
				AAGATCCGGA			1920
45				CTGAACCTGG			1980
45				ATCTCAGTGG			2040
				GAAGCATTCC			2100
				ATCCTTAAAT			2160
				ACTATATCCC			2220 2280
50				GATGACTTCT TGTGTGATAT			2340
50				ATTAAAAAGA			2400
				ATCGCTGGCC			2460
				CCAGTTAACG			2520
				ATATTCATCT			2580
55				TGTTGTGGAA			2640
				TTAAAGAAGC			2700
	TCCAGCTCTT	CAAATTCCTT	ACAGTCAAGC	AGTAACTCCA	CTAACTCCAC	CACACTGCTA	2760
				GGGAATGGAA			2820
<i>c</i> 0				GTGTGCCTTC			2880
60				AATGGGAAAG		TCTCAGAAGG	2940
	ACTTCAAAGC	GGGGAAGCTT	ACACTTTATT	GAGCAAATGT	GA		
	•	14 Protein	_				
65		cession #:					
03	1	11	21	31 .	41	51	
				(i	 PDVTLSLLPS	60
						TVPQNQHITN	120
						NTMNACAVIA	180
70				LOCDLODPIV			240
, 0				PIGEIQPLSP			300
				NVNTTSAPPV			360
						NFSNTTISLT	420
						LMNNLPAHDM	480
75						TLKHINPSQD	540
						LSRTSVLPAQ	600
	MMALTFITYI	GCGLSSIFLS	VTLVTYLAFE	KIRRDYPSKI	LIQLCAALLI	LNLVFLLDSW	660
	IALYKMQGLO	ISVAVFLHYF	LLVSFTWMGL	EAFHMYLALV	KVFNTYIRKY	ILKFCIVGWG	720
00	VPAVVVTIII	TISPDNYGLG	SYGKFPNGSF	DDFCWINNNA	. VFYITVVGYF	CVIFLLNVSM	780
80						PVNVTFMYLF	840
						LKKQTVNQGV	
					GVSPSVQNGI	VCLHDFTGKQ	960
	HMFNEKEDS	: NGKGRMALRE	TSKRGSLHFI	EQM			
85	Con In No.	15 DNA seq	nience				
0.5	acd In was				21	70	

			ı #: Eos seç	Ineuce			
	1	ence: 129	21	31	41	51	
5	שוריביינייייייייייייייייייייייייייייייייי	CTGTCACCCA	GTGTGGCCAT	GTTGGGAGAA	COLLEGE	TTTACTCACC	60
•			CATTTGTCTT				120
			GTCACCACCA				180
			AATCACTATA TTTGTCATCT				240 300
10			TAAAGAAAGC				360
			GTCTCTAAGT				420
			GAATGCATGT				480 540
			TGACCTGCAG				600
15			CAGCCAATCC				660
			CTCTTTTGCT				720 780
			CATGCCCCCA				840
20			CCCACCTCCT				900
20			CACTACCAGC				960
			TGAGAACCAA CGCAGGAGAA				1020 1080
	TCCCCGCCTG	ACATGCTGGC	CCCTCTGGCT	CAAAGATTGC	TGAAAGTAGT	GGATGACATT	1140
25			AAACACGACT				1200
23			CAGTAGTTTC GGAAACCCAA				1260 1320
	CTTCCTTCAT	CGCTGATGAA	TAATTTACCA	GCTCATGACA	TGGAGCTAGC	TTCCAGGGTT	1380
			ACCTGCTTTG				1440
30			ATCGAGTGTT GCACATCAAC				1500 1560
-			AAATGGTGGC				1620
			TGAAACCATC				1680
			GACATCTGTG GCTTTCATCA				1740 1800
35			GAGGGATTAC				1860
			GGTCTTCCTC				1920
			GGCTGTATTT CCATATGTAC				1980 2040
			ATTCTGCATT				2100
40			CCCAGATAAC				2160
			CTGCTGGATC				2220 2280
			GAAGAAGCAA				2340
45	GACCTCAGGA	GTATCGCTGG	CCTTACATTT	TTACTGGGAA	TAACTTGGGG	CTTTGCCTTC	2400
45			CGTGACCTTC				2460 2520
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	GCTACTAATG	GTTTAAAGAA	GCAGACTGTA	AACCAAGGAG	TGTCCAGCTC	TTCAAATTCC	2640
50			CACTAACTCC				2700 2760
20			TCACGATTTC				2820
	GAAGATTCCT	GCAATGGGAA	AGGCCGTATG				2880
	TTACACTTTA	TTGAGCAAAT	GTGA				
55		16 Protein cession #:	sequence Eos sequenc	e			
	1	11	21	31	41	51	
	MARGABOOSH 	VCPTEEVI.I.T	PKIFLVIICL	HUMINTSLEE	I DTDNSSI.SPP	PDVTLSLLPS	60
60	NETEKTKITI	VKTFNASGVK	PORNICNLSS	ICNDSAFFRG	EIMFQYDKES	TVPQNQHITN	120
	GTLTGVLSLS	ELNTLNCTFT	IKLNNTMNAC	AVIAALERVK	IRPMEHCCCS	VRIPCPSSPE	180
			RGPPFSSSQS ASSPAIDMPP				240 300
			TSSISDLENQ				360
65			GLQLNFSNTT				420
			LPSSLMNNLP NVTVTLKHIN				480 540
	VKDRRLNETI	CTCSHLTSFG	VLLDLSRTSV	LPAOMMALTE	ITYIGCGLSS	IFLSVTLVTY	600
70	IAPBKIRRDY	PSKILIQLCA	ALLLLNLVPL	LDSWIALYKM	QGLCISVAVF	LHYFLLVSFT	660
70			IRKYILKFCI				720 780
			VGYFCVIFLL FAWGPVNVTF			VAKENVRKOW	840
	RRYLCCGKLR	LAENSDWSKT	ATNGLKKQTV	NQGVSSSSNS	LQSSSNSTNS	TTLLVNNDCS	900
75	VHASGNGNAS LHFIEQM	TERNGVSFSV	ONGDVCLHDF	TGKQHMFNEK	EDSCNGKGRM	ALRRTSKRGS	960
		17 DNA seq					
		id Accession	n #: Eos se 811	daeuce			
80	1	11	21	31	41	51	
	1				 		60
	TTCAAGATAT	TCCTTGTCAT	CATTTGTCTT	CATGTCGTTC	TGGTAACATC	TTTACTGACG CCTGGAAGAA	120
0.5	GATACTGATA	ATTCCAGTTT	GTCACCACCA	CCTGAGGTTC	AAACAACAAG	CCTCAATGAT	180
85	GTTACTTTA	GCTTACTCCC	TTCAAACGAA	ACAGGCGTC	AACCCCAGAG	AAATATCTGC	240

		CTATTTGCAA					300
		GCACTGTTCC					360
		GTGAATTAAA TAATGTGTGC					420 480
5		ATAATACAAT					540
•		TGGAACACTG					600
		AGCTTCAGTG					660
		CATTTTCTTC					720
10		CCAAAGCTAC					780
10		CTCCAATAGG					840
		CTGCCATTGA					900
		TCTCCGGCAC					960
		CGAATGTCAA TTTCTGATCT					1020 1080
15		AGCCTAACCT					1140
10		ACATGCTGGC					1200
		TGAACTTTTC					1260
		GAGTGAATGC					1320
20		AGGTTTCTCT					1380
20		CGCTGATGAA					1440
		TTTTTGAAAC					1500
		ACGTCATATC					1560
		TCACATTAAA ACTTGGGCAG					1620
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		ACCTATCTAG					1800
		TTGGTTGTGG					1860
		AAAAGATCCG					1920
		TGCTGAACCT					1980
30		GCATCTCAGT					2040
	TGGATGGGCC	TAGAAGCATT	CCATATGTAC	CTGGCCCTTG	TCAAAGTATT	TAATACTTAC	2100
		ACATCCTTAA					2160
		TGACTATATC					2220
35		CGGATGACTT					2280
22		TCTGTGTGAT					2340
		GAATTAAAAA					2400
		GTATCGCTGG					2460 2520
		GACCAGTTAA TCATATTCAT					2520
40		TTTGTTGTGG					2640
••		GGGTCTCTTT					2700
					ATGGGAAAGG		2760
		WCW1G111WW					
		CTTCAAAGCG					2.00
45							
45	CTCAGAAGGA Seq ID NO:	CTTCAAAGCG 18 Protein	GGGAAGCTTA sequence	CACTTTATTG			2.00
45	Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: F	GGGAAGCTTA sequence Sos sequence	CACTITATIG	AGCAAATGTG	Α	2.00
45	CTCAGAAGGA Seq ID NO:	CTTCAAAGCG 18 Protein	GGGAAGCTTA sequence	CACTTTATTG			2.00
	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11	GGGAAGCTTA sequence Sos sequence 21	CACTITATIG	AGCAAATGTG	a 51 	
45 50	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH	CTTCAAAGCG 18 Protein cession #: H 11 VGRTEEVLLT	GGGAAGCTTA sequence Sos sequence 21 FKIFLVIICL	CACTITATIG 31 HVVLVTSLEE	AGCAAATGTG 41 DTDNSSLSPP	A 51 PEVETTSLND	60
	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH VTLSLLPSNE	CTTCAAAGCG 18 Protein cession #: H 11 VGRTEEVLLT TGVKPQRNIC	GGGAAGCTTA sequence cos sequence 21 FKIFLVIICL NLSSICNDSA	CACTITATIG 31 HVVLVTSLEE FFRGEIMPQY	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ	A 51 PEVETTSLND HITNGTLTGV	
	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH VTLSLLPSNE LSLSELKRSB	CTTCAAAGCG 18 Protein cession #: H 11 VGRTEEVLLT	GGGAAGCTTA sequence Cos sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE	CACTITATIG 31 HVVLVTSLEE FFRGEIMPQY AQSTLNCTFT	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC	A 51 PEVETTSLND HITNGTLTGV AVIAALERVK	60 120
	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11	GGGAAGCTTA sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ	CACTITATIG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP	AGCAAATGTG 41 DTDMSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL	60 120 180
50	CTCAGAAGGA Seq ID NO: Protein Acc WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPRATSFA QTHYSGTPPP	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPPDYSPVTH VKASFSSPTV	GGGAAGCTTA sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS	CACTITATIG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ	51 	60 120 180 240 300 360
	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVT WKASFSSPTV MINQVSRLLH	GGGAAGCTTA sequence Sos sequence 21 FKIFLVIICL NUSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA	CACTITATIG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSSQS ASSPAIDMEP TSSISDLENQ GLQLNPSNTT	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPNE VLQMEKALSL ISLTSPSLAL	60 120 180 240 300 360 420
50	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINGVSRLLH NTTTFVAQDP	GGGAAGCTTA sequence 21 KIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ	CACTTTATTG 31	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV	60 120 180 240 300 360 420 480
50	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTTPVAQDP FQDPSLENLS	GGGAAGCTTA sequence 21 FRIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV	CACTITATIG 31 HVVLVTSLEB PFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR	41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAC KGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSFSLAL SHDMELASRV PSQDELTVRC	60 120 180 240 300 360 420 480 540
50 55	CTCAGAAGGA Seq ID NO: Protein Acc NVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPRATSFA QTHYSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG	CTTCAAAGCG 18 Protein cession #: 8 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS	GGGAAGCTTA sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAB ELEKLQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI	CACTTTATTG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF	60 120 180 240 300 360 420 480 540 600
50 55	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTL5LLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINGVSRLLH NTTTPVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY	GGGAAGCTTA sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAPEKIRDY	CACTTTATTG 31	41 DIDNSSLSPP DKESTVPONO IKLINITMNAC IKSSIDLENO GIQLIPSITT LPSSLMINLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL SLTSPSSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM	60 120 180 240 300 360 420 480 540 600
50	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EVRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT	GGGAAGCTTA sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAPEKIRRDY WMGLEAFHMY	CACTTTATTG 31 HVVLVTSLEB FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY	41	51	60 120 180 240 300 360 420 480 540 600 660 720
50 55	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY YGLGSYGKPP	GGGAAGCTTA sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKIQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAPEKIRRDY WMGLEAPHMY MGSPDDFCWI	CACTITATIG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHE PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLIVENLITE CTCSHLISFG PSKILIQLCA LKLVKVFNTY NNNAVFYITV	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSG ASSPAIDMPP TSSISDLENQ GLQLNFSNTLP LPSSLMNNLP LVTVTLKHIN VLLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTURC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV	60 120 180 240 300 360 420 480 540 600
50 55	CTCAGAAGGA Seq ID NO: Protein Acc WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPRATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFPETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKKQ	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EVRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT	GGGAAGCTTA Sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSV VKDRRLNETI IAPEKIRDY WMGLEAFHMY MGSPDDFCMI DLRSIAGLTF	CACTITATIG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTII CTCSHLTSFG PSKILIQLCA LALVKVFNTY LLGITWGFAF	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLE UPSSLMNLE UPSSLMNLE LPSSLMNLE LPS	51	60 120 180 240 300 360 420 540 600 660 780
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPS EPPPYSPVTH VKASFSSPTV MINQVSRLLH NTTTPVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFY LGAQRKTSIQ	GGGAAGCTTA sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAB ELEKLQCDLQ NVPSIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRLNETI LISYVISSSV WMGLEAFHMY MGSPDDFCMI DLRSIAGLTF RRYLCCGKLR	CACTTTATTG 31	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLE UPSSLMNLE UPSSLMNLE LPSSLMNLE LPS	51	60 120 180 240 360 420 480 540 660 720 780 840
50 55	CTCAGAAGGA Seq ID NO: Protein Acc I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSP QFMFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFPIFIFYC GKQHMFNEKE	CTTCAAAGCG 18 Protein cession #: I 11	GGGAAGCTTA sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKIQCDLO NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRDY WMGLEAFHMY MGSPDDFCMI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL	CACTTTATTG 31	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLE UPSSLMNLE UPSSLMNLE LPSSLMNLE LPS	51	60 120 180 240 360 420 480 540 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINDOVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKPP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequ	GGGAAGCTTA sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAPEKIRRDY WMGLEAPHMY NGSPDDFCMI RRYLCCGKLR LRRTSKRGSL LENCE	CACTTTATTG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITY NNNAVFYITY LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLE UPSSLMNLE VLLDLSRTSV ALLLLNLVFL IRKYILKFCL VGYFCVIFLL PAWGPVNVTF	51	60 120 180 240 360 420 480 540 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LMKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH HTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession	GGGAAGCTTA sequence Cos sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAB ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAPEKIRRDY WMGLEAFHMY NGSPDDFCMI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LERTSKRGSL	CACTTTATTG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITY NNNAVFYITY LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLE UPSSLMNLE VLLDLSRTSV ALLLLNLVFL IRKYILKFCL VGYFCVIFLL PAWGPVNVTF	51	60 120 180 240 360 420 480 540 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTPVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKPP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession Lence: 1.36	GGGAAGCTTA sequence Cos sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAB ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLL LERTSKRGSL LECCE 1 #: Eos second	CACTTTATIG 31 HVVLVTSLER PFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGPAF LAENSGNAST HFIEQM Quence	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTL LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSFELAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIRNTL NGDVCLHDPT	60 120 180 240 360 420 480 540 660 720 780 840
50556065	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTTY LHYFLLVSFT YGLGSYGKPP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 136	GGGAAGCTTA sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKIQCDLO SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAPEKIRRDY WMGSLEAPHMY MGSPDDFCMI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LENCE 1#: EOS 5e 21	CACTTTATTG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITY NNNAVFYITY LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLE UPSSLMNLE VLLDLSRTSV ALLLLNLVFL IRKYILKFCL VGYFCVIFLL PAWGPVNVTF	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV MYLFAIPNTL	60 120 180 240 360 420 480 540 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LMKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSPT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession lence: 136 11	GGGAAGCTTA sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAB ELEKLQCDLQ NVPSIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYVISSSV WMGLEAFHMY NGSPDDFCMI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL lence 1 #: Eos se 045 21	CACTTTATTG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGPAF LAENSGNAST HPIEQM QUENCE 31	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKPCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPNP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTY LDSWIALIYK VGWGVPAVVV NVSMFIVVLV MYLFAIFNTI NGDVCLHDFT	60 120 180 300 360 420 540 600 720 780 840 900
50556065	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINQUSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ DSCNGKGRMA 19 DNA sequid Accession cence: 130 11 CTGTCAGGCA	GGGAAGCTTA sequence Cos sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LERTSKRGSL LERTSKRGSL LERTSKRGSL 1 #: Eos se 045 21 GTGTGGCCAT	CACTTTATIG 31 HVVLVTSLEB PFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLISFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HPIEQM QUENCE 31 GTTGGCAGAA	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTI- LPSSLMINLP NVIVTLKHIN VILLDLSRTSV ALLLLNLVPL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSFSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG	60 120 180 240 360 420 540 600 720 780 840 900
50556065	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAGCG 18 Protein 28sion #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTPVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY YGLGSYGKPP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq id Accession ience: 136 11 CTGTCAGGCA TCCTTGTCAT	GGGAAGCTTA Sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAPEKIRRDY MGSLEAPHMY MGSPDDFCMI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LRRTSKRGSL 10 #: Eos se 21 CHICAGCCAT GTGTGGCCAT CATTGTCTT	CACTITATIG 31 HVVLVTSLER FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HPIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINTMNAC RGPPFSSSG ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLNLVFL FRKYLKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VSMGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA	60 120 180 300 360 420 540 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acci	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINQUSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ DSCNGKGRMA 19 DNA sequid Accession cence: 130 11 CTGTCAGGCA	GGGAAGCTTA sequence 21 KIFLVIICL NLSSICNDSA TYPIMCATAS TYPIMCATAS ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYVISSSV VKDRRLNETI LAFEKIRRDY WMGLEAPHMY MGSPDDFCMI LRRTSKRGSL LRRTSKRGSL LRRTSKRGSL 18: EOS SE 045 21 GTGTGGCCAT GTCACCACCA	CACTTTATTG 31 HVVLVTSLEB FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPROVIDIVN QRLLKVVDDI ANLTVRNLTR CTCSHLTSFR CTCSHLTSFR CTCSHLTSFR LALVKVFNTY NNNAVFYITV NNNAVFYITV LLGITWGFAF LAENSGNAST HPIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVVI NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC	60 120 180 240 360 420 480 600 600 720 780 840 900
50556065	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTPVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKPP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession lence: 130 11 CTGTCAGGCA TCCTTGTCAT ATCAGGTTA ATCAGGTTTA ATGAGGTTGA CAGAAAAAAA	GGGAAGCTTA sequence Cos sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKORRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCMI DLRSIAGLTF RRYLCCGKL LERTSKRGSL LENCE 1 #: Eos se 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAGC	CACTTTATTG 31 HVVLVTSLER PFRGEIMPQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGPAF LAENSGNAST HPIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAATG ATAGTAAAAA	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTI LPSSLMINLP NVIVILKHIN VLLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAGT CCTTCAATGC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSFELAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIRNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTCAGGCGTC	60 120 180 240 360 420 480 660 720 780 840 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acci MVFSVRQCGH VTL5LLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil I ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCTCCAGA TCAAACGAAA AAACCCCAGA	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINDOVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKPP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 130 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTTA ATGAGATAAA GAAATAATCTG	GGGAAGCTTA sequence 21 KifiviicL	CACTTTATIG 31 HVVLVTSLEB FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVF1IT NNNAVF1IT ANNAVF1T LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGGTC CCTGCTAAAT CTCAATGAAAA TCTAATTGCA	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFL ERMGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG ATGACTCAGC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSIAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA	60 120 180 300 360 420 480 540 660 720 780 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acci WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LSLSELKRSE LSPNEHCCCS SQVPRATSFA QTHYSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Acc Coding sequil ATGGTTTTCT TTCAAGATAT GGTACTGATA CCCTCCTCCA TCAAACGAAA AAACCCCAGA GGTGAGATCA	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LMKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession lence: 136 11 CTGTCAGGCA TCCTTGTCAT ATGAGGTTGA CAGAAAAAAC GAAATATCTG TGTTTCAATA	GGGAAGCTTA sequence Cos sequence 21 FKIFILVIICL NLSSICNDSA TYPIMCATAB ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYVISSSV WKGRLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LENCE 1 #: Eos se 045 21 GTGTGGCCAT CAATTTGTCA AACAACAAGC TAAAATCACTC CAATTTGTCA TGATAAAGAA	CACTTTATTG 31 HVVLVTSLEB FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMENSIGTIT ANLTVRNLTR CTCSHLTSFG FSRILIGCA LALVKVFNTY NNNAVFYITV LIGITWGPAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA TCTAATTGCA AGCACTGTTC	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNILP NVTVTLKHIN VLLDLSRTSV VLLDLSRTSV IRKYILKFCI VGYFCVIFLL PAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TTGGTAACATC TATCTGTTGT TTACTTTAAG CCTCAATGC ATGACTCAGC CCCCAGAATCA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALIYM VGWGVPAVVV NVSMFIVVLV MYLFAIPNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGGA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC TTCAGGCGTC TTCAGGCGTC ATTTTTTAGA ACATATAACG	60 120 180 240 360 420 540 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ LGAQRKTSIQ 19 DNA sequid Accession lence: 130 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTGA CAGAAAAAAC GAAATATCTG TGTTTCAATA TTAACTGGAGT TAACTGGAGT TTAATTGGAGT TTAATTGGAGT TTATTGAGGT TTATCAGGTT TAACTGGAGT TTAATTGGAGT TTAATTGGAGT TTAATTGGAGT TTATTCAATA TTAACTGGAGT	GGGAAGCTTA sequence Cos sequence 21 FRIFILVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA LISYVISSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF REYLCCGKLR LRRTSKRGSL LERTSKRGSL 1	CACTTTATIG 31	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTI- LPSSLMINLP NVIVILKHIN VILLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGA AACGCTCAGA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSFSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA	60 120 180 240 360 420 540 600 720 780 840 900 60 120 180 240 360 420 360 420
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINDOVSRLLH NTTTPVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKPP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 130 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATTCAGGTTT ATTCAGGTTA TTCAGTTT TGTTCAATA TAACTGGAGT TATTCAATTA TAACTGGAGT TCCTTTCAATTA TAACTGGAGT TCCTTTAAGTTA TAACTGGAGT TCCTTAAGTGA	GGGAAGCTTA sequence 21 Kifiviicl NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAPEKIRRDY MMGLEAPHMY NGSPDDFCMI LRSTAGLTF RRYLCCGKLR LRRTSKRGSL LENCE 1 #: EOS SE 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAGGC TAAAATTGTCA TGATAAAGAAA CCTGTCTCTCA GACTTACTTT GACTTACTTT	CACTTTATIG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFITY NNNAVFITY NNNAVFITY CTCSHLTSFG GTTGGCAGAA CATGTTCGTTC CCTGCTAAAT CTCAATGATG ATGGTAATAA ATGATTTGCA AGGCACTGTTC AGTGAATTAA ATAATGTGTG ATTGGAATTAA ATAATGTGTG ATGGAATTAA ATAATGTGTG ATGGAATTAA ATAATGTGTG	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGA CCTCCAGAA ACGCTCAGA CTACAGAA ACGCTCAGA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSIAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALTKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA GGCCCAAAGG	60 120 180 300 360 420 480 540 660 720 780 900 60 120 180 240 300 420 420 420 420
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acci WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LIPMEHCCCS SQVPKATSFA QTHYSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QCKPIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil I ATGGTTTTCT TTCAAGATAT CCTCCTCCA TCAAACGAAA AAACCCAGAA GGTGAGATCA AATGGCACCTA ACCTGCACA ACCTGCACA ACCTGCACA ACCTGCACA ACCTGCACA ACCTGCACAT ACCCTGCACA ACCTGCACAT ACCCTGCACA ACCTGCACAT ACCCTGCACA ACATTAAATT	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINOVSRLLH MITTTVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSPT YGLGSYGKFS UAKENVRKQW DSCNGKGRMA 19 DNA seq id Accession Lence: 13d 11 CTGTCAGGCA TCCTTGTCAT ATCAGGTTA ATCAGGTTA ATCAGGTTA TATCAGGTTA TATCAGGTTA TATCAGGTTA TGAATATCTG TGTTTCAATA TAACTGGAGTA GTACATTCAC	GGGAAGCTTA sequence 21 FKIFLVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI 1APEKIRRDY WMGLEAPHMY MGSPDDFCMI LRRTSKRGSL LRRTSKRGSL LRRTSKRGSL 1015 GTGTGGCCAT CATTACTAT TATAAAGAA CCTTACTTAT TATAAAGAA CCTTACTTT AATAAAACTG AACTACTTT AATAAAACTG GACTACTTT AATAAAACTG	CACTTTATTG 31 HVVLVTSLEB FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPROVIDIVA QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVF1IT LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAATACAA AGCACTGTTC AGTGAATTAA AGCACTGTTC AGTGAATTAA ATAATGTG	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNPSNTT LPSSLMNNLP NVTLVTLKHIN VLLDLSRTSV ALLLINLVPL IRKYILKPCI VGYFCVIPLL FAMGPVFFV ERNGVSFSVQ 41 CTGAAGAAGT TGATACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGC CCCAGAATCA AACGCTCAGA CTACAGCAGA TGAATGCATG	SI PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTR LDSWIALYKM VGWGVPAVVV NVSMFIVVLV NYSMFIVVLV STACKACACACACACACACACACACACACACACACACACAC	60 120 180 360 420 360 420 780 840 900 60 120 180 240 300 480 540 600
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acci WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LSLSELKRSE LSPMENCCCS SQVPKATSFA QTHYSGTPPP GSLEPNLAGE AVIRNASSP QFNFFETPAL VFWDLGRNGG ITYIGGLSS QGLCISVAVF TILITISPDN QLCRIKKKG GGLGISVAVF TILITISPDN QLCRIKKKG Seq ID NO: Nucleic Ac: Coding sequ 1 ATGGTTTTCT TTCAAGATAT TGTAAGGATAT CCCTCCCAA ACACCAGA GGTGAGATCA AAACCCCAGA AGGTGAGATCA AATGGCACCT ACCCTGCAAA ACATTAAATT GCCGCTTTGG	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTFTVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ UAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 130 11 CTGTCAGGCA TCCTTGTCAT ATTCAGTTTA ATTCAGTTTA ATTCAGTTGA CAGAAAAACC GAAATATCG GAAATATCG TGTTTCAATA TAACTGGAGT TCCTTAGTAA TAACTGGAGT CCCTAAGTGA AAAGAGTAAAA AAAGAGTAAAA AAAGAGTAAAA	GGGAAGCTTA sequence Cos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKORRINETI IAPEKIRRDY WMGLEAFHMY NGSPDDFCMI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LRRTSKRGSL Jence 1 #: Eos se 045 21 GTGTGGCCAT GTCACCACCA AACAACAAGC TAAAATCACT CAATTTGTCTT AATAAAACTG GACTTACTTT AATAAAACTG GATTCGACCAC	CACTTTATIG 31 HVVLVTSLEB FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAST HPIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTAC CCTGATAC CCTGCTAAAT CTCAATGATG ATAGTAAAAA ATCGTATCAA ATGAAATATCAA ATGAAACACT	AGCAAATGTG 41 DTDNSSLSPP DKBSTVPQNQ IKLINTMNAC KGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLLNLVFL IRKYILKFCI VGYFCVIFLL PAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTCAATGC ATGACTCAGA CTACAGCAGA ACGCTCAGA TGAATGCATG GCTGCTGTTC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV NYSMFIVVLV MYLFAIPNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTTATGCC CTTATTTTAGA GCCCAAAGC GCTCAACAAA GGCCCAAAGC TGCTGCAATA TGTCAGGATA	60 120 180 240 360 420 540 600 720 780 840 900 60 120 180 300 300 420 480 540 660
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acci WYFSVRQCGH VTLSLLPSNE LSLSELKRSBE IRPMEHCCCS SQVPKATSFA QTHYSGTPPP GSLEPNLAGE AVIRWASSP QFNFFETPAL VFWDLGRINGG ITYIGOGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFFIFIPYC GKQHMFNEKB Seq ID NO: Nucleic Ac: Coding sequity I ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCTCCA TCAAACGAAA AAACCCCAGA AAACCCCAGA GGTGAGATCA ACATTAAATT GCCCTTTGG CCCTTGCCCTT	CTTCAAAGCG 18 Protein cession #: I 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession lence: 130 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTGA ATTCCAGTTGA ATTCCAGTTGA CAGAAAAAAC GAAATATCTG TGTTTCAATA TAACTGGAGT CCCTAAGTGA CCCTCAGGAAAAC CCTCCCCAGA	GGGAAGCTTA sequence Cos sequence 21 FRIFIVIICL NLSSICNDSA TYPIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLOVSLETQ LISYVISSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LERTSKRGSL LERTSKRGSL 1 #: Eos se 045 21 GTGTGGCCAT GATTTGTCTT GTCACCACCA AACAACAGC TAAAATCACT TAAAATCAC TGATAAAGAA CCTGTCTCTTA AACTAACAAC GATTGGACCA AGAGTTGGGA	CACTTTATIG 31	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTI- LPSSLMINLP NVIVTLKHIN VILLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGC CCCAGAATCA AACGCTCAGA CTACAGCAGA TGAATGCATG GTGACCTGCA GTGACCTGCA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSFELAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGMGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GGTCAACAAAA GGCCCAAAGC TGCTGCAATA TGTCAGGATA GGATCCCATT	60 120 180 240 360 420 540 600 600 720 780 840 900 60 120 180 240 360 420 360 420 540 600 600 600 600 600 600 600 600 600 6
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acci	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WKASFSSPTV WKNOVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFS VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession Lence: 136 11 1 CTGTCAGGCA TCTCTGTCAT ATGAGTTAA TATGAGTTAA TATGAGTTAA TATGAGTTAA TAACTGGAGT TTTCAATA TAACTGGAGT GAAATATCTG GGTACATCAC AAAGAGTAAA CCTCCCCAGA CTGACCATCC	GGGAAGCTTA sequence 21 KifiviicL Sequence 21 KifiviicL NLSSICNDSA TYPIMCATAS ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYVISSSV VKDRRLNETI LAFEKIRRDY WMGLEAPHMY MGSPDDFCMI LAFEKIRRDY MGLEAPHMY MGSPDDFCMI LAFTSKRGSL LRRTSKRGSL LRRTSKRGSL 18: EOS SE 14: EOS SE 15: EOS SE 16: EOS SE 17: EOS SE 17: EOS SE 17: EOS SE 18: EOS	CACTTTATIG 31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPROVIDIVN QRLLKVVDDI ANLTVRNLTR CTCSHLTSFC FSRILIQLCA LALVKVFNTY NNNAVFYITV NNNAVFYITV LIGITMGFAF LAENSGNAST HPIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAA ATGTGAATTAA ATGTGAATTAA ATGGAACACT AAGGTTCAGT CCCATTTCTT AGTTTTTTT	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNPSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FAMGPVTFF ERNGVSFSVQ 41 CTGAAGAAGT TGATGACTTCAATGC ATGACTCAGC CCCAGAATCA AACGCTCAGA CTACAGCAGA TGAATGCATGC GTGACTGCA GCTGCTGTCA GCTGCTGCA CCAGCCAATC	SI PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVVV NVSMFIVVVV STATE TTTACTGACG CCTGGAAGGA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATCTTTTTAGA ACATATAACG GCTCAACAAAA GGGCCCAAAGC TGCTGCAATA TGTCAGGATA GGATCCCATT CATCCCATT CATCCCATT CATCCCATT	60 120 180 360 420 540 600 720 780 900 60 120 180 240 360 480 540 660 720 780
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acci WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LSLSELKRSE LSTEPNLAGE AVIRVASTPPP GSLEPNLAGE AVIRVASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil ATGGTTTTCT TTCAAGATAT GCTACTCCA TCAAACGAAA AAACCCCAGA AGTGGAGATCA AATGGCACCT ACCTGCCAT ACCTGCCAT GCCGCCTTTGG CCCTCCCTTTGGTCTTGGTGTCTTGGTGTCTTGGTGTCTTGGTGTCTTGGTGCTCGGGGTGCTCGGGGTGCTCGGGGTGCTCGGGGTGCTCGGGGTCCTTCGGTGGT	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LMKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession lence: 136 11 CTGTCAGGCA TCCTTGTCAT ATGAGGTTGA TATCCAGTTT ATGAGGTTGA CAGAAAAAC GAAATATCTG TGTTTCAATA TAACTGGAGT TCCTTAGTGAT TAACTGGAGT CCTAAGTGA GTACATTCAC AAAGAGTAAA CCTCCCCAGA ACTGCATCC CCACTGTGCT	GGGAAGCTTA sequence cos sequence 21 FKIFILVIICL NLSSICNDSA TYPIMCATAB ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYVISSSV VKDRRLNETI LISPKIRRDY WMGLEAFHMY NGSPDDFCMI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LRRTSKRGSL 1 GTGTGGCCAT CAATTTGTCA TGATAAGGAA CCTGTCTCTA GACTTACTCA TGATAAGCA AGGATTGGGC AGGATTGGGCA AGGATTGGGCCA TGATAAGCA AGGATTGGGCCA AGGATTGGGCCA AGGATTGGGCCA AGGATTGGGCCA AGGATTGGGCCA AGGATTGGGCCA AGGATTGGGCCA AGGATTGGGCCA AGGATTGGGCCA ATTCCCAGGTC	CACTTTATTG 31 HVVLVTSLEB FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSRILIGCA LALVKVFNTY NNNAVFYITV LIGITWGFAF LAENSGNAST HFIEQM 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA ATGAAATTACAA ATGAATTACAA ATGAATTACAA ATGAATCAA ATGGAACACT AAGCTTCAGTTC CCAATGTTC CCAATGTTC AGTGAATTAA ATGAATCAA ATGAATCAA ATGAACACT AAGCTTCAGTTC CCAATGTTCTC CCCAATGTTC CCCAATGTT	AGCAAATGTG 41 DTDNSSLSPP DKESTVPQNQ IKLINITMAG RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNILP NVTVTLKHIN VLLDLSRTSV ALLLLINLVFL IRKYILKFCI VGYFCVIFLL PAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TTGGTAACATC ATGACTCAGC ATGACTCAGC ATGACTCAGG ATGACTCAGG CTACAGCAGA TGAATGCATG GCTGCTGTTC GTGACCTGCCA CCAGCCAATC CCTCTTTTGC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSFELAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGMGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GGTCAACAAAA GGCCCAAAGC TGCTGCAATA TGTCAGGATA GGATCCCATT	60 120 180 240 360 420 540 660 720 780 840 900 60 120 360 420 480 540 660 720 780 840 840 840

	CCCCAGCCTT	CAGCTCCCAT	AGCTTCCAGC	CCTGCCATTG	ACATGCCCCC	ACAGTCTGAA	960
	ACGATCTCTT	CCCCTATGCC	CCAAACCCAT	GTCTCCGGCA	CCCCACCTCC	TGTGAAAGCC	1020
	TCATTTTCCT	CTCCCACCGT	GTCTGCCCCT	GCGAATGTCA	ACACTACCAG	CGCACCTCCT	1080
_			CACCAGCAGT				1140
5			GGGCAGCCTG				1200
			TTCCCCGCCT				1260
			TGGCCTACAG				1320
			GGCTGTGATC				1380 1440
10			TGCAAATCTT TCTTCCTTCA				1500
10			TCAGTTCAAT				1560
			TCTGATCAGC				1620
			AAACGTGACA				1680
			TGTATTTTGG				1740
15			TGTCAAAGAC				1800
			CGTTCTGCTG				1860
			CATTACATAT				1920
			CATAGCTTTT				1980
20			TGCTCTGCTT				2040
20			GCAAGGCCTC				2100 2160
			ATGGATGGGC CATCCGAAAA				2220
			GACCATCATC				2280
			CAATGGTTCA				2340
25			GGTGGGATAT				2400
	ATGTTCATTG	TGGTCCTGGT	TCAGCTCTGT	CGAATTAAAA	AGAAGAAGCA	ACTGGGAGCC	2460
	CAGCGAAAAA	CCAGTATTCA	AGACCTCAGG	AGTATCGCTG	GCCTTACATT	TTTACTGGGA	2520
	ATAACTTGGG	GCTTTGCCTT	CTTTGCCTGG	GGACCAGTTA	ACGTGACCTT	CATGTATCTG	2580
20			ACAAGGATTT				2640
30			GAGGCGGTAT				2700
			TGCTACTAAT				2760 2820
			CTTACAGTCA AGTACAGGCA				2820
			TCAGAATGGA				2940
35			GGAAGATTCC				3000
-			CTTACACTTT				
	Seq ID NO:	20 Protein	sequence:				
40	Protein Acc	cession #: 1	Eos sequence	2			
40	1	11	21	31	41	51	
	1	1	1	1	1	1	
	MVFSVRQCGH	 VGRTEEVLLT	 FKIFLVIICL	 HVVLVTSLEE			60
	MVFSVRQCGH PSSNEVETTS	 VGRTEEVLLT LNDVTLSLLP	SNETEKTKIT	HVVLVTSLEE IVKTFNASGV	KPQRNICNLS	SICNDSAFFR	120
45	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE	VGRTEEVLLT LNDVTLSLLP STVPQNQHIT	SNETEKTKIT NGTLTGVLSL	HVVLVTSLEE IVKTFNASGV SELKRSELNK	KPQRNICNLS TLQTLSETYF	SICNDSAFFR IMCATAEAQS	120 180
45	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL	VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI	SNETEKTKIT NGTLTGVLSL AALERVKIRP	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI	KPORNICNLS TLOTLSETYF PCPSSPEELG	SICNDSAFFR IMCATAEAQS KLQCDLQDPI	120 180 240
45	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP	VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS	120 180 240 300
45	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS	VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSPVTHNVP SFSSPTVSAP	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP	120 180 240
	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS	VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL	120 180 240 300 360
45 50	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ	VGRTEEVLLT LMDVTLSLLP STVPONQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE	120 180 240 300 360 420
	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTPTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ MSIGTITLPS TVRNLTRNVT	VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW	HVVLVTSLBE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN FVNASSFNTT FFETPALFQD DLGRNGGRGG	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP GVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC	120 180 240 300 360 420 480 540
	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA	SNETEKTKIT NGTLITGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK	120 180 240 300 360 420 480 540 600 660
	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL	VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS	SNETEKTKIT NGTLTGVLSL AALERVKIRD VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TPVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL	120 180 240 300 360 420 480 540 600 660 720
50	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTPTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVPNTYIRK	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVMASSFNTI FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAP FLLLVSPTWMG GSYGKFPNGS	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGETQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHWYLAL PDDFCWINNN	120 180 240 300 360 420 480 540 600 660 720 780
	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLINLVFLLDS YILKFCIVGW FCVIFLLNVS	SNETEKTKIT NGTLITGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC	HVVLVTSLBE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSEVITNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL SVSDNGCSVKD SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG	120 180 240 300 360 420 480 540 660 720 780 840
50	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILLQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW GCVIPLINVS GFVNVTFMYL	SNETEKTKIT NGTLITGVLSI AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFN WIALYKMQGL GVPAVVTII MFIVVLVQLC FAIFNTLQGF	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL FIKKKQLGA FIFIFYCVAK	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKO SVTLVTVIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVEKQWRRY	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFILIG LCCGKLRLAE	120 180 240 300 360 420 480 540 660 720 780 840 900
50	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT TSHLTSFGVLL ILLQLCAALL VKVPNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNV GEVNVTFMYL GLKKQTVNQG	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGLA SENSTNSTTL	KPQRNICNLS TLQTLSTYF PCPSSPEELG DYSPVTINVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP SVENLSLIS WSDNGCSVKO SVTLVTYIAP FLLVSFTMMG GSYGKPPNGS QRKTSIODLR ENVEKQMERY LVNNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGBIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRIAE SGNGNASTER	120 180 240 300 360 420 480 540 660 720 780 840
50 55	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT TSHLTSFGVLL ILLQLCAALL VKVPNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNV GEVNVTFMYL GLKKQTVNQG	SNETEKTKIT NGTLITGVLSI AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFN WIALYKMQGL GVPAVVTII MFIVVLVQLC FAIFNTLQGF	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGLA SENSTNSTTL	KPQRNICNLS TLQTLSTYF PCPSSPEELG DYSPVTINVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP SVENLSLIS WSDNGCSVKO SVTLVTYIAP FLLVSFTMMG GSYGKPPNGS QRKTSIODLR ENVEKQMERY LVNNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGBIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRIAE SGNGNASTER	120 180 240 300 360 420 480 540 660 720 780 840 900
50	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLMCTFTIKL VCLADHPRGP PQPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKHITSFGVLL ILLQLCAALL VKVENTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE LSDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW GFVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WTALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSTYF PCPSSPEELG DYSPVTINVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP SVENLSLIS WSDNGCSVKO SVTLVTYIAP FLLVSFTMMG GSYGKPPNGS QRKTSIODLR ENVEKQMERY LVNNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGBIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRIAE SGNGNASTER	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TIMCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT TSHLTSFGVLL ILLQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MFIVVLVQLC FAIFMTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSTYF PCPSSPEELG DYSPVTINVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP SVENLSLIS WSDNGCSVKO SVTLVTYIAP FLLVSFTMMG GSYGKPPNGS QRKTSIODLR ENVEKQMERY LVNNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGBIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRIAE SGNGNASTER	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TIMCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT TSHLTSFGVLL ILLQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GEVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WITALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMPNEKEDS LUENCE #: NM_005 3117	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFHLY LTISPDHYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTIL CNGKGRMALR	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSEVITAVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSPTMMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNICSVHA RTSKRGSLHF	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGETQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHWIAL PDDFCWINNN SIAGLTFILG LCCGKLRLAE SGNGNASTER IEQM	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TIMCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT TSHLTSFGVLL ILLQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MFIVVLVQLC FAIFMTLQGF VSSSNSLQS QHMFNEKEDS uence n #: NM_005	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSTYF PCPSSPEELG DYSPVTINVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP SVENLSLIS WSDNGCSVKO SVTLVTYIAP FLLVSFTMMG GSYGKPPNGS QRKTSIODLR ENVEKQMERY LVNNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGBIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRIAE SGNGNASTER	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLMCTFTIKL VCLADHPRGP PQPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILLQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1	VGRTEEVLLT VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SIMMNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq	SNETEKTKIT NGTLTGVLSIL NGTLTGVLSIL VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTIL MFIVVLVQLL FAIFNTLOGF VSSSSNSLQS QHMFNEKEDS LUENCE n #: NM_005 3117 21	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CTSVAVPLHY LTISPDNYGL RIKKKQLGA FIFIFYCVA SSNSTNSTTL CNGKGRMALR 756.1	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP QVSRLLHSPP SVSLNTLSLIS WSDNGCSVKD SVTLVTYIAP FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVEKQMERY LVNNDCSVHA RTSKRGSLHF	SICNDSAFFR IMCATAEAGS KAQCDLQDPI SPIGBIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLIG LCCGKLRLAE SGNGNASTER IEQM	120 180 240 360 420 540 660 720 780 840 960
50 55	MVFSVRQCGH PSSNEVETTS GEMMPOYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL UKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GEVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITV GYPAVVVTII MFIVVLVQLC FAIFNTLQGP VSSSSNSLQS QHMFNEKEDS LUCIC M#: NM_005 3117 21 CGGGCAGGTGT	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT DIGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGGT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVIENVP SFSSPTVSAP QVSRLHSSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVYIAF FLLVSFTMMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGETOPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG CTCGCGGTCA	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTTT	SNETEKTKIT NGTLITGVESI NGTLITGVESI VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GUPAVVTII MFIVVLOLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21 CGGCAGGTGT CGGCAGGTGT	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGGSVKD WSDNGGSVKD SVTLVTYIAF FLLVSPTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCCACTTT ATGTTGGCAG	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA	120 180 240 360 420 480 660 720 840 900 960
50 55 60	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILLQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDMSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG GCTCAGCCCGGGTCA GTTTTACTGA	VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD UTLKHINPSQ DLSRTSVLPA LLINLVFILDS YILKFCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT	SNETEKTKIT NGTLITGVLSI NGTLITGVLSI VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE n #: NM_005 3117 21 CGGGCAGGTGT CTCTGTCAGG ATTCCTTGTC	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVMASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAP FLLVSPTWMG GSYGKFPNGS QRKTSIQDLR ENVEKQMERY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTIT TCTCCACTIT ATGTTGGCAG TTCATGTGGT	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGETOPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA	120 180 240 360 420 480 660 720 840 900 960
50556065	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGAAG GTCAGTTTTG	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YLLKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCCTCCTC	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GUPAVVTII MFIVVLOLC FAIFNTLQGP VSSSSNSLQS QHMFNEKEDS uence n #: NM_005 3117 21 CGGCAGGTGT CTGTCAGG ATTCCTGTCAGT TAATTCCAGT CAATAAGGTT	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GGAACACAA	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD WSDNGCSVKD SVTLVTVIAF FLLVSPTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCAATGTCGT CACCTGCTAA	SICNDSAFFR IMCATAEAGS KAQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA AATTATCTGTT TGTTACTTTA	120 180 240 360 420 540 660 720 780 840 960
50 55 60	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDMSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGATG AGCTTACTCC	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accessio	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI NGTLTGVKSIR VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFMEKEDS LUCIC HE NM_005 3117 CGGCAGGTGT CTCTGTCAGG ATTCCTGTC TAATTCCAGT TAATTCCAGT AACGAAAAA	HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR RTSKRGSLHF 41 TCTCCACTIT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATAGTAAA	SICNDSAFFR IMCATAEAGS IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACCTTTA AACCTTCAAT	120 180 240 360 420 540 660 720 780 840 960 120 180 240 300 360
50556065	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILLQLCAALL VKVENTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GGTTCAGGCGG	VGRTEEVLLT VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCUIPLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCCTCCTC CTTCAAACGA TCAAACCCA	SNETEKTKIT NGTLTGVLSIL NGTLTGVLSIL NGTLTGVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLOGF VSSSSNSLQS QHMFNEKEDS LUCIC H#: NM_00S 3117 - 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTA AACAGAAATATC	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKOLGA FIFIFYCVAK SSMSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACACAA ACTAAAATCA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP QVSRLLHSPP STVADPANL PSLENLSLIS WSDNGCSVKD SVYLVTYIAF FLLVSFTMMG GSYGKPPNGS QRKTSIQDLR RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCAATGTCAT CACCTGCTAA GCCTCAATGA CATCTATTTG	SICNDSAFFR IMCATAEAQS KAQCDLQDPI SPIGELQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA CAATGACTCA	120 180 240 360 420 660 660 780 780 840 960 120 180 240 300 360 420
50556065	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA AGCTTACTCG AGCTTACTCG GCTTCAGGCG GCATTTTTA	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LINLVFLLDS YILKFCIVGW FCVIFLLNVS GEVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGGA CCCCTCCTC CTTCAAACGA CCCCTCCTC CTTCAAACGA TCAAACCCCA GAGGTTGAGGTT	SNETEKTKIT NGTLTGVLSIL NGTLTGVLSIL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY GYPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LUCIC CTGTGTGGG ATTCCTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA GAGAAAATATC CATGTTTCAA	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFHLY LTISPDHYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCAA TGCAATTTGT TATGATAAAG	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTENVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP STVANDPANL PSLENLSLIS WSDNGCSVKO SVTLVTYIAF FLLVSFTMMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTTGT TCACTGCTTA GCCTCAATGA CTATATTAG CAACACCTGTTATTATC AAAGCACTGT	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGETOPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA ACTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT TCATGCATCA TCACCAGAAT	120 180 240 360 420 540 660 780 840 900 960 120 180 360 420 360 420
50556065	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIKL AVFYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTCAGTATG AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAA	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTCA ACCCCTCCTC CTTCAAACGA TCAAACCCCA GGATGGTAGCAC CGAATGGCAC	SNETEKTKIT NGTLTGVLSL NGTLTGVLSL VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVTII MFIVVLOLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LICE M#: NM_00S 3117 21 CGGGCAGGTGT CTGTCTCAGG ATTCCTTGTC TAATTCCAGT TAATTCCAGT CAATGAGAAAAA GAGAAAAAA CGAGAAAAAA CTTAACTGGA	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCAC GGAACAGAAA ACTAAAATCA TGCAATTTGT TGTGAATTTGT TGTGAATTTGT TGTGAATTGTAAAG GTCCTGTCTC	KPQRNICNLS TLQTLSSTYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTVIAF FLLVSFTWMG GSYGKFPNGS QKKTSIQDLR ENVEKQWRRY LVNNDCSVHA TTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA CCTCTAATGA CCTCTAATGA CCTCTATTGA CATCTATTG TAAGTGAATT TAAGTGAATT	SICNDSAFFR IMCATAEAGS KAQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGGAT AAAACGGTCA	120 180 240 360 420 540 660 720 780 960 120 180 240 360 420 420 540
5055606570	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILLQLCAALL VKVPNTYIRV NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG GCTCCAGGCGG AGCTTACTGA TCCCTGGAGG AGCTTACTGA GTTTACTGA GTCTCAGGCG GCATTTTTA CAACATATAA GAGCTCAACA	VGRTEEVLLT VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YTLKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCAG GGATGGTTTT CGTTCAAGAT AAGATACTGA CCCCTTCTTC CTTCAAGAT AAGATACCCA GAGGTGAGAT CGAATGGCAC AAACCCTGCA	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI NGTLTGVKSIR VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN QMMALTFITY WTALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLOGF VSSSNSLQS QHMFNEKEDS LECC TAITOLOGF CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA GAGAAATATC CATGTTTCAA GAGAAATATC CATGTTTCAA GAGAAATATC CATGTTTCAA CATGAAGAA AACCTTAACTGGA AACCCTAAGT	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKQLGA FIFIFYCVA SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGC ATCATTTGTC ATCATTTGTC TTGTCACCAC GAAACACAA ACTAAAATCA TGCAATTTGT TATGATAAAG GTCCTGTCTC GAGACTTACT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP QVSRLHSPS QVSRLHSPS VSDRGCSVKD SYTLVTIAP FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVEKQMERY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT TCTCCACTTT ATGTTGGTAG CCTCAATGA CCTCAATGA CATCTATTTG AAAGCACTGT TAAAGTGAATT TAAAGTGAATT TTATAATGTG	SICNDSAFFR IMCATAEROS KAQCDLQDPI SPIGBIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTPLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAGAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA TGAATGACTCA TCAATGACTCA TGCTACAGCA	120 180 240 360 420 660 660 780 900 960 120 180 240 300 480 540 600
50556065	MVFSVRQCGH PSSNEVETTS GEIMPOYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG GTCTGCGGGTCA GTTTTACTGA GTCAGTTTTG AGCTTACTCC GCTTCAGGOG GCATTTTTTA GCACATATAA GAGCCCAAA	VGRTEEVLLT VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMMNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GEKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession cence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGGA CCCCTCCTC CTTCAAACGA TCAAACGA TCAAACGA AGACCCTGCA AAACCCTGCA AAACCCTGCA AGCACTTAAA	SNETEKTKIT NGTLTGVLSIL NGTLTGVLSIL NGTLTGVLSQV TISSPMPQTH MEKALSLGSI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLOGF VSSSNSLQS QHMFNEKEDS LUCCE M#: NM_005 3117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGATAA GAGAAATATC CATGTTTCAA CTTAACTGGA AACCCTAAGT TTGTACATTC	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCAA TGCAATTTGTC TTGTCACCAC GAAACTAAAACA TGCAATTTGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAAC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP QVSRLHSPP STVADPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAP GSYGKPPNGS QRKTSIODLR ENVEKQMEN LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TCTCATTGTGCAG CCTCATTAA GCTCTATTTG AAGCACTGT TAAGTGAAA CTATTATTTG AAGCACTGT TAAGTGAAATTT TATGTGAAATTT TATGTGAATATTT GAAGCACTGT TAGTGAAATTT TATGTAAATTT TGAATAATTGT TGAATAATTGT TGAATAATTGT TGAATAATTAT	SICNDSAFFR IMCATAEAQS KAQCDLQDPI SPIGELQDPI SPIGELQDPI SPIGELQDPI SPIGELQDPI SANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLILG SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTT TGTTACTTTT TATTACTTTT TATTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGAAT AAAACGCTCA ATGATACGA AATGAATGCA AATGAATGCA	120 180 240 360 420 660 660 780 840 900 960 120 180 240 300 360 420 480 540 660
5055606570	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq I AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTCAGCTG GTCAGCTG GCTTCAGCGG GCATTTTTTA GAGCTCAACA GAGGCCCAAA TGTGCTGCAAA TGTGCTGCAAA	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YLLKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA CCCCCTCCTC CTTCAAACGA TCAAACCCA AAACCCTGCA AAACCCGCTTT	SNETEKTKIT NGTLTGVLSL NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVVTII WIALYKMQGL GVPAVVVTII WIALYKMQGL FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LUCCE M#: NM_005 3117 21 CGGGCAGGTGT CATGTCTCAGG ATTCCTTGTC TAATTCCAGT AACAGAAAAA GAGAAATATC CATGTTCAA CTTAACTGGA AACCTTAAGTT TTGTACATTC GGAAAGAGTA	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC ACGAACAAAAACAA ACTAAAATCA TGCAATTTGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAAC AAGATTCGAC	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTVIAF FLLVSFTWMG GSYGKFPNGS QKKTSIQDLR ENVEKQWRRY LVNNDCSVHA TTCTCCACTTT ATGTTGGCAG TTCATGTGTATCA CTATATTGT CACCTGCTAA CATCTATTTG CACCTGCTAATCA CTATATATATGT TAAGTGAATT TTAAATGTGAATT TTAAATGTGAACC CAATGGAACA CCAATGAACA CCAATGAAC	SICNDSAFFR IMCATAEAGS KAQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGGAT AAAAGGCTCA TCCCCAGGAT AAAAGGCTCA TCTGCTGTTGTT TCTGTACTCAGCA AATGAATGCA CTGCTGCTGT	120 180 240 360 420 540 660 720 780 960 120 180 240 360 420 420 540 600 600 600 600 600 720 720 720 720 720 720 720 720 720 7
5055606570	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVNGY ITWGFAFFAW NSDMSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTCTTACTGA GCTTCAGGCG GCATTTTTA GAGCTCAACA GAGGCCCAACA CAGAGCCCAACA TGTGCTGCAA TCTGCTGCAA TCTGCTGCAA	VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LINLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession id Accession cance: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA ACCCTCTC CTTCAAACGA TCAAACCCA GAGGTGAGAT TGAAACCCA AACCCTGCA GCACATTAAA TAGCCGCTTT TACCCTGCCC	SNETEKTKIT NGTLTGVLSIL NGTLTGVLSIL NGTLTGVLSIV VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS UENCE n #: NM_005 3117 21 CGGCAGGTGT CACTGTCAGG ATTCCTTGTC TAATTCCAGT TAACAGAANAA GAGAAATATC CATGTTTCAA CATGTTTCAA TTACCAGTT AACAGAANAA CTTAACTGGA AACCCTAAGT TTGTACATTC GGGAAAGAGTA TTGTACATTC GGGAAAGAGTA TTCCTCCCCA	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC TGTGTACCAC GAAACAA ACTAAAATCA TGCAATTTAGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAAC AAGATTAGAC AAGATTAGAC GAAGATTGGC GAGAGTTGGC GAGAGTTGGC GAGAGTTGGC GAGAGTTGGC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR RTSKRGSLEF 41 TCTCCACTIT TCTCCACTIT TCTCCACTTT ACGTGCAG GCCTCAATGA GCCTCAATGA CATCTATTGG AAAGCACTGT TTAAGTGAATT TTAAGTGAATT TTAAATGTG TGAATAATAC GAAAGCATTCA GAAAGCATTCA	SICNDSAFFR IMCATAEAQS KAQCDLQDPI SPIGELQDPI SPIGELQDPI SPIGELQDPI SPIGELQDPI SANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLIG SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTT TGTTACTTTT TGTTACTTTT TATTACTTTT TATTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGAAT AAAACGCTCA ATGATACGAC AATGAATGCA	120 180 240 360 420 540 660 720 780 840 960 180 240 300 420 420 480 660 720 780
505560657075	MVFSVRQCGH PSSNEVETTS GEMMPOYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Coding seq 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTTA AGCTTACTCC GCTTCAGGCG GCATTTTTTA AGCTTACTCC GCTTCAGGCG GCATTTTTTA AGCTTACTCC GCTTCAGGCG GCATTTTTA AGCTCAACA GAGGCCCAAA TGTGCTGCAAC CAGGGCCCAAA TGTGCTGCAAC CAGGGCCCAAA TCTGTCAGGAG CAGGATCCCA	VGRTEEVLLT VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFLLNVS GPVNVTFMYL GEKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCAG GGATGGTTT TCGTTCAAACGA TCAAACCCAG GAATGCAC GAATGCAC GAATGCAC GAATGCAC GAATGCAC GAATGCAC GAATGCAC TTGCCCTCCTC TTGCTCTTCTCTT	SNETEKTKIT NGTLTGVLSIL NGTLTGVLSIL NGTLTGVLSQV VPRATVLSQV VISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLOGF VSSSSNSLQS QHMFNEKEDS LUCIC CGGCAGGTGT CTCTTCAGG ATTCCTGTCAGG TAATTCCAGT AACAGAATAA GGGAAATATC CATGTTTCAA CTTAACTGGG AACCTAAGT TTGTACATTC GGAAGAGTTA TTCCTCCCCA TTGTCCCCCA	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFOD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKKOLGA FIFIFYCVAK SSMSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACACAA ACTAAAATCA TGCAATTTGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAAC AAGATTCGAC GAGAGTTGGCC CGAGACTTACT CGAGACTTACT CGAGACTTACT CGAGACTTACT CGAGACTTACT CGAGACTTACT CGAGACTTACT CGAGACTTACT CGAGACTTACT CCACAGTGGCC CCACCTTGCCC CCACCTTCCC CCACCTTGCCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTCC CCACCTTGCC CCACCTTGCC CCACCTTGCC CCACCTTCC CCACCTTGCC CCACCTTGCC CCACCTTCC CCAC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTINVP SFSSPTVSAP QVSRLLHSPP QVSRLLHSPP STVADPANL PSLENLSLIS WSDNGCSVKD SVYLVTYIAP FLLVSPTMMG GSYGKPPNGS QRKTSIQDLR ENVEKQMERY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG GCTCAATGA CTCTATGTGAG CTTATAGTAGA CTATAGTAGAA CTATATTTT AAAGCACTGT TAAGTGAAT TTATATATGT TGAATAATAC CAATGGAACC CAACATTTTC CACCTGTTTA GGAAGCTTCA GAAAGCTTCA GAAAGCTTCA GAAAGCTTCA GAAAGCTTCA GAAAGCTTTCA CACCATTTTC CACCTTTTTC CACCACTTTTC CACCACTTTC CACCACTTTC CACCACTTTC CACCACTTTC CACCACTTTTC CACCACTTTC CACCACTTTC CACCACTTTC CACCACTTTC CACCACTTTTC CACCACTTTC CACCACTTTTC CACCACTTTC CACCACTTTTC CACCACTTTTC CACCACTTTC	SICNDSAFFR IMCATAEROS KAQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA TGTTACTTTA TGTTACTTTA TAAACGCTCA TCCCCAGAAT TCCCCAGAAT TCCCAGCA AATGAATGCA TCCCCAGCA AATGAATGCA TCCCCAGCA CTGCTGCTGT TGTTACCTTG TGTTACCTGT	120 180 240 360 420 660 780 840 900 960 120 120 120 120 240 300 360 420 420 780 840 900
5055606570	MVFSVRQCGH PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVPNTYIRK AVFFITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq 1 AGCCAGCCCG GCTCGGGGTCA GTTTTACTGA GCTCAGCGG GCATTTTTA AGCTTACTCG GCTTCAGGCG GCATTTTTA AGGCTCAACA GAGGCCCAAC TCATCCAGG CAGGATCCCA CAGGATCCCAG GCAGGATCCCA CAGGATCCCAG CAGGATCCCAG CAGGATCCCAG CAGGATCCCAG CCATCCCAG CCATCCCAG CCATCCCAG CCATCCCAG CCAGCCCCAC CCATCCCAG CCAGCCCCAC CCATCCCAG CCATCCAG CCATCCCAG CCATCCAG CCATCCCAG CCATCCCAG CCATCCCAG CCATCCCAG CCATCCCAG CCATCCCAG CCATCCCAG CCATCCCAC CCATCCAC CCATCCCAC CCATCCAC CCATCCCAC CCATCCAC	VGRTEEVLLT VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPONQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YLLKFCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTA ACCCCTCCT CTTCAAACGA TCAAACCCCA AAACCCTGCA AAACCCTGCA AAACCCTGCA TTGTCTTGTC	SNETEKTKIT NGTLTGVESI NGTLTGVESI NGTLTGVESI VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LUCIC MF. IM_005 3117 21 CGGCAGGTGT CATCTGTCAGG ATTCCTGTCAGG ATTCCTGTCAGG ATTCCTGTCAGG TAATTCCAGT TAATTCCAGT TAATTCCAGT TAATTCCAGT TAATTCAGT TAATTCAGT TAATTCAGT TAATTCAGT TAATTCAGT TGACATTCA CTTAACTGGA ACCCTAAGT TTCTCCCCA TGCTGACCAT GGCCACTGTG ACCTGTGACCAT GGCCACTGTG ACCTGTGACCAT	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVPLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 31 GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCAG ACTAAAATCA TGCAATTTGTC TATGATAAAG GTCCTGTCTC GAGACTACT ACAATAAAC AAGATTCGC CTTTCCCAGG CCACTTGGCC CTTTCCCAGG CCACTTGGCC CTTTCCCAGG CCACATTGGCC CTTTCCCAGG CCACATTGGCC CTTTCCCAGG	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVKQWERY LVNNDCSVHA TTCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA CATCTATTTG TAAGTGAATA CATCTATTTG TAAGTGAATT TAATATGTG TGAATAATAC CAATGAACACTGT TAAGTGAATT TAAGTGAATT TAAGTGAATT CAATGAATT CAATGAATAATAC CAATGAACAC GAAAGCTTCA CACCATTTC CACCATTCC CCCCAAACC CCCTCTCCAAT	SICNDSAFFR IMCATAERQS KAQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGAAT AAAACGCTCA TCCCCAGAAT AAAACGCTCA TCCTGCTGT GTGTGACCTG TTCCAGCCAA AATGAATGCA CTGCTGCTGT GTGTGACCTG TTCCAGCCAA AATGAATCA TCCCAGCAAT AAACGCTCA TCCCAGCAAT AAACGCTCA TCCCAGCAAT AAACGCTCAT TCCAGCCAAT TACCTCTTTT AGGGGAGATT	120 180 240 360 420 660 720 780 840 960 120 180 240 420 420 420 480 660 780 960
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505560657075	MVFSVRQCGH PSSNEVETTS GEIMFOYDKE TINCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac Coding seq I AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTTTACTGA GTCTCAGCCG GCTTCAGGCG GCATTTTTG AGCTTACTCC GCTTCAGGCA TCCTGCAGAG TCCTGCAGAG TCCTGCAGAG TCCTGCAGAG TCCTGCAGAG TCCTGCAGAG TCCACCCAG TCTGTCAGCAG TCGTGCAGA TCGTGCAGAG TCCATCCCAG GCTGAGCCCTC CAACCCCTTT CCACAGTCTC CCACGTCTGAAAG	VGRTEEVLLT VGRTEEVLLT VGRTEEVLLT LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LINLVFLLDS YILKFCIVGW FCVIFLLNVS GEVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37 11 AGGAGGCGAG GGATGGTTT CGTTCAAGAA TCAAACCCA CCCCTCCTC CTTCAAAGAA TCAAACCCAA CGAATGGAGT CGAATGGCAC TTGCTGTCT TACCCTGCCC TTGTCTGTCT TGGTGCCTCG CAAACGATCTC CAACCAACGATCTCC CAACCAACGATCTCC CAAACGATCTCC CAAACGATCTCC CAAACGATCTCC CAAACGATCTCC CAAACGATCTCC CCCCATCTCC CAAACGATCTCC CACCCAGCCC CAAACGATCTCC CCCCATCTCC CCCCATCTCCCCCCCCCC	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI NGTLTGVLSI AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFN WIALYKMQGL GVPAVVTII MFIVVLOLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LUCIC USSSSNSLQS QHMFNEKEDS LUCIC TANTICAGG ATTCCTTGTC TAATTCCAGG ATTCCTTGTC TAATTCAGGT AACAGAAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA AACCTTAGGT TTGTACATTC GGAAAGAGTA TTCTTCCCCA TTTCCCCCA TTCCCCCATGT CTTCCCCTATG TTCAGCTCCC TTCCCCTATG TTCACCCTATG TTCACCCCTATG TTCACCCTATG TTCCTCCCCACC TTCCCCTATG TTCCTCCCCACC TTCCCCTATG TTCCTCCCACC TTCCCCTATG TTCCTCCCCACC TTCCCCTATG TTCCTCCCCACC TTCCCCTATG TTCCTCCCCACC TTCCCCTATG TCCTCCCCACC TTCCCCTATG TCCTCCCCACC	HVVLVTSLEE HVVLVTSLEE IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFHLY LTISPDHYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC GAGACTAGACA TGCAATTTGT GAGATTTGT ACAATTAAAA GTAAAATCA ACGAAGTTGGC CACGTGGCC CCTTTCCCAGG CCACAAGTCC CACAACCC CTTCCCAGG CCACAACCC CTTCTCCAGG CCACAACCC CTTCTCCCAGG CCACAACCC CTTCTCCCAGG CCACAACCC CTTCTCCCAGG CCACAACCC CTTCTCCCAGG CCACAACCC CTTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCCC CTTTCCCCAGG CCCCAAACCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCCC CTTCTCCCAGG CCCCAAACCC CTTTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CCCCAAACCC CTTCTCCCAGG CTTCTCCCAGC CTTCTCCCAGG CTTTCTCCAGG CTTCTCCCAGG CTTTCTCCCAGG CTTCTCCCAGG CTTTCTCCCAGG CTTCTCCCAGG CTTTCTCCCAGG CTTTCTCCCAGG CTTTCTCCCAGG CTTCTCCCAGG CTTTCTCCCAGG CTTTCTCCAGG CTTTCTCCAGG CTTTCTCCCAGG CTTCTCCCAGG CTTTCTCCCAGG CTTCTCCCAGG CTTTCTCCCAGG C	KPQRNICNLS TLQTLSETYP PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTVIAF FLLVSPTWMG GSYGKFPNGS QKKTSIQDLR ENVRKQWRRY LVNNDCSVHA TTCTCCACTIT ATGTTGGCAG TTCATGTCST CACCTGCTAA CATCTATTTG GCCTCAATGA CATCTATTTG TAAATGAAAT TTAAATGAAT TTAAATGAAT CAATGAATC CAATGAACA CAATGAACA CAATGAACA CACATTTTC CCACAAACC CCTCCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT ATGTTCCCG CTCCCAATGC CTCCCCAATGC CCTCTCCAAT	SICNDSAFFR IMCATAEAGS IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGCAT AAAAAGCTCA TGCTGCTGT TGTGACCTG TTCCAGCCAA TTCCTCTTTT AGGGGAGATT TCACATGCCC CACCCCACCT CACACCTACC	120 180 240 300 360 420 780 900 960 120 180 240 360 420 480 540 600 600 600 600 720 780 840 900 960
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				AGAAACGTGA			1740
				TGTGTATTTT			1800
10				TCTGTCAAAG			1860
10				GGCGTTCTGC			1920
				TTCATTACAT			1980
				TACATAGCTT			2040
				GCTGCTCTGC			2100
15				ATGCAAGGCC			2160
13				ACATGGATGG			2220
				TACATCCGAA			2280
				GTGACCATCA			2340
				CCCAATGGTT			2400
20				GTGGTGGGAT			2460
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				CAAGACCTCA			2580
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				TTTTATTCTC			3240
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				AAAATGTAAG			3780
				AGATGCCCCC			3840
45	TGGGTCATGG	TTTGACAAAC	AGAGTGAGAG	ACCATATTTT	AGCCCCACTC	ACCCTCTTGG	3900
43	GTGCACGACC	TGTACAGCCA	AACACAGCAT	CCAATATGAA	TACCCATCCC	CTGACCGCAT	3960
				AAGATGTTTA			4020
				TCAGGAAAAT			4080
				CTTTAGGAAC			4140
50				AAAAATCATA			4200
J U				TGGTACACTC			4260
				CAGTGACAAG			4320
				CATGTATCGA			4380
				ATCTGCTTGA			4440
55				TAAGTCTTTC			4500
22				CCATAGTAAT			4560
				ATTTATTTAA		TITATATGIT	4620
	AAAATCAAAA	ATGTTAAAAT	CAATGAAATA	AATTTGCAGT	TAAGA		
			-				
60		22 Protein					
OU	Protein Ac	cession #: 1	NP_005747.1				
	į	11	21	31	41	51	
	1.	1	1	1	1	1	
				HVVLVTSLEE			60
65				NICNLSSICN			120
05						TFTIKLNNTM	180
				SPEELEKLOC			240
				VTHNVPSPIG			300
				NVNAGARVTG			360
70				LLHSPPDMLA			420
70				QDPANLQVSL			480
				NLSLISYVIS			540
						SFGVLLDLSR	600
				VTYIAFEKIR			660
75						NTYIRKYILK	720
75				KPPNGSPDDF			780
						Paffawgpvn	840
						SKTATNGLKK	900
						PSVQNGDVCL	960
00	HDPTGKQHMF	NEKEDSCNGK	GRMALRRTSK	RGSLHFIEQM			
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06	1	11	2 1	31	41	51	
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	GAGACATTCC	TCAATTGCTT	AGACATATTC	TGAGCCTACA	GCAGAGGAAC	CTCCAGTCTC	60
			GATTCTGATT				120
							180
			TAGAACCGTA				
-	CCTGTTAATC	CAAGGTCTTT	AGAAAAACTT	GAAATTATTC	CTGCAAGCCA	ATTTTGTCCA	240
5	CGTGTTGAGA	TCATTGCTAC	AATGAAAAAG	AAGGGTGAGA	AGAGATGTCT	GAATCCAGAA	300
-			ACTGAAAGCA				360
			ATCGATGCAG				420
	CCTCTCCCAT	CACTTCCCTA	CATGGAGTAT	ATGTCAAGCC	ATAATTGTTC	TTAGTTTGCA	480
			ATGATGGTCA				540
10							
10			AGCTATTCAG				600
	GCTCTACTGA	GGTGCTATGT	TCTTAGTGGA	TGTTCTGACC	CTGCTTCAAA	TATTTCCCTC	660
	ACCUTTCCCA	TOTTOCAAGG	GTACTAAGGA	ATCTTTCTGC	THEST STATES	ATCAGAATTC	720
							780
			AAGGTATGCA				
	ACTTCATGGA	CTTCCACTGC	CATCCTCCCA	AGGGGCCCAA	ATTCTTTCAG	TGGCTACCTA	840
15	CATACAATTC	CAAACACATA	CAGGAAGGTA	GAAATATCTG	AAAATGTATG	TGTAAGTATT	900
			ACAAAGTATA				960
	TTTCAGTGTA	CATGGAATAA	CATGTAATTA	AGTACTATGT	ATCAATGAGT	AACAGGAAAA	1020
	TTTTAAAAAT	ACAGATAGAT	ATATGCTCTG	CATGTTACAT	AAGATAAATG	TGCTGAATGG	1080
			ACTCTCCTGG				
20	IIIICAAAIA	WWW.IOWOG1	ACICICCIGG	WWITIIW			
20							
	Seg ID NO:	24 Protein	sequence				
		ession #: N	_				
	1	11	21	31	41	51	
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25	MNOTATIJICC	LIFLTLEGIO	GVPLSRTVRC	TCISISNOPY	NPRSLEKLET	IPASOFCPRV	60
					WE KULLINGE		
	ETTATMKKKG	EKRCLNPESK	AIKNLLKAVS	KEMSKRSP			
	Seg ID NO:	25 DNA sequ	ence				
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20			1 #: XM_030	227			
30	Coding sequ	ence: 11	L19				
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			CGGGGCGGGC				60
	AGCAAGTTTG	GAGCTGAATT	TCGTCGGTTT	TCGCTGGAAA	GATCAAAACC	TGGAAAATTT	120
35							180
55			ACAACATGTT				
	GGCTATGCAG	ACATCCATGG	AGACTTACTA	CCTATAAATA	ATGATGATAA	TTATCACAAA	240
	CCTCTTTCAA	CCCCCAATCC	ACTGCTTAGG	ם ברב דדד ברב ברב ברב ברב ברב ברב ברב ברב	AAAAGAAGGA	AGAAGCAGAC	300
			CACGCTAATA				360
	CGTCCTGACA	ACCATAGAAA	AAAGCCACAT	ATAGTCATTA	GTATGCCCCA	AGACTTTAGA	420
40	CCTCTCTCTT	CTATTATACA	CGTGGATATT	CTCCCAGAAA	OCCATOCTAG.	GGTACGTCTT	480
			ACCCCTAGGA				540
	GTAACACCAC	ATGGCTTAGA	AAAGGTTCCA	GGGATCTTTA	TATCCAGGCT	TGTCCCAGGA	600
			ACTATTAGCT				660
	ATAGAAGTTT	CAGGGAAGAG	CCTTGATCAA	GTAACAGACA	TGATGATTGC	AAATAGCCGT	720
45	AACCTCATCA	TAACAGTGAG	ACCGGCAAAC	CAGAGGAATA	ATGTTGTGAG	GAACAGTCGG	780
							840
			GTCTACTGAT				
	GAACCAAGCT	TTGAGCCAGA	GGATGAAGAC	AGCGAAGAAG	ATGACATTAT	CATTGAAGAC	900
			TCCAAAAGCT				960
50			TGAGTCTGGA				1020
50	AGCTTAGCAG	CCATAGCAAG	CAGCTCAAAC	ACGGAATTTG	AAACACATGC	TCCAGATCAA	1080
	AAACTCTTAG	AAGAAGATGG	AACAATCATA	ACATTATGA			
	seq ID NO:	26 Protein	sequence				
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55	1	11	21	31	41	51	
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	1		1	1	1	1	
	MNRSHRHGAG	SGCLGTMEVK	SKFGAEFRRF	SLERSKPGKF	EEFYGLLOHV	HKIPNVDVLV	60
			AVSTANPLLR				120
60			PVSSIIDVDI				180
60	VTPHGLEKVP	GIFISRLVPG	GLAQSTGLLA	VNDEVLEVNG	IEVSGKSLDQ	VTDMMIANSR	240
			TSGSSGQSTD				300
			LUIELSFESG	GWGETESNEA	PLAATASSSN	TEFETHAPDQ	360
	KLLEEDGTII	TL					
65	Com TD NO	22 DV2					
05		27 DNA seq					
	Nucleic Ac	id Accessio	n #: NM_003	667.1			
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70	ATGGACACCT	CCCCCCCCCC	بالثلاث لساريين		י י	GCTGGCGACC	60
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						CTGTCATTGC	120
	GAGCCCGACG	GCAGGATGTT	GCTCAGGGTG	GACTGCTCCG	ACCTGGGGCT	CTCGGAGCTG	180
						CATCAGTCAG	240
75						TGCGGGAAAC	300
75	GCTCTGACAT	ACATTCCCAA	GGGAGCATTC	ACTGGCCTTT	ACAGTCTTAA	AGTTCTTATG	360
						GCGAAGCCTT	420
						TTTCAGTGGC	480
	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAATGCGT	TAACAGAAAT	CCCCGTCCAG	540
							600
90						AATACACCAC	
80	ATACCAGACT	ATGCCTTTGG	AAACCTCTCC	AGCTTGGTAG	TTCTACATCT	CCATAACAAT	660
						GACTTTAGAT	720
						CAACCTTAAA	780
	GAACTACATT	TCTATGACAA	TCCCATCCAR	TTTGTTGGGA	GATCTGCTTT	TCAACATTTA	840
						TCCTGATTTA	
85							
(1)	ACIGGAACTO	CANACTIGGA	CHARTCHEACT	TTAACTGGAG	CACAGATETE	ATCTCTTCCT	960

	CAAACCGTCT	GCAATCAGTT	ACCTAATCTC	CAAGTGCTAG	ATCTGTCTTA	CAACCTATTA	1020
	GAAGATTTAC	CCAGTTTTTC	AGTCTGCCAA	AAGCTTCAGA	AAATTGACCT	AAGACATAAT	1080
		AAATTAAAGT					1140
5		ACAAAATTGC					1200
)	ATAAAGCTGG	ACCTATOGTC	CAACCTCCTG	TCGTCTTTTC	CTATAACTGG	GTTACATGGT	1260
	TTAACTCACT	TAAAATTAAC	AGGAAATCAT	GCCTTACAGA	GCTTGATATC	ATCTGAAAAC	1320
		TCAAGGTTAT					1380
		CCTATAAGAT					1440
	GACCTTCATA	AGAAAGATGC	TGGAATGTTT	CAGGCTCAAG	ATGAACGTGA	CCTTGAAGAT	1500
10	TTCCTCCTTC	ACTTTGAGGA	AGACCTCAAA	CCCCPTCATT	CACTGCAGTG	TTCACCTTCC	1560
							1620
		TCAAACCCTG					
	TGGACCATAG	CAGTTCTGGC	ACTTACTTGT	AATGCTTTGG	TGACTTCAAC	AGTTTTCAGA	1680
	TCCCCTCTGT	ACATTTCCCC	CATTAAACTG	TTAATTGGGG	TCATCGCAGC	AGTGAACATG	1740
		TCTCCAGTGC					1800
15							
13		GTGCCTGGTG					1860
	ATTTTTGCTT	CAGAATCATC	TGTTTTCCTG	CTTACTCTGG	CAGCCCTGGA	GCGTGGGTTC	1920
	TCTGTGAAAT	ATTCTGCAAA	ATTTGAAACG	AAAGCTCCAT	TTTCTAGCCT	GAAAGTAATC	1980
		GTGCCCTGCT					2040
							2100
20		CCTCCCCTCT					
20	TACATGGTCG	CTCTCATCTT	GCTCAATTCC	CTTTGCTTCC	TCATGATGAC	CATTGCCTAC	2160
	ACCAAGCTCT	ACTGCAATTT	GGACAAGGGA	GACCTGGAGA	ATATTTGGGA	CTGCTCTATG	2220
		TTGCCCTGTT					2280
		CCTCTTTAAT					2340
	CTTCTGGTGG	TAGTCCCACT	TCCTGCATGT	CTCAATCCCC	TTCTCTACAT	CTTGTTCAAT	2400
25	CCTCACTTTA	AGGAGGATCT	GGTGAGCCTG	AGAAAGCAAA	CCTACGTCTG	GACAAGATCA	2460
							2520
		GCTTGATGTC					
		TGGTAACCTT					2580
	GTGCCATCAC	CAGCTTATCC	AGTGACTGAG	AGCTGCCATC	TTTCCTCTGT	GGCATTTGTC	2640
	CCATGTCTTA					•	
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	Sea ID NO:	28 Protein	sequence				
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	1	11	21	31	41	51	
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35	MDTSRLGVLL	SLPVLLQLAT	GGSSPRSGVL	LRGCPTHCHC	EPDGRMLLRV	DCSDLGLSEL	60
		LDLSMNNISQ					120
		TEALQNLRSL					180
	AFRSLSALQA	MTLALNKIHH	IPDYAFGNLS	SLVVLHLHNN	RIHSLGKKCF	DGLHSLETLD	240
		TAIRTLSNLK					300
40							360
70		LTGAQISSLP					
		QQLLSLRSLN					420
	LTHLKLTGNH	ALQSLISSEN	FPELKVIEMP	YAYOCCAFGV	CENAYKISNO	WNKGDNSSMD	480
	DITTENDACHE	QAQDERDLED	Pt t negent v	NT UPUCCEDE	DCDDKDCEUT.	T.DCWT.TDTCW	540
4.5		NALVTSTVFR					600
45	ARHGAWWENG	VGCHVIGFLS	IFASESSVFL	LTLAALERGF	SVKYSAKFET	KAPFSSLKVI	660
	TLICALIALT	MAAVPLLGGS	KVCA CDI.CI.D	I.DECEDSTMC	VMVAT.TT.UNG	LCFLMMTTAY	720
		DLENIWDCSM					780
	LLVVVPLPAC	LNPLLYILFN	PHFKEDLVSL	RKQTYVWTRS	KHPSLMSINS	DDVEKQSCDS	840
	TOALVTFTSS	SITYDLPPSS	VPSPAYPVTE	SCHLSSVAFV	PCL		
50							
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	Seq ID NO:	29 DNA sequ	ience				
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			. 44/6				
	Coding sequ						
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55			21 	31	41		
55	1	11	1		1		60
55	1 GGCACGAGTA	11 GGGGTGGOGG	 GTCAGTGCTG	CTCGGGGGCT	TCTCCATCCA	 GGTCCCTGGA	
55	I GGCACGAGTA GTTCCTGGTC	11 GGGGTGGCGG CCTGGAGCTC	 GTCAGTGCTG CGCACTTGGC	CTCGGGGGCT GCGCAACCTG	 TCTCCATCCA CGTGAGGCAG	 GGTCCCTGGA CGCGACTCTG	120
55	I GGCACGAGTA GTTCCTGGTC	11 GGGGTGGOGG	 GTCAGTGCTG CGCACTTGGC	CTCGGGGGCT GCGCAACCTG	 TCTCCATCCA CGTGAGGCAG	 GGTCCCTGGA CGCGACTCTG	120 180
	I GGCACGAGTA GTTCCTGGTC GCGACTGGCC	11 GGGGTGGCGG CCTGGAGCTC	GTCAGTGCTG CGCACTTGGC TCCCGGGCTG	CTCGGGGGCT GCGCAACCTG AGGACTATGA	 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC	GGTCCCTGGA CGCGACTCTG ACCATTGGCA	120
55 60	I GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA	11 GGGGTGGCGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC	GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT	120 180
	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT	11 GGGGTGGOGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TGACTATGGC	GTCAGTGCTG GGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG	120 180 240 300
	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT	11 GGGGTGGOGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TGACTATGGC TCGTGAACTG	GTCAGTGCTG GGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG	120 180 240 300 360
	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA	11 GGGGTGGCGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TGACTATGGC TCCTGAACTG	GTCAGTGCTG GCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG TGGAATATTG	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA	120 180 240 300 360 420
	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC	11 GGGGTGGGGG CCTGGAGCTC GGCCGCTGC TGGCTGACTG TCGTGAACTG TACAACACTG AAAGGGAACC	GTCAGTGCTG GCACTTGGC TCCCGGGCTG CAGAAGATCCA TCCATGACAG AAACATCCAA ATACATTGTAA AAGGAAAGGC	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGA AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGCCAAG ACAGATGCTT TTACTATGAT TGAAGAGGGG TGAAGAGTTT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCGAG	120 180 240 300 360
60	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGC ACCGGACCAA GTGTAATTAC	11 GGGGTGGGGG CCTGGAGCTC GGCCGCTGC TGGCGGTGC TGGTGAACTG TACAACACTG AAAGGGAACC	GTCAGTGCTG GCACTTGGC TCCCGGGCTG CAGAAGATCCA TCCATGACAG AAACATCCAA ATACATTGTAA AAGGAAAGGC	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGA AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGCCAAG ACAGATGCTT TTACTATGAT TGAAGAGGGG TGAAGAGTTT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCGAG	120 180 240 300 360 420 480
60	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCA GTGTAATTAC TGATGACTCA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TGACTATGGC TACAACACTG TACAACACTG AAAGGGAACC GTTGACTCTG	GTCAGTGCTG GTCAGTGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGCTAGAA AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGAGGGG TGAAGAGTTT ACGAAGTGAT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGCCTA GTTCTTCCAAG GGTGGTCATA	120 180 240 300 360 420 480 540
	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA TGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTAC CCGTATTGCA	11 GGGGTGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TCGTGAACTG TACAACACTG AAAGGAACC GTTGACTCTG TCGGGATCTT	GTCAGTGCTG GGCACTTGGC TCCCGGGCTG TCCATGACAG TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGG GCCCTGAAGG AAACCAGCCA	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAGAGA AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTTCCT	TCTCCATCCA CCTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGGT TGAAGAGTGTT ACGAAGTGAT GGATGGCAAG	GSTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCCGAG GGTGGTCATA CAAAACGTCA	120 180 240 300 360 420 480 540
60	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA TGAATTACCT ACCGGACCAA GTGTAATTAC TGATGACTCA ACCGTATTGCA AGCTTGGAGA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TCGCTGACTGC TACAACACTG AAAGGGAACC GTTGACTCTC TCGGGATCTT CTTTGGGCTA	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCTGAAGG AAACCAGCA AGCAAGCA	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGAGAAGAG AACTGGTAGA ACATCGTTCG TGGAATATTG AATACCTAGA AATGCCACAG ATGTTTCCT TAAACCATGA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTGTA ACGAAGTGAAG GGATGGCAAG CACCAGTTTT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCGAG GGTGTCATA CAAAACGTCA GCAAAAACAT	120 180 240 300 360 420 480 540 600
60	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA TGAATTACCT ACCGGACCAA GTGTAATTAC TGATGACTCA ACCGTATTGCA AGCTTGGAGA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TCGCTGACTGC TACAACACTG AAAGGGAACC GTTGACTCTC TCGGGATCTT CTTTGGGCTA	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCTGAAGG AAACCAGCA AGCAAGCA	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGAGAAGAG AACTGGTAGA ACATCGTTCG TGGAATATTG AATACCTAGA AATGCCACAG ATGTTTCCT TAAACCATGA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTGTA ACGAAGTGAAG GGATGGCAAG CACCAGTTTT	GSTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCCGAG GGTGGTCATA CAAAACGTCA	120 180 240 300 360 420 480 540 600 660 720
60	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA ACGTTTGGAA AGCTTGGAGA	11 GGGGTGGGG CCTGGAGCT GGCCATGCCT TGACTATGGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTCT TCGGGATCTT TCTTTGGGCTA ACCTTATTAC	GTCAGTGCTG GCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA AGCTAGAAATAT ATGTCTCCTG	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACCTAGA AATGCCACAG ATGTTTTCCT TAAACCATGA AACAATGA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT CGAAGTGAT TCACAGGTTT TCGCATGTCC	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG GGATTATTG GATCTTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAACAT TACAATGAGA	120 180 240 300 360 420 480 540 600 660 720
60	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGGAAGAACT TGAATTGCT ACCGGACCAA GTGTAATTAC TGATCACTCA CCGTATTGCA AGCTTGGAGA ATGTTGGCAC ARTCAGATAT	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TCGTGAACTG TACAACACTG AAAGGGAACC GTTGACTCTG TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG	GTCAGTGCTG GTCAGTGCTG GCGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAAATAT ATGTCTCCTG GGCTGCTTGC	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AACCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTTCCT TAAACCATGA AACAAATGAA TGTATGAGTT	I TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGCCAA ACAGATGCTT TTACTATGAT TGAAGAGGG TGAAGAGTTT ACGAAGTGAT GGATGCCAAGTCAT TGCATGTCC ATGTGCATTA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT	120 180 240 300 360 420 480 540 600 660 720 780
60 65	GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA ACCGTATTGCA AGCTTGGAGA ATTTGCTTGCAAC ATTACAGCTTT	11 GGGGTGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TACAACACTG AAAGGAACC GTTGACTCTG TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG GAAACCAGCCA GCTAGAATAT ATGTCTCCTG GGCTGCTTGC GAACTCGCTG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AACTGGAGA AACTGAGAC TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTTCCT TAAACCATGA AACAAATGAA TGTATGAGTT GGAAAATCAG	TCTCCATCCA TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTA ACGAAGTGTT ACGAAGTGTT TCGCATGCCAAG CACGAGTTTT TCGCATGCCAAA AGAAGGCAAA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG CGGATTATTG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT TTCAGGCGAA	120 180 240 300 360 420 480 540 600 660 720 780 840
60	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA TGATGACTCA CCGTATTGCA AGCTTGGAGA TTGTTGGCAC AATCAGATAT TTACAGCTTT TTCCATACCG	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCGTGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTCT CCGGGATCTT CCTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAG TTACTCTGAT TTACTCTGAT	GTCAGTGCTG GTCAGTGGCTG CGGACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTCTCCTG GGACTGCTGGGAACTGCGTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AACTGGAGAA ACATCGTTCG TGGAATATTG AATACCACAGA ATGCTACACAGA AACAAATGAA TGTATGAGTAT GGAAAATCAG AAAATTATTACAAAATTAAAAATTAAAAAATTAAAAAAAA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTGTA ACGAAGTGAT CACCAGTTTT TCGCATGTCC ATGTGCATTA AGAAGGCAAA GAGGAATTTA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAAG CGGATTATG GATCTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT TTCAGGCGAA AACTTAAAGG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
60 65	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA TGATGACTCA CCGTATTGCA AGCTTGGAGA TTGTTGGCAC AATCAGATAT TTACAGCTTT TTCCATACCG	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCGTGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTCT CCGGGATCTT CCTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAG TTACTCTGAT TTACTCTGAT	GTCAGTGCTG GTCAGTGGCTG CGGACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTCTCCTG GGACTGCTGGGAACTGCGTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTGGAACTGCTG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AACTGGAGAA ACATCGTTCG TGGAATATTG AATACCACAGA ATGCTACACAGA AACAAATGAA TGTATGAGTAT GGAAAATCAG AAAATTATTACAAAATTAAAAATTAAAAAATTAAAAAAAA	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTGTA ACGAAGTGAT CACCAGTTTT TCGCATGTCC ATGTGCATTA AGAAGGCAAA GAGGAATTTA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAAG CGGATTATG GATCTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT TTCAGGCGAA AACTTAAAGG	120 180 240 300 360 420 480 540 600 660 720 780 840
60 65	GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA ACGTAATTAC CCGTATTGCA AGCTTGGAGA TTGTTGGCAC AATCAGATAT TTACAGCTTT TTCCATACCG	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TCGTGAACTG AAAGGGAACC GTTGACTCTG TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT	GTCAGTGCTG GTCAGTGCTG GCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTCTCCTG GGCTGCTTGC GAACTCGCTTG GAATATTGAATG	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACCTAGA AATGCCACAG ATGTTTTCCT TAAACCATGA AACAAATGAA TGTATGAGTT GGAAAATCAG AAATTAATAC TTGAGAACCC	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGT TGAAGAGTTT ACGAAGTGAT TCACAGATTAT TCGCATGTCC ATGTGCATTA AGAAGCCAAA GAGGATGTTA TTTAATAGCA	GGTCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAG GATCTTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTTA GCAAAACATT TACAATGAGA ATGCTCCAT TTCAGGCGAA AACTTAAAGG GATTTAGAGGA AACTTAAAGG GATTTGGTTG	120 180 240 300 420 480 540 600 660 720 780 840 900 960
60 65	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTACT TGATCACTCA CCGTATTGCA AGCTTGGAGA AGCTTGGAGA TGTTGGCAC AATCAGATAT TTCCATACCG CAGACGAGCA CAGACGAGCA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TACAACACTG AAAGGGAACC GTTGACTCTG TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAT	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCA AAACATCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTCTCCTG GGCTGCTTGC GAACTCGCTG GAACTCGCTG GAACTCAAATAT CTTCAAATG CTTCAGAGAAATTC	CTCGGGGGCT CGCAACCTG AGGACTATGA AGGACTATGA AACCTGAGAA AACATGTTCG TGGAATATTG AATACTTAGA AATCACACA ATGTTTCCT TAAACCATGA AACAAATGAA TGTATGAGTT GGAAAATCAG AAATTATTAC TTGAGAACCC GAGGGGGACA	TCTCCATCCA TCTCCATCCA AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT CGATGGCAAG CACCAGTTTT TCGCATGTCC ATGTGCATTA AGAAGGCAAA AGAAGGCAAA ATTAGCAAGAGA	GGTCCCTGGA CGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG GGATTATTG GATCTGGCTA GTTCTTCTAGG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTCAAGG AACTTAAAGG GATTTGGGTG CCAGAAAAAT CCAGAAAAAT	120 180 240 300 420 480 540 600 650 720 780 900 960
60 65	GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC CCGTATTGGAA AGCTTGGAGA TTGTTGGCAA TTATTACGATCT TTCCATACCG ATTACCATCG CCGACGAGTAC CGCACGAGTTC	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TACAACACTG AAAGGAACC TCTGGACTTC TCTGGACTTC TCTGGCTATC TCTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AGGAAGAAAT CAGCCCTGTA	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTCTCCTG GGACTTGCCTG GAATTGAATG GAAGAAATTC CTTGAGAGAA TTGAGTGAGC TTGAGAGAA TTGAGTGAGC	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AACTGAGAA AATACTTAGA AATACCACAG AACAAATGAA AGGACAATGAT GGAAAATCAG AAATTATGAGAACCC GAGGGGCACA TGAAACTGAA TGAAACTGAA	TCTCCATCCA TCTCCATCCA TCTCAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTAACAGATGGTT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTT TCGCATGTCC ATGTGCATA AGAAGGCAAA GAGGATGTTA AGAAGGCAAA AGAGGCAAA ATTAGAAGA GGAATTCAG	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG GGACTCTG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AATGCTCAT TTCAGGCGAA AACTTAAAGG GATTTGGTTG CCAGAAAAAT TTACAGGAGC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
60 65 70	GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC CCGTATTGGAA AGCTTGGAGA TTGTTGGCAA TTATTACGATCT TTCCATACCG ATTACCATCG CCGACGAGTAC CGCACGAGTTC	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TACAACACTG AAAGGAACC TCTGGACTTC TCTGGACTTC TCTGGCTATC TCTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AGGAAGAAAT CAGCCCTGTA	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTCTCCTG GGACTTGCCTG GAATTGAATG GAAGAAATTC CTTGAGAGAA TTGAGTGAGC TTGAGAGAA TTGAGTGAGC	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AACTGAGAA AATACTTAGA AATACCACAG AACAAATGAA AGGACAATGAT GGAAAATCAG AAATTATGAGAACCC GAGGGGCACA TGAAACTGAA TGAAACTGAA	TCTCCATCCA TCTCCATCCA TCTCAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTAACAGATGGTT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTT TCGCATGTCC ATGTGCATA AGAAGGCAAA GAGGATGTTA AGAAGGCAAA GAGGATGTTA ATTAATAGG GGAATTCAG	GGTCCCTGGA CGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG GGATTATTG GATCTGGCTA GTTCTTCTAGG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTCAAGG AACTTAAAGG GATTTGGGTG CCAGAAAAAT CCAGAAAAAT	120 180 240 300 420 480 540 600 650 720 780 900 960
60 65 70	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA AGCTTGGAGA TTGTTGGCAC ATCAGATAT TTACAGCTTT TTCCATACCG ATTACCATCG CAGACGAGCC CGCAGGATTC CGCAGGAGTC	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TCGTGAACTG TACACACTG AAAGGGAACC GTTGACTCT TCGTGATCTT TCTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA ATTACTCTGAT ACCTTCTGTT AAGAAGAAA TCACTCTGAT ACCTCTATTAC CTGCCAGATA ACCTTCTGTT AAGAAGAAA TCACTAAAGCA	GTCAGTGCTG GTCAGTGGC GCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTCTCCTG GGACTGCTGC GAACTCGCTG GAACTCGCTG GAATTGAATG TTGAGAGAAA TTGAGAGAAA ATGAGAGAAA	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACCACAGA ATGCTACACAGA AACAAATGAA TGTATGAGTAT GGAAAATCAG AAATTATTAC TTGAGAACCC GAGGGCGACA TGAAACTGAA GATTGAAGAC	TCTCCATCCA CGTAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT CGCATGTCC ATGTGCATTT TCGCATGTCC ATGTGCATTA TTAATAGCA ATTAGAAGCAAA GAGGATGTTA TTTAATAGCA ATTAGAGAGG GGAAATTCAG GAAAGACACA GAAAGACACA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAAG CGGATTATTG GATCTTGGCTA GATCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT TTCAGGCGAA AACTTAAAGG GATTTGGTTG CCAGAAAAAC TTACAGGAGC TACAGGAGAC GAGAATTTATAGGGAGC GAGCTTTGTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
60 65	GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA AGCTTGATA CCGTATTGCA AGCTTGGAGA ATTCAGATAT TTACAGCTTT TTCCATACCG CAGACGAGCA CGCAGGATTC GAGACGAGCC GAGACGAGGC GTTCGTGAGAG	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TCGTGAACTG TACAACACTG AAAGGGAACC GTTGACTCTG TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT AAGAAGAAAT CAGCCCTGTA TCCAAAGCA ACTACCAGAGA	GTCAGTGCTG GTCAGTGCTG GCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTCTCCTG GGATGCTTGC GAACTGCTG GAACTGAATG TTGAGTGAAT TTGAGTGAGA ATGGTTGAGAAATTC	CTCGGGGGCT CGCAACCTG AGGACTATGA AGACTAAGA AACCTGAGAA AACATCGTTCG TGGAATATTG AATACTTAGA AATACCACAG ATGTTTTCCT TAAACCATGA AACAAATGAA TGTATGAGTT GGAAAATCAG AAATTAATAG CTTGAGAACCC GAGGCCGACA TGAAACTGAA GATTGGAGGCA CTAGAGCAGA	TCTCCATCCA CCTCAGGCAG AGTGTTGTAC CGTGAGGCAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT TCGCATGTCC ATGTCCATGTCATTACATT AGAAGGCAAA AGAAGGAATTAA ATTAAATAGA ATTACGAGAG AATTCTGTG AAAAGAACAA	GGTCCCTGGA CGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTCAAG GATTTAGGTG GATTTAGGTG CAGAAAAAT TTCAGGCGAA TTCAGGAGC GATTTGGTG CAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGAACTACA	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140
60 65 70	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GCGAACGAA GTGTAATTAC TGATGACTCA AGCTTGGAGA AGCTTGGAGA TTGTTGGCAC AATCAGATAT TTACAGCTTT TTCCATACCG ATTACCATCG ATTACCATCG ATTACCATCG ATTACCATCG CAGACGAGCA CGCAGGATTC GAGAGCGAGGCA GCTTCGTGAGAG	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCC TGACTATGGC TGACTATGACTG AAAGGGAACC TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAT ACCTTCTGTT AAGAAGAAAAT TCTCAAAGCA ACTAGCAGAAA ACTAGCAGAAA ACTAGCAGAAA ACTAGCAGAAA GGAACGGAAAA GGGACGGAAAA GGGACGGAAAA GGGACGGAAAA GGGACAGAAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAGAAACGGAAGAA	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTCTCCTG GAATTGAATG GAAGAAATTC CTTGAGAGAA TTGAGTGAGG AGAAAATTG AAGAAATTC TTGAGTGAGG AGAAAACTGG TTCCTGTCTCCTG	CTCGGGGGCT CGCAACCTG AGGACTATGA AGGACTATGA AGGACTAGGA AGGCTGAGA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG AACAAATGAA AGGACAAGTAA TGTATGAGTC GGAGAGACA TTGAGAACC TGAGACCGAG TGAACTGAA CTAGAGACC TGAACCGAGA TGAACCGAGA TGAACCGAGA TGAACCGAGA TGGACAGAGA	TCTCCATCCA TCTCCATCCA TCTCCATCCA AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTT CGCATGCCA AGAGGATTT AGAAGGAAT ATTAATAGCA ATTAGGAGGA GAAATTCAG GAAACAACAAG AAATCTGTTG TCCAGAACTT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG CGGATTATTG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTAAAGG GATTTGGTTG TCAGGCGAA AACTTAAAGG GATTTGGTTG CCAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGACTACA CTTAATCTTC	120 180 240 300 360 420 540 600 650 720 780 840 900 1020 1080 1140 1200 1260
60 65 70	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTGCT ACCGGACCAA TGATGACTCA AGCTTGGGAG ATCAGATAT TTACAGCTT TTCCATACCG ATTACCATCG CAGACGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGAGCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTAAA CATCCTCAGT	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTCT TCTGGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAAT CCGCCCTGTA TCTCAAAGCA ACTACCAGAA ACTACCAGAAA ACTACCAGAAA ATTACTAGAAAAAATATACAAAAAAAAAA	GTCAGTGCTG GTCAGTGGCTG CGGACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTCTCCTG GAATTGAATAG GAATTGAATG TTGAGAGAA TTGAGTGAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG AATACTTAGA AATACCACAG AACAAATGAT TGGAAATCATGA AACAAATGAA TGTATGAGAACCA GAAGTACAGA GAATTATAC GAAAATCAGA AATTATAC TTGAGAACCA GAGGCGCAC GAGGCAGACA GATTGAGACAGA TGAAACTGAA TGAGACAGA TGAGACAGA TGAGACAGAA TCAGTGGGGAA TCAGTGGGGAA	TCTCCATCCA TCTCCATCCA ACTGTGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT TCGCATGCCAT AGGAGGCAAA AGAAGGCAAA AGAAGGCAAA AGAAGGCAAA ATTAGGAGG GGAAATTCAG GGAAATTCAG GAAGAACAG AAATCTGTTG TCCAGAACTT AAGTAAAGAG	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATG GATCTTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCTCCAT TTCAGGCGAA AACTTAAAGG GATTTTGGTTG CCAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGAACTACA	120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1260 1320
60 65 70	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTGCT ACCGGACCAA TGATGACTCA AGCTTGGGAG ATCAGATAT TTACAGCTT TTCCATACCG ATTACCATCG CAGACGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGGAGCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGAGCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTCA ACCAGGAGTAAA CATCCTCAGT	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTCT TCTGGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAAT CCGCCCTGTA TCTCAAAGCA ACTACCAGAA ACTACCAGAAA ACTACCAGAAA ATTACTAGAAAAAATATACAAAAAAAAAA	GTCAGTGCTG GTCAGTGGCTG CGGACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTCTCCTG GAATTGAATAG GAATTGAATG TTGAGAGAA TTGAGTGAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG AATACTTAGA AATACCACAG AACAAATGAT TGGAAATCATGA AACAAATGAA TGTATGAGAACCA GAAGTACAGA GAATTATAC GAAAATCAGA AATTATAC TTGAGAACCA GAGGCGCAC GAGGCAGACA GATTGAGACAGA TGAAACTGAA TGAGACAGA TGAGACAGA TGAGACAGAA TCAGTGGGGAA TCAGTGGGGAA	TCTCCATCCA TCTCCATCCA ACTGTGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT TCGCATGCCAT AGGAGGCAAA AGAAGGCAAA AGAAGGCAAA AGAAGGCAAA ATTAGGAGG GGAAATTCAG GGAAATTCAG GAAGAACAG AAATCTGTTG TCCAGAACTT AAGTAAAGAG	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG CGGATTATTG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTAAAGG GATTTGGTTG TCAGGCGAA AACTTAAAGG GATTTGGTTG CCAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGACTACA CTTAATCTTC	120 180 240 300 360 420 540 600 650 720 780 840 900 1020 1080 1140 1200 1260
60 65 70	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGATTGCT ACCGGACCAA ACTTGGAGA ATTGATGACA ACTTGGAGA TTTACAGCTTT TTCCATACCG CAGACGAGCA CGCAGGATCA CGCAGGATCA CGCAGGATCA CGCAGGATCA CGCAGGATCA CGCAGGATCA GCTTGCTAAA CATCCTCAGT GGAGTGAGA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TCGTGAACTG AAAGGGAACC GTTGACTCTG TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT AAGAAGAAAT CAGCCCTGTT ATCTCTGAT ACTACACAGAG ACTAGCAGAA ACTAGCAGAG ATTAAAAAG ATTACAGAG ATTAAAAAG TTCTAAAAG TTCTAAAAAG TTCTAAAAAG TTCTAAAAAG TTCTAAAAAAG TTCTAAAAAAG TTCTAAAAAAAAAA	GTCAGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTCTCCTG GAACTGCTTGC GAACTGGAAGA TTGAGTGAGAA TTGAGTGAGAA GACAAACTGG TTCCTGTCTCCTC AAAGTTCAT CAGCTCACAT CACCTCACAT CACC	CTCGGGGGCT CGCAACCTG AGGACTATGA GAGGAAGAG AAGCTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCTACATGA ATGTTTTCCT TAAACCATGA ACATAGATTT GGAAAATGAA TGTATGAGTT GGAAAATGAA AATTATTAG AAATTATAG AAATTATAG TTGAGAACCC GAGGGCGACA TGAAACTGAA CTAGAGCAGA TGGAAGTAA TCAGTGGGG CTAGTGGGG CTAGTGGGG CTAGTGGGG	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC CGTGAGGCAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT TGGATGCCAAG CACCAGTTTT TCGCATGTCC ATGTGCATTA AGAAGGCAAA AGAGGATGTTA TTTAATAGCA ATTAGGAGAG GAAAATTCAG GAAACTCGTTG TCCAGAACTT ACGAAAGAG AAATCTGTTG TCCAGAACTT AAGTAAAGAG GTGCAAGGAC	GGTCCCTGGA CGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TTCAGGCGAA AACTTCAAG AACCTTCAT TTCAGGCGAA AACTTAAAG CAGAAAAAT TTACAGGAC GAGCTTTGTG AAGAACTACA CTTAATCTTC AACATCATGA CTTAATCATCA	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1140 1200 1250 1380
60 65 70 75	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGGAAGACT TGATTGCT ACCGGACCAA AGCTTGGAGA AGCTTGGAGA AGCTTGGAGA TTGATGGCAC AATCAGATAT TTACAGCTTT TTCCATACCG CAGACGAGCA CGCAGGATTC GAGACGAGC GTTGCTGAGAG GCTTGCTAAA CATCCTCAGA GCTTGCTAAA CATCCTCAGAGA GGCTTGCAGAGA GGCTTGCAGAGAG	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TACAACACTG AAAGGAACC GTTGACTCTG TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAT CCAGCCCTGTA TCTCAAAGCA ACTAGCAGAG ACTACCAGAG ATTAAGAGA TTCTGAGAGT TCTCAAAGCA ACTACCAGAG GGAACGGAG TTCTGAGGT TTCTGAGGT TTCTGAGGT TTCTGAGGT	TCAGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCA TACATTGTAA AAGGAAAGGC GCCTGAAGG AAACCAGCA GCTAGAAGA ATGTCTCTG GAATTGTAATG GAATTGTAATG GAATTGTAATG GAAGAAATTC CTTGAGAGAA TTGAGTGAGA ATGATTAATG TTGAGTGAG	CTCGGGGGCT CGCAACCTG AGGACTATGA AGGACTATGA AGACTGAGAA AACCTGGGAGAAAATACTTAGA AACAATGAA AACAAATGAA TGTATGAGTT GGAAAATCAG AAATTATAC TTGAGAACCC GAGGGGGACA TGAAACTGAA GATTGGAGC CTAGAGCAG TGAAACTGAA CTAGAGCAGA CTAGAGCAGA CTAGAGCAGA CTAGAGCAGA CCTAGAGCAA CCTAGAGCAA CCTAGAGCAA CCTAGAGCAA CCTAGAGCAA CCTAGAGCAA CCTAGAGCAA CCTAGAGACAA CCTAGAGCAA CCTAGAGCAA CCTAGAGCAA	TCTCCATCCA TCTCCATCCA TCTCCATGCAG AGTGTTGTAC TGATGGCAAG ACAGATGGTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT TCGCATGTCC ATGTGCATAG AGAAGGCAAA TTTAATAGCA AGAAGAACAG GGAAATTCAG GAAGAACTT TCGCATGTC TCCAGAACTTT AATAGCAA AATAGCAA AATAGCAA AAATCTGTTG TCCAGAACTT AAGTAAAGAAC TCCAGAACTT AAGTAAAGAAC TTCAGAACAC TATTGAGAAC TATTGAGAAC TATTGAGAAC TATTGAGAAC TATTGAGAAC TATTGAGAAC TATTGAGAAC TATTGAGAAC TATTGAGAAC TTTTGAGAAC TTTGAGAAC TTTTGAGAAC TTTGAGAAC TTTTGAGAAC TTTGAGAAC TTTTGAGAAC TTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAAC TTTTGAGAC TTTTTGAGAC TTTTTGAGAC TTTTTTTTTT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAGG GGATTATTG GATCTGGCTA GTTCTTCTAGG GGTGGTCATA CAAAACGTCA GCAAAACGTCA GCAAAACGTCA TACAATGAGA AACTTAAAGG CAATTAAAGG CAATTAAAGG CAGTTTACAGGAGC CAGCATTGGTG CAGAAAAAT TTACAGGAGC CAGCTTTCTC AACATCATCA CTTAATCTTC AACATCATCA CTTAATCTTC AACATCATCA CTTAATCTTC AACATCATCA CTTAATCTAC AACATCATCA CTTAATCACAC CTTAATCACAC	120 180 240 300 360 420 540 6600 650 720 780 840 900 1020 1020 1140 1200 1260 1380 1440
60 65 70	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAC TGAATTACCT ACCGGACCAC TGATGACTCA TGATGACTCA ATTCTTGGCAC AATCAGATAT TTTCCATACCG ATTACCATCG CAGACGAGCA CGCAGGATTC GAGACGAGCA TTGCTTAGAGA CATCCTCAGT GGAGTTAGAGA CATCTCAGT GGAGTTCAGAGA GGCTTCACAGT GGAGTTAGAAA CATCCTCAGT GGAGTTAGAAA CGCTCTCAGT GGAGTTAGAAA CGCTTCACAGT	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TCGTGAACTG TACACACTG TACACACTG AAAGGGAACC GTTGACTCT CTGTGACTTG TCTTGGGCTA ACCTTATTAC CTGGTCATTA ACCTTATTAC ACCTCATTA ACCTTCTGTT AAGAAGAAA TTACTCTGAT CTGCAGAGG GGAACGGAAG AATTAAGAAG ATTACTAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TGCCCAGCTG ACCACCTGT ACCCACCTG	GTCAGTGCTG GTCAGTGGCTG GCGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTTTCCTG GAATTGATAG GAACTCGCTG GAATTGAATG GAAGAAATTC CTTGAGAGAA TTGAGTGAGC AGAGAAGAAC GCCAACTGCTCCTC AAAGTTCATT CAGGCTCAAG GGCATGCCCAAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGACTAAGA AAGCTGAGAA AAGCTGAGA AATACTTAGA AATACCACAG AACAAATGAA ACAAAATGAA ACATTAGTTAGAAACCAC GAAGACGAAC TGAAACTAGA CCACGGACA TGAAACTGAA CTAGAGCAGA CTAGAGCAGA TGAAACTGAA CCACGGGACA TGAACTCAAA CCACGGAAGA ACCCTGTCAGA AGCCAGGTAG	TCTCCATCCA TCTCCATCCA TCTCCATCCA AGTGTGTAC TGATGGCAAG ACAGATGCTT TTACATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTT TCGCATGTCC ATGTGCATA AGAAGTATA AGAAGGCAAA AGAGGAATTTA TTTATAGACA GAAATTCAG GAAATTCAG GAAATTCAG GAAATTCAG GAAATTCAG GAAATTCAG AAATTCTTT TCCAGAACTT AAGTAAAGAG ATTGAGAAA AAGAACAAG AATTGAGAAA AAGAACAAG CTATTGAGAAA AAGAACAAG	GGTCCCTGGA CGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG GGAGTTATG GATCTGGCTA GTTCTTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTAAAGG GATTATTGGTA TACAGGAGA AACTTAAAGG GATTTGGTTG AAGACTTCTTC AAGACATACA CTTAATCTTC AACATCATGA CTTAATCTTC AACATCATGA AACTTACAACA CTTAATCTTC AACATCATGA AATTACCAACA AGCTGTGTAC	120 180 240 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1380
60 65 70 75	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAC TGAATTACCT ACCGGACCAC TGATGACTCA TGATGACTCA ATTCTTGGCAC AATCAGATAT TTTCCATACCG ATTACCATCG CAGACGAGCA CGCAGGATTC GAGACGAGCA TTGCTTAGAGA CATCCTCAGT GGAGTTAGAGA CATCTCAGT GGAGTTCAGAGA GGCTTCACAGT GGAGTTAGAAA CATCCTCAGT GGAGTTAGAAA CGCTCTCAGT GGAGTTAGAAA CGCTTCACAGT	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TCGTGAACTG TACACACTG TACACACTG AAAGGGAACC GTTGACTCT CTGTGACTTG TCTTGGGCTA ACCTTATTAC CTGGTCATTA ACCTTATTAC ACCTCATTA ACCTTCTGTT AAGAAGAAA TTACTCTGAT CTGCAGAGG GGAACGGAAG AATTAAGAAG ATTACTAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TTCTCAGAGT TGCCCAGCTG ACCACCTGT ACCCACCTG	GTCAGTGCTG GTCAGTGGCTG GCGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCCA GCTAGAATAT ATGTTTCCTG GAATTGATAG GAACTCGCTG GAATTGAATG GAAGAAATTC CTTGAGAGAA TTGAGTGAGC AGAGAAGAAC GCCAACTGCTCCTC AAAGTTCATT CAGGCTCAAG GGCATGCCCAAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGACTAAGA AAGCTGAGAA AAGCTGAGA AATACTTAGA AATACCACAG AACAAATGAA ACAAAATGAA ACATTAGTTAGAAACCAC GAAGACGAAC TGAAACTAGA CCACGGACA TGAAACTGAA CTAGAGCAGA CTAGAGCAGA TGAAACTGAA CCACGGGACA TGAACTCAAA CCACGGAAGA ACCCTGTCAGA AGCCAGGTAG	TCTCCATCCA TCTCCATCCA TCTCCATCCA AGTGTGTAC TGATGGCAAG ACAGATGCTT TTACATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTT TCGCATGTCC ATGTGCATA AGAAGTATA AGAAGGCAAA AGAGGAATTTA TTTATAGACA GAAATTCAG GAAATTCAG GAAATTCAG GAAATTCAG GAAATTCAG GAAATTCAG AAATTCTTT TCCAGAACTT AAGTAAAGAG ATTGAGAAA AAGAACAAG AATTGAGAAA AAGAACAAG CTATTGAGAAA AAGAACAAG	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAGG GGATTATTG GATCTGGCTA GTTCTTCTAGG GGTGGTCATA CAAAACGTCA GCAAAACGTCA GCAAAACGTCA TACAATGAGA AACTTAAAGG CAATTAAAGG CAATTAAAGG CAGTTTACAGGAGC CAGCATTGGTG CAGAAAAAT TTACAGGAGC CAGCTTTCTC AACATCATCA CTTAATCTTC AACATCATCA CTTAATCTTC AACATCATCA CTTAATCTTC AACATCATCA CTTAATCTAC AACATCATCA CTTAATCACAC CTTAATCACAC	120 180 240 300 360 420 540 6600 650 720 780 840 900 1020 1020 1140 1200 1260 1380 1440
60 65 70 75	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA AGCTTGGAC AGTGTAATTAC CGTATTGCA AGCTTGGAGA TTTCCATACCG ATTACAGCTTT TTCCATACCG ATTACAGCTTC CGAGACGAGC CGAGGATTC GGAGGAGGC GCTTGCTAAA CATCCTCAGT GGAGTGAGAA CATCTCAGT GGAAAAGAG AGATTACAGAAAACAG AGATTACAGAAAACAG AGAAAACAGAAAACAGAAAACACACCTCAAGAAAACAGAAAACAGAAAACAGAAAACAACACACAC	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTCT TCTGGGATCTT TCTTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA ACTACTGT AAGAAGAAAA TTACTCTGAT ACTTCTGAT ACTTCTGAT ACTTCTGAT TCTCAAAGCA ACTAGCAGAG AATTAAAGAG TTCTGAGAGT TCTCAAAGCA ACTAGCAGAGT ACTAGCAGAGT ACTAGCAGAGT ACTAGCAGAGT ACTAGCAGATCTCTGATAGACACCCTGACTG ACTACCACCCTGACTG ACTACCACCCCTGACTG ACTACCACCCCTGACTG ACTACCACCCC ATTACCCACCCC GGGAGCCAACCC ATTACCCACCCC ACTACCACCCC ATTACCCACCC	GTCAGTGCTG GTCAGTGGCTG CGGACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTCTCCTG GGACTTGAGAGA TTGAGAGAA TTGAGTGAG AGGAAACTGG TTGAGAGAA TTGAGTGAG CAGACTCGCTG CAGACTGGTG CTTGAGAGAA TTGAGTGAGC AGAGAAACTGG TCCTGTCTG CAAAGTTCATT CAGCTCACT CAGCTCACAT TTTAAAGACT	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AAGCTGAGAA ACATCGTTCG AATACTTAGA AATACTACATA AATACCATGA AACAAATGAA ACATATGAT GGAAAATCAG AAATTATAC GAGAGCGCACA TGAGACCAC GAGGCGCACA CTAGAGCAGA TCAGACCAG ATCAGACCAG ATCAGACCAG CTAGAGCAGA CCCTCTCAGA AGCCAGTAG AGCAGTAG AGCAGTAG AGCCAGTAG	TCTCCATCCA TCTCCATCCA TCTAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TCAAGGAGGG TGAAGAGTTT TCGCATGCCA ATGCCAAG AGAGTTT TCGCATGTCC ATGTCCATTAATAGCA AGAAGGCAAA AGAAGGCAAA AATACGAGAG GGAAATTCAG GGAAATCAG GGAAATCAG TCCAGAACTT AAGTAAAGAG TATTGAGAAA AGACACAG TGCTGTAGTG TCCTTAGGAC TGCTGTAGTG	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATG GATCTGGCTA GTTCTCGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACCTCCAT TTCAGGCGAA AACTTAAAGG GATTTGGTTG CAGAAAAAA TTACCAGC GAGCTTTGTG AAGAACTACA CAGAAAAAA CTTAATCTTC AACATCATCA CTGAAGAAAA AATTACCAAC CTGAAGAAAA AATTACCAC CTGAAGAAAA AATTACCAC CTGAAGAAAA AATTACCAC CTGAAGAAAA AATTACCAC CTGAAGAAAA AATTACCAC CTGAAGAAAA CTGAAGAAAAA CTGAAGAAAA CTGAAGAAAAA CTGAAGAAAAAA CTGAAGAAAAA CTGAAGAAAAAAA CTGAAGAAAAAA CTGAAGAAAAAAAAA CTGAAGAAAAAAAAA CTGAAGAAAAAAAAAA	120 180 240 300 360 480 540 600 780 840 960 1020 1140 1260 1320 1380 1440 1500
60 65 70 75	GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTGCT ACCGGACCAA AGCTTGACTA CCGTAATTAC CCGTATTGCA AGCTTGGAGA ATTCAGATAT TTACAGCTTT TTCCATACCG CAGACGAGCC GAGACGAGCC GAGACGAGCC GTTCCTAGAG GCTTCCTAGAG GCTTCCTAGAG GCTTCCTAGAG AGACTAGAA AGATCTAAA AGGCTTCACGC TGAAAAGCAG AGGATGTAAA AGGATCTAGAA AGGATCATAG AGGCTCCATGA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT CGGCCATGCCT TGACTATGGC TCGTGAACTG TACAACACTG TACAACACTG TCGGGATCTT CTTTGGGCTA TACCTCGAT TACCTCGAT AAGAAGAAAT TACTCTGAT AAGAAGAAAT TCTCAAAGCA ACTACCAGAG GGAACGGAAG AATTAAGAGG ATTAAGAGT TCCCAGCTG ACGACTGGAT TCCCAGCTG ACTACCAGAG AATTAAGAGG AATTAAGAGG AATTAACAACA CAGATCCTG ACGATCCTG ATTACCAACC GCCATGCCTTA	TCGGTGCTG GTCAGTGGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGC GCCTGAAGG AAACCAGCCA GCTAGAAGATAT ATGTCTCCTG GAATTGTAATG GAATTGAATGG TAGAGTGAGA TGGGTGAGGA TGGGTGAGGA TGGGTGAGGA TGCGCTG CAGAAACTGG TTCCTGTCTC CAGAGAACTCG TTCCTGTCTC CAGGCTCAAG GGCATGCGCT TTTAAAGACT TCTGTATAG	CTCGGGGGCT CGCAACCTG AGGACTATGA AGGACTATGA AGACTGAGAA AACCTGAGAA AATACTTAGA AATACTTAGA AATACTAGA AACAAATGAA TGTATGAGTT GGAAAATGAA AGAAATGAA CGAGGAACC GGGGGGACA TGAAACTGAA GATTGGAGACC CTAGAGCAGA TCAAGTCAGA CCTAGTCGAGA CCTAGTCGAGA CCTAGTCAGA AGCCAGGTAG AGCCAGGTAGA AGCCAGGTAGA AGCCAGGTAGA AGCCAGGTAGA ACCATGATAA	TCTCCATCCA CCTCAGCAG AGTGTTGTAC CGTGAGGCAG AGTGTTGTAC TGATGGCAAG TGATGGCAAG TGAAGAGGTTT TCGCATGTCC AGGAGGCAAA AGGAGGCAAA AGAAGCAAA ATTAGCAA ATTAGCAGAGG GAAATTCAG GAAGAACTGTA AGAAGAACACAG GTGCAAGACTT TCCAGAACTT TCCAGAACTT AAGTAAGAA ATTAGCAA ATTAGCAAACACACA TCCAGAACTT AAGTAAAGAA TTTAGTAAGAA TTTAGTAAGAA TTTAGTAAGAA TTTAGGAACTT AAGTAAAGAAC TATTGAGAAA TTTAGGAACAC TATTGAGAAA TGCTGTAAGGAC TGCTGTAGTG TTCCGGAATT TTTCGGAATT	GGTCCCTGGA CGGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG GGATTATTG GATCTGGCTA GTTCTTCTAGG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTAAAGG GATTTAGGTTG CCAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGAACTACAC CTTAATCTTC AACATCATGA CTTAATCTTC AACATCATGA AACTTAAAGC AGCTTTGTG AAGAACAAAA AATTACCAAC CTGAATAAAC TTGAAGAAAA AATTACCAAC AGCTGTGTAC TTGAATACTT GGTTTTACTG	120 180 240 300 360 420 540 660 720 780 840 960 1020 1140 1200 1140 1320 1380 1440 1560 1620
60 65 70 75	1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GCGAAGAACA GTGTAATTAC TGAATTACA CCGTATTGCA AGCTTGGAGA AGCTTGGAGA ATTAGCTTACAG ATTACAGCTT TTCCATACCG ATTACCATCG CAGAGCAGGA CAGAGCAGGCA GCTGCTAGAG GCTTCCTAAA CATCCTCAGT GGAGCTAGGA GCTTCCTAAA CATCTCAGAT GGAGCTAGAG GGCTTCACGG TGAAAAGCAG AGGATTAAA AGCTTCAAGA TGAAAAGCAG AGGATTAAA GCCTCTCAGCA TGAAAAGCAG AGGATTAAA GCCCCATAGA TTCTTCAGCA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT CGGCCATGCCT TGACTATGGC TACAACACTG AAAGGGAACC TCGGGATCTT CTTTGGGCTA ACCTTATTAC CTGGTCATTAC TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAT TCTCAAAGCA GGAACGAAG ATTAAGAG TTCTGAGGAG TTCTGAGGAG AATTAAGAG AATTAAGAG AATTAAGAG AATTAAGAG AATTAAGAG TTCTGAGAGT TGCCCAGCTG ACAGATCCTG ACTACCACC GCACACCCTT ACTATTGTAC	GTCAGTGCTG GTCAGTGGCTG CGGACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCTGAAGG AAACCAGCCA GCTAGAAGA ATGTCTCCTG GAATTGTAA TGAGTGAGG AGAGAAATT CTTGAGAGAA TTGAGTGAGG AGAGAAATT CAGGTCACAG GCCACACTGCTG CAAGGTCACAT TCTGTTAAGG TTCTGTATAGT CGGCCTCAGG GCATGCGCT TCTTAAAGAT TCTGTATAGT AAAATGTTCA	CTCGGGGGCT CGCAACCTG AGGACTATGA AGGACTATGA AGGACTATGA AGGACTAGA AGGCTGAGA AAGCTGAGA AATACTTAGA AATACCACAG AACAAATGAA ACAACAATGAA AGGAGAACCAG AAATTATTAC TTGAGAACC TGAGAGCAGA TGAACTGAA CTAGAGCAGA TGAACTGAA CTAGAGCAGA TGAGCAGA ACCACGTAG AGCCAGGTAG AGCCAGGTAG AGCCAGGTAG AGCCAGGTAG AGCCAGGTAG AGCCAGGTAG AGCCAGGTAG ACACATGATA	TCTCCATCCA TCTCCATCCA TCTCCATCCA AGTGTGTAC AGTGTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTT CGCATGTCC ATGTGCCATA AGAAGGATATTA AGAAGGAAAA ATTAGAAGAG AATTCAGAACAGA AAATCTGTTG TCCAAGACTT AAGTAAAGAG AAATCTGTTG TCCAAGACTT AAGTAAAGAG AGACCACAG TCTCAAGACT TATTAGAAAA AGAGACACAG TGCTGTAGTTG TTTCGGAATT TTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTTCT	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG CGGATTATG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTAAAGG GATTTTTGTAG GATTTTTCAGG GATTATTGTTCAG GAAAAACAT TTCAGGCGAA AACTTAAAGG GATTTTGTT CCAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGAACTACA CTTAATCTTC AACATCATGA CTGAAGAAAA AATTACCAAC AGCTGTGTAC TTGAATACTT GGTTTTACTG TTTTAAAGAC	120 180 240 300 360 420 540 600 660 780 840 900 1020 1080 1120 1320 1380 1500 1500 1500 1680
60 65 70 75 80	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA AGCTTGGAC AGTGTAATTAC TGATGACTCA AGCTTGGAA AGCTTGGAGA TTTTCGCAC ATTCAGCTT TTCCATACCG ATTACCATCG CAGACGAGC TTCGTGAGAG GCTTCGTAAA CATCCTCAGT GGAGTGAGAA CATCCTCAGT GGAGTTAACA CATCCTCAGT GGAGTTAACA CATCCTCAGT GGAGTTAACA CATCCTCAGT GGAGTTAACA CATCTTCAGT TGAAAACAG AGGATTAAAA AGGTTAAAA AGGTCAATAT TTTCACGCA TTCTTCAGCA ATATTATAAA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTTG TCTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAA TTACTCTGAT TCTGAAGCA ACTAGCAGAG ACTAGCAGAG AATTAAGAAG AATTAAGAAG AATTAAGAAG AATTAAGAAG TTCTGAGTCTG ACCAGCTG ACCAGCTG ACCAGCTG ACTACCACCC GCCATGCCTT ACTATTGTAC AAGAATACTT	GTCAGTGCTG GTCAGTGGCTG GCGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTTTCCTG GAATTGAAAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGTGAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AAGCTGAGAA AAGCTGAGA AAGCTGAGAA AATACTTAGA AATACTTAGA AATACCACAG AACAAATGAA ACAAATGAA ACATTAGATTG GGAAAATCAG AAATTATTAC TTGAGAACCC GAGGGGCACA TGAAACTGAA CCTGTCAGA CCTGTCAGA AGCCAGGTAG GATATTCAAA ACACATGATA CATTTAATTT	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT TCGCATGCCAT TCGCATGCCAT AGAAGTATA AGAAGGCAAA AGAGGCAAAA GAGGATGTTA TTTAATAGCA GAAATTCATTA GAAAGTCAT AAGTAAAGAG GAAATTCAG GAAACACAG AAATTCAGTG TCCAGAACTT AAGTAAAGAG TCCAGAACTT AAGTAAAGAG TCCAGAACTT TATTGAGAAA TTGAGAAA TTGAGAAA TTGAGAAA TTGAGAAC TGCTGTAGTG TTTCTTCTTCTCTC CTGTGTGTGA	GGTCCCTGGA CGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG GGGATTATG GATCTGGCTA GTTCTTCGAG GGTGGTCATA ACAAACGTCA GCAAAAACAT TACAATGAGA AACCTCAAT TTCAGGCGAA AACTTAAAGG GATTTGGTTG CCAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGAACTACA ACTTAATCTC AACATCATGA CTTAATCTTC AACATCATGA CTTAATCTTC AACATCATGA CTTAATCTTC AACATCATGA CTTAATCTTC AACATCATGA CTTAATCTTC AACATCATGA CTTGAAGAAAA AATTACCAAC AGCTGTGTAC TTGAATACTT GGTTTTAAGAAC TTTTAAGAAC TTTTAAGAAC TTTTAAGAAC TTTTAAGAAC	120 180 240 300 360 420 540 600 720 780 960 1020 1080 1140 1260 1380 1440 1500 1500 1680 1740
60 65 70 75	1 GGCACGAGTA GTTCCTGGTC GCCACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA AGCTTGGAC AGTGTAATTAC TGATGACTCA AGCTTGGAA AGCTTGGAGA TTTTCGCAC ATTCAGCTT TTCCATACCG ATTACCATCG CAGACGAGC TTCGTGAGAG GCTTCGTAAA CATCCTCAGT GGAGTGAGAA CATCCTCAGT GGAGTTAACA CATCCTCAGT GGAGTTAACA CATCCTCAGT GGAGTTAACA CATCCTCAGT GGAGTTAACA CATCTTCAGT TGAAAACAG AGGATTAAAA AGGTTAAAA AGGTCAATAT TTTCACGCA TTCTTCAGCA ATATTATAAA	11 GGGGTGGGGG CCTGGAGCTC GGCCATGCCT TGACTATGGC TGACTATGGC TACACACTG AAAGGGAACC GTTGACTTG TCTTGGGCTA ACCTTATTAC CTGGTCATTG TAGCCAGAAA TTACTCTGAT ACCTTCTGTT AAGAAGAAAA TTACTCTGAT TCTGAAGCA ACTAGCAGAG ACTAGCAGAG AATTAAGAAG AATTAAGAAG AATTAAGAAG AATTAAGAAG TTCTGAGTCTG ACCAGCTG ACCAGCTG ACCAGCTG ACTACCACCC GCCATGCCTT ACTATTGTAC AAGAATACTT	GTCAGTGCTG GTCAGTGGCTG GCGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA GCTAGAATAT ATGTTTCCTG GAATTGAAAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGAGAA TTGAGTGAG	CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AAGCTGAGAA AAGCTGAGA AAGCTGAGAA AATACTTAGA AATACTTAGA AATACCACAG AACAAATGAA ACAAATGAA ACATTAGATTG GGAAAATCAG AAATTATTAC TTGAGAACCC GAGGGGCACA TGAAACTGAA CCTGTCAGA CCTGTCAGA AGCCAGGTAG GATATTCAAA ACACATGATA CATTTAATTT	TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT TCGCATGCCAT TCGCATGCCAT AGAAGTATA AGAAGGCAAA AGAGGCAAAA GAGGATGTTA TTTAATAGCA GAAATTCATTA GAAAGTCAT AAGTAAAGAG GAAATTCAG GAAACACAG AAATTCAGTG TCCAGAACTT AAGTAAAGAG TCCAGAACTT AAGTAAAGAG TCCAGAACTT TATTGAGAAA TTGAGAAA TTGAGAAA TTGAGAAA TTGAGAAC TGCTGTAGTG TTTCTTCTTCTCTC CTGTGTGTGA	GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCAGG CGGATTATG GATCTGGCTA GTTCTTCTGAG GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA AACTTAAAGG GATTTTTGTAG GATTTTTCAGG GATTATTGTTCAG GAAAAACAT TTCAGGCGAA AACTTAAAGG GATTTTGTT CCAGAAAAAT TTACAGGAGC GAGCTTTGTG AAGAACTACA CTTAATCTTC AACATCATGA CTGAAGAAAA AATTACCAAC AGCTGTGTAC TTGAATACTT GGTTTTACTG TTTTAAAGAC	120 180 240 300 360 420 540 600 720 780 960 1020 1080 1140 1260 1380 1440 1500 1500 1680 1740

5	TATGCAGGAA TGTCATGTCT CCAGTTAGAT TCTGTAGTTC TTTTTTTCTG TAAAAGAATT	AGATTTAAAT GCAATTTGGT AAATCTGTTA TTTAACAGAA	TTTAAGTCTG CATTAATACC GCTTTGTGAA	AGATTTTAAA ATGACATCTT AATTCATCAC	TGTTTTTGAG GCTTATAAAT TGTGATGTTT	CTTAGAAAAC ATTCCATTGC GTATTCTTTT	1860 1920 1980 2040 2100
10	Seq ID NO: Protein Acc			31	41	51	
	ELKHPNIVRY	YDRIIDRTNT	ROQKIRRKSD TLYIVMEYCE DLKPANVFLD	GGDLASVITK	GTKERQYLDE	EFVLRVMTQL	60 120 180
15	YYMSPEQMNR SDELNEIITR	MSYNEKSDIW MLNLKDYHRP IQLQERERAL	SLGCLLYELC SVEEILENPL KAREERLEOK	ALMPPFTAPS IADLVADEQR EQELCVRERL	QKELAGKIRE RNLERRGRQL AEDKLARAEN	GKFRRIPYRY GEPEKSQDSS LLKNYSLLKE	240 300 360 420
20	QLRAQALSDI						
	Seq ID NO: Nucleic Aci Coding sequ	d Accession	1 #: NM_0202	42			
25	1	11	21	31	41	51	
25	CACTCCCCC	CCCTCCACTC	GGGAGGTGGA	CCCF CCCCC	CCV didectariani	CCCATCCAC	60
	GGGTGAGGGC GTCTAACCAA	GCTATGGCAC CCAAGTAATG	CCGGCTGCAA AAGGTGATGC	AACTGAGTTA CATCAAAGTT	CGCAGCGTGA TTTGTGCGAA	CAAATGGTCA TTCGTCCTCC	120 180
30			CTGATGGAGA CCAACCCTGA				240 300
50			AATCTGTATT				360
			GTACCATCTT				420
			CTGAATCTGA				480
35			TGTTTTCCTT				540 600
55			AGTGTTCCTT CTGGACTGTA				660
			AGGTGGTAAC				720
			GTGTGGCATC				780
40			CAATAGAGTC				840
40			TGGTGGATTT				900
			AGGAAGCAGG				960
			TACTACGGGA			TTTGCTACAG	1020 1080
			GATCCAGGTG				1140
45						CCCAAGGAAA	1200
			AAGTGAAGAG				1260
						ACTATATGGA	1320 1380
						AGTCTCTGAT TTCAATCTAA	1440
50						TCCACAAGGA	1500
	ATCCCGGGGA	GGTTTTCTGC	CTGAGGAGCA	GGATCGTTTG	CTCTCAGAAT	TAAGGAATGA	1560
						ATGCTATGGA	1620
						TGAAAAGAGC AAATAAGTGG	1680 1740
55						AAGAGCCATG	1800
						CAGAGCTGAA	1860
						AGCTAGAATT	1920
						TTTTGGAAGC	1980
60			CCAAGGCCTA			CTGAAACACT	2040 2100
-	AAGCCCTGAA	ATGGGAAGCT	TTGGCTCTCT	ATACACTCAG	AATTCTAGCA	TATTAGATAA	2160
	TGATATATTA	AATGAGCCAG	TTCCTCCTGA	GATGAATGAA	CAAGCTTTTG	AGGCCATTTC	2220
	TGAAGAGCTT	AGAACAGTGC	AGGAACAAAT	GAGTGCTCTT	CAAGCCAAAC	TGGATGAAGA	2280
65						ATTCTACCCA	
05						AAGAGCTTCT ATGACTTTTT	
	GAAAAGTGAG	GTACATGACC	TGCGAGTAGT	CCTTCATTCT	GCTGACAAGG	AGCTTTCTTC	2520
	AGTGAAATTG	GAATATAGTT	CATTCAAAAC	GAATCAGGAG	AAAGAATTCA	ACAAACTTTC	2580
70						ACGAAAAGCT	
70	GCTTGAGAGC	AAAGCCTGCC	TACAGGATTC	CTATGACAAC	TTACAAGAAA	TAATGAAATT AAACTCTGAA	2700
	TGAGATTGAC	AATAATTGA	TGGAGCTTCT	TGAGGCAGAA	AAAGAACGCA	ATAACAAATT	2820
						AAGTTCTTGA	
75	GGCTGTACGT	CAGGAGAAAC	AGAAAGAGAC	GGCCAAGTGT	GAGCAGCAGA	TGGCAAAAGT	2940
75	ACAGAAACTA	GAAGAGAGCT	TGCTTGCTAC	TGAAAAAGTG	ATCAGTTCCC	TGGAAAAGTC	3000
						AGCTAAGAAC	
•						AGGACATAAA TCAAGAAGCA	-
						CTGAGGACAT	
80	AGAGAGGGAT	ATGCTCTGTG	AGGACCTGGC	TCATGCCACT	GAGCAGCTGA	ACATGCTCAC	3300
	AGAGGCCTCA	AAAAAACACI	CGGGGCTGCT	GCAGTCTGCC	CAGGAAGAAC	TGACCAAGAA	3360
	GGAAGCCCTG	ATTCAGGAAC	TTCAGCACAA	GCTAAACCAA	AAGAAAGAGG	AAGTAGAACA	3420
	GAAGAAGAAT	GAATATAACI	TCAAAATGAG	GCAACTAGAA	CATGTGATGG	ATTCTGCTGC	3480
85	TGAGGATCCC	CAGAGTCCTA	AGACACCACC	TCACTTTCAA	ACACATTIGO	CAAAACTCCT TGGAACACCT	3600
05	GGANACACAA	GAACAAGAGA	. MONAGATGG	MAGAGCCICI	. nnunctici		2000

		CTAAATGAAG					3660
	GCAGTTGCGT	GAAATGGAAA	ACCTACGCCT	GGAAAGTCAG	CAGTTAATAG	AGAAAAACTG	3720
		GGTCAGCTGG					3780
		CAACAGCTGA					3840
5							
,		GTTGAAGAAA					3900
		AAAGAGATGG					3960
	TTTGGAGTCT	AAAGCATTCC	AGGAAAAAGA	ACAACTGAGA	TCAAAGCTGG	AAGAAATGTA	4020
		GAGAGAACAT					4080
10		Aatggaaagt					4140
10	AGTGCGACTA	AAGAAGGAAA	ATGTCAGGCT	TGCTGAGGAG	ACAGAAAAGT	TGCGTGCCGA	4200
	AAATGTATTT	TTAAAAGAAA	AGAAAAGAAG	TGAATCTTGA	GGATTCCGGT	CAGCTACCTA	4260
		TGTTTGAAGA					4320
		TGAATTTATG					4380
		TGATGAACAT					4440
15	ATTAAGTGGC	CTACTTCAAG	GCTTTGAATC	AACTTAAGGG	AAAACCTTTT	GTCTTTGTAA	4500
		CTGTAGCTAA					4560
		ATCTCCTTTG					4620
	CCTGCAGTGA	GTTTAATGAC	TGACTTAGTA	GCAGGTACAA	GAAGCAAACT	TGTTAATATA	4680
	GATTATTTT	GTATTCTTAC	TTTAGGTATT	TTACTTGAGC	ATTTTCCATG	actgtaaata	4740
20	AAGCCATTTT	TTAAGATAAA	AAAAAAAAA	AAAAA			
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23		1			CCI DODONE O	I COMOTA	
		SVTNGQSNQP					60
	LHSNPEPKTF	TFDHVADVDT	TQESVFATVA	KSIVESCMSG	YNGTIFAYGQ	TGSGKTFTMM	120
	GPSESDNFSH	NLRGVIPRSF	EYLFSLIDRE	KEKAGAGKSF	LCKCSFIEIY	NEQIYDLLDS	180
		I KKGVFVVGA					240
30							300
50		NEIVNIRTSL					
		RHVCYRDSKL					360
	KLIKNKAVVN	EDTQGNVSQL	OABVKRLKEO	LAELASGOTP	PESFLTRDKK	KTNYMEYFQE	420
		EKKSLIEKVT					480
							540
25		SELRNEIQTL					
35	AQTIAKLEKA	PSEISGMEKS	DKNQQGFSPK	AQKEPCLFAN	TEKLKAQLLQ	IQTELNNSKQ	600
	EYEEFKELTR	KRQLELESEL	QSLOKANLNL	ENLLEATKAC	KRQEVSQLNK	IHAETLKIIT	660
		RPVPKLSPEM					720
							780
		AKLDEEEHKN					
40	VLEKQLQETQ	TKNDFLKSEV	HDLRVVLHSA	DKELSSVKLE	YSSFKTNOEK	EFNKLSERHM	840
40	HVOLOLDNLR	LENEKLLESK	ACLODSYDNL	QEIMKFEIDO	LSRNLQNFKK	ENETLKSDLN	900
		ERNNKLSLQF					960
							1020
		SSLEKSRDSD					
		VLIKKQEVDI					1080
	KHSGLLOSAO	EELTKKEALI	OELOHKLNOK	KEEVEOKKNE	YNFKMRQLEH	VMDSAAEDPQ	1140
45		HLAKLLETQE					1200
							1260
		LIEKNWLLQG					
		EEVQSALYNK					1320
	RTSQEMEMLR	KQVECLAEEN	GKLVGHQNLH	QKIQYVVRLK	KENVRLAEET	EKLRAENVFL	1380
	KEKKRSES	-	-				
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		AGGATTTAAG					60
		AAAATAAGTT					120
		ATACTACAGA					180
60		ACTGGTTGAG					240
UU		TAAATAAAT					300
	GATAAATATG	GCCAAAATGA	GAGTTTTGCT	AGAATTCAAG	TGAGATTTGC	TGAATTAAAA	360
		AGCCAGATGA					420
						TAATGTCAAA	480
		AACTTCTTCA					540
65							
$o_{\mathcal{I}}$		TGCGGAATTT					600
		CAGCATCTAC					660
	CATTTACAGA	ATAGGAACAA	CAGTTGTGAT	TCCAGAGGAC	AGACTACTAA	AGCCAGGTTT	720
						TTCATTGAGA	780
70		AAACTAAACA					840
70						Gaaaagacaa	900
	ACCTCTAGAT	CAGAATGCCG	AGATTTGGTT	GTGCCTGGAT	CTAAACCAAG	TGGAAATGAT	960
						ACCTCTGGTG	1020
							1080
						GAATAAAACG	
75						AGAGGTTCCA	1140
75	GAGAGTAACC	AGAAACAGTG	GCAATCTAAG	AGAAAGTCAG	AGTGTATTAA	CCAGAATCCT	1200
	CCTCCATCTT	CAAATCACTC	GCAGATTOY	GAGTTAGCCC	GAAAAGTTAA	TACAGAGCAG	1260
							1320
	8 8 8 77 R F		ACCIGICITY				
	AAACATACCA			サイツアス カインス へろん	CAAGCAGCAA	TACCTTGGAT	1380
	ACATCTAAAT	GGTTTGACCC					
	ACATCTAAAT GATTACATGA	GCTTTGACCC	AACTCCAGTT	GTAAAGAATG	ACTITCCACC	TGCTTGTCAG	1440
80	ACATCTAAAT GATTACATGA	GCTTTGACCC	AACTCCAGTT	GTAAAGAATG	ACTITCCACC	TGCTTGTCAG	
80	ACATCTAAAT GATTACATGA TTGTCAACAC	GGTTTGACCC GCTGTTTTAG CTTATGGCCA	AACTCCAGTT ACCTGCCTGT	GTAAAGAATG TTCCAGCAGC	ACTITICACO AACAGCATCA	TGCTTGTCAG AATACTTGCC	1440 1500
80	ACATCTAAAT GATTACATGA TTGTCAACAC ACTCCACTTO	GGTTTGACCC GCTGTTTTAG CTTATGGCCA AAAATTTACA	AACTCCAGTT ACCTGCCTGT GGTTTTAGCA	GTAAAGAATG TTCCAGCAGC TCTTCTTCAG	ACTITCCACC AACAGCATCA CAAATGAATG	TGCTTGTCAG AATACTTGCC CATTTCGGTT	1440 1500 1560
80	ACATCTAAAT GATTACATGA TTGTCAACAC ACTCCACTTC AAAGGAAGAA	GGTTTGACCC GCTGTTTTAG CTTATGGCCA AAAATTTACA TTTATTCCAT	AACTCCAGTT ACCTGCCTGT GGTTTTAGCA	GTAAAGAATG TTCCAGCAGC TCTTCTTCAG ATAGGAAGTG	ACTITCCACC AACAGCATCA CAAATGAATG GAGGTTCAAG	TGCTTGTCAG AATACTTGCC CATTTCGGTT CAAGGTATTT	1440 1500 1560 1620
80	ACATCTAAAT GATTACATGA TTGTCAACAC ACTCCACTTC AAAGGAAGAA CAGGTGTTAA	GGTTTGACCC GCTGTTTTAG CTTATGGCCA AAAATTTACA TTTATTCCAT ATGAAAAGAA	AACTCCAGTT ACCTGCCTGT GGTTTTAGCA TTTAAAGCAG ACAGATATAT	GTAAAGAATG TTCCAGCAGC TCTTCTTCAG ATAGGAAGTG GCTATAAAAT	ACTITICACO AACAGCATCA CAAATGAATG GAGGTTCAAG ATGTGAACTT	: TGCTTGTCAG AATACTTGCC CATTTCGGTT CAAGGTATTT 'AGAAGAAGCA	1440 1500 1560 1620 1680
	ACATCTAAAT GATTACATGA TTGTCAACAC ACTCCACTTC AAAGGAAGAA CAGGTGTTAA	GGTTTGACCC GCTGTTTTAG CTTATGGCCA AAAATTTACA TTTATTCCAT ATGAAAAGAA	AACTCCAGTT ACCTGCCTGT GGTTTTAGCA TTTAAAGCAG ACAGATATAT	GTAAAGAATG TTCCAGCAGC TCTTCTTCAG ATAGGAAGTG GCTATAAAAT	ACTITICACO AACAGCATCA CAAATGAATG GAGGTTCAAG ATGTGAACTT	: TGCTTGTCAG AATACTTGCC CATTTCGGTT CAAGGTATTT 'AGAAGAAGCA	1440 1500 1560 1620
80 85	ACATCTAAAT GATTACATGA TTGTCAACAC ACTCCACTTC AAAGGAAGAA CAGGTGTTAA GATAACCAAA	GGTTTGACCC GCTGTTTTAG CTTATGGCCA AAAATTTACA TTTATTCCAT ATGAAAAGAA CTCTTGATAG	AACTCCAGTT ACCTGCCTGT GGTTTTAGCA TTTAAAGCAG ACAGATATAT TTACCGGAAC	GTAAAGAATG TTCCAGCAGC TCTTCTTCAG ATAGGAAGTG GCTATAAAAT	ACTTTCCACC AACAGCATCA CAAATGAATG GAGGTTCAAG ATGTGAACTT ATTTGAATAA	TGCTTGTCAG AATACTTGCC CATTTCGGTT CAAGGTATTT	1440 1500 1560 1620 1680 1740

	GTAATGGAGT	GTGGAAATAT	TGATCTTAAT	AGTTGGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
	CCATGGGAAC	GCAAGAGTTA	CTGGAAAAAT	ATGTTAGAGG	CAGTTCACAC	AATCCATCAA	1920
		TTCACAGTGA					1980
		ATTTTGGGAT					2040
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		ATGGGAAATC					2160
		TGTACTATAT					2220
	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTCC	CGATATTCCA	2280
	GAGAAAGATC	TTCAAGATGT	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
10		AGCTCCTGGC					2400
		GAACCACTGA					2460
		CCATTTTGAA					2520
	AGTCATAATT	CTTCATCCTC.	CAAGACTTTT	GAAAAAAAA	GGGGAAAAA	ATGA	
1 =							
15	Seq ID NO:	34 Protein	sequence:				
		ession #: A					
	1	11	21	31	41	51	
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20		LTIDSIMNKV					60
20	NPEDWLSLLL	KLEKNSVPLS	DALLNKLIGR	YSQAIEALPP	DKYGQNESFA	RIQVRPAELK	120
	AIQEPDDARD	YFQMARANCK	KFAFVHISFA	QFELSQGNVK	KSKQLLQKAV	ERGAVPLEML	180
	EIALRNLNLO	KKQLLSEEEK	KNLSASTVLT	AOESFSGSLG	HLONRNNSCD	SRGOTTKARF	240
		ABIGYRNSLR					300
		VPGSKPSGND					360
25							420
23		TKEYQEPEVP					
		SVSKQSPPIS					480
		FQQQQHQILA					540
	QVLNEKKQIY	AIKYVNLEEA	DNOTLDSYRN	BIAYLNKLQQ	HSDKIIRLYD	YEITDQYIYM	600
	VMECGNIDLN	SWLKKKKSID	PWERKSYWKN	MLEAVHTIHO	HGIVHSDLKP	ANFLIVDGML	660
30		MOPDTTSVVK					720
50							780
		KTPFQQIINQ					
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	SHNSSSSKTF	EKKRGKK					
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35	Seg ID NO:	35 DNA sequ	ience				
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		ence: 851					
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	1	11	4+	31	41	31	
40		1	1	1	1	1	
40		CGTCTGCTGT					60
	CCCTCCCTGG	GATCTACACA	GACCATGGCC	TTGCCAACGG	CTCGACCCCT	GTTGGGGTCC	120
	TGTGGGACCC	CCGCCCTCGG	CAGCCTCCTG	TTCCTGCTCT	TCAGCCTCGG	ATGGGTGCAG	180
		CCCTGGCTGG					240
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45		GCCTGAGCAC					360
73							
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		ACGCCCTCCC					480
	GGGCCCCAGG	CCTGCACCCG	TTTCTTCTCC	CGCATCACGA	AGGCCAATGT	GGACCTGCTC	540
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50	CGGGGGTCTC	TGCTGAGCGA	GGCTGATGTG	CGGGCTCTGG	GAGGCCTGGC	TTGCGACCTG	660
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	GAGAGCCTCA	TCTTCTACAA	GAAGTGGGAG	CTGGAAGCCT	GCGTGGATGC	GGCCCTGCTG:	1080
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		TGGATGAGCT					1200
60		TCCTCAAGAT					1260
-		AGGCTTTGCT					1320
	AGGGGGGG	AUGUTTIGUT	TOWNGTCARC	ANNUGUCACG	MANIGAGICC	TONOGIOGOC	
		ACCGCTTTGT					1380
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						CCACCCCAAG	2040
		CTCAGTAAAC					
75					-nov-		
, ,	Com TD 170	26 80-5-1-					
		36 Protein					
		cession #: 1					
	1	11	21	31	41	51	
00		l		1	1		
80	MALPTARPLL	GSCGTPALGS	LLPLLFSLGW	VQPSRTLAGE	TGQEAAPLDG	VLANPPNISS	60
						PPEDLDALPL	120
						GVRGSLLSBA	180
						GPPYGPPSTW	240
0.5	SVSTMDALRG	LLPVLGQPII				PRFRREVEKT	300
85	ACPSGKKARE	IDESLIPYKK	WELBACVDAA	LLATQMDRVN	AIPFTYEQLD	VLKHKLDELY	360

5	GRGQLDKDTL RLAFQNMNGS KLLGPHVEGL	HLGYLPLKMS DTLTAFYPGY EYFVKIQSFL KABERHRPVR TVLALLLAST	LCSLSPEELS GGAPTEDLKA DWILRQRQDD	SVPPSSIWAV LSQQNVSMDL	RPQDLDTCDP ATFMKLRTDA	RQLDVLYPKA VLPLTVAEVQ	420 480 540 600
	Nucleic Act	37 DNA sequid Accession	#: NM_0134	104.1			
10	1	11 CTCCCGTCTG	21 	31 CGGACAGAGA	41 GCTACCGGTG	51 GACCCACGGT	60
15	GCCTCCCTCC CTGTGGGGAC	CTGGGATCTA CGCCCTGGCA CTGGCTGGAG	CACAGACCAT GCCTCCTGTT	GGCCTTGCAA CCTGCTCTTC	CGGCTCGACC AGCCTCGGAT	CCTGTTGGTC GGGTGCATCC	120 180 240
15	AACCCCCCAT GGTGTCCGGC	AACATTTCCA CTGAGCACGG TCAACAGAGC	GCCTCTCCCC	TCGCCAACTC GGAGCTGGCT	CTTGGCTTCC	CGTGTGCGGA CACAGAAGAA	300 360 420
20	GGACCTGGAC GCCCCAGGCC	GCCCTCCCAT TGCACCCGTT CCCGAGCGAC	TGGACCTGCT TCTTCTCCCG	GCTATTCCTC CATCACGAAG	AACCCAGATG GCCAATGTGG	CGTTCTCGGG ACCTGCTCCC	480 540 600
	GGGGTCTCTG TGGGCGCTTT	CTGAGCGAGG GTGGCCGAGT CAGGACCAGC	CTGATGTGCG CGGCCGAAGT	GGCTCTGGGA GCTGCTACCC	GGCCTGGCTT CGGCTGGTGA	GCGACCTGCC GCTGCCCGGG	660 720 780
25	CTACGGCCCC CGTGCTGGGC	CCGTCGACAT CAGCCCATCA CGGGACCCAT	GGTCTGTCTC TCCGCAGCAT	CACGATGGAC CČCGCAGGGC	GCTCTGCGGG ATCGTGGCCG	GCCTGCTGCC CGTGGCGGCA	840 900 960
30	CCGGCGGGAA GAGCCTCATC	GTGGAGAAGA TTCTACAAGA GACCGCGTGA	CAGCCTGTCC AGTGGGAGCT	TTCAGGCAAG GGAAGCCTGC	AAGGCCCGCG GTGGATGCGG	AGATAGACGA CCCTGCTGGC	1020 1080 1140
	GCATAAACTG CTACCTCTTC	GATGAGCTCT CTCAAGATGA GCTTTGCTTG	ACCCACAAGG GCCCTGAGGA	TTACCCCGAG CATTCGCAAG	TCTGTGATCC TGGAATGTGA	AGCACCTGGG CGTCCCTGGA	1200 1260 1320
35	GCGGCCCCTC AGACAAAGAC	CCACAGGTGG ACCCTAGACA CTGAGCTCCG	CCACCCTGAT CCCTGACCGC	CGACCGCTTT CTTCTACCCT	GTGAAGGGAA GGGTACCTGT	GGGGCCAGCT GCTCCCTCAG	1380 1440 1500
40	GAACATGAAC	GACCCAAGGC GGGTCCGAAT AAGGCGCTCA	ACTTCGTGAA	GATCCAGTCC	TTCCTGGGTG	GGGCCCCCAC	1560 1620 1680
40	CCACGTGGAG GCAGCGGCAG	GATGOGGTGC GGCCTGAAGG GACGACCTGG	CGGAGGAGCG ACACGCTGGG	GCACCGCCCG GCTGGGGCTA	GTGCGGGACT CAGGGCGGCA	GGATCCTACG TCCCCAACGG	1740 1800 1860
45	ACCTGGACCT CCACTCCCTT	CTAGACCTCA GTTCTCACCG GCTGGCCCCA TTCCACCCCA	TCCTGGCACT GCCCTGCTGG	GCTCCTAGCC GGATCCCCGC	TCCACCCTGG CTGGCCAGGA	CCTGAGGGCC GCAGGCACGG	1920 1980 2040 2100
50	Protein Ac	38 Protein cession #: 1		31	41	51	
		SCGDRPGSLL EVSGLSTERV	 FLLFSLGWVH	 PARTLAGETG	 TESAPLGGVL	 TTPHNISSLS	60 120
55	LLFLNPDAFS RALGGLACDL STMDALRGLL	GPQACTRFFS PGRFVAESAE PVLGQPIIRS ESLIFYKKWE	RITKANVDLL VLLPRLVSCP IPQGIVAAWR	PRGAPERQRL GPLDQDQQEA QRSSRDPSWR	LPAALACWGV ARAALQGGGP QPERTILRPR	RGSLLSEADV PYGPPSTWSV FRREVEKTAC	180 240 300 360
60	GYPESVIQHL IDRFVKGRGQ VLYPKARLAF TVAEVQKLLG	GYLFLKMSPE LDKDTLDTLT QNMNGSEYFV	DIRKWNVTSL AFYPGYLCSL KIQSPLGGAP RHRPVRDWIL	ETLKALLEVD SPEELSSVPP TEDLKALSQQ	RGHEMSPQAP SSIWAVRPQD NVSMDLATFM	RRPLPQVATL	420 480 540
65	Nucleic Ac	39 DNA seq id Accessio uence: 11	n. #: NM_001: 362				
70	CCCGAGTTTG TTCGTGATGG		CTGGATCAAA GAACAGOGTC	ATCACCCTTA ACCATTCGGG	TTCTGGTGTA TCACCCAGGT		60 120 180 240
75	TTGGTGTTCC ACGTCCAGCT GCTACGCTGC	TCATCGGCAT ACACCCTGTC TGCACGTGCT	GCCCATGGAG CTGCAAGCTG GACGCTCAGC	TTCTACAGCA CACACTTTCC TTTGAGCGCT	TCATCTGGAA TCTTCGAGGC ACATCGCCAT		300 360 420 480
80	GTCACCTCCG GTGAACGTGC CAGCCCGAGA CAGTCCAGCA	CCCTGGTGGC CCAGCCACCG CCTCCAATAT TCTTCGGCGC	ACTGCCCTTG GGGTCTCACT GTCCATCTGT CTTCGTGGTC	TGCAACCTCT ACCAACCTCT TACCTCGTGG	TGGGTACTGA CCAGCACCCG CCAGCCGCTG TCCTGCTCTC	GTACCCCTG CCACCACGAG GACCGTGTTC CGTAGCCTTC GGCCGGGGGC	540 600 660 720
85	ACGCGGCCTC ACCATCATCT	CGCAGCTGAG CTCCTGAGGCT	GAAGTCCGAG GATTGTTGTG	AGCGAAGAGA ACATTGGCCG	GCAGGACCGC TATGCTGGAT	CAGGAGGCAG GCCCAACCAG CTACTTCCGG	840 900

5	CCGCTCCTGT TGCCGCCTGT ACCACCGACA TCTGCAAGGA TCTAAGTCCC	TCCTCCTCCC ACACGGTGTC CGCTGCAGCA GCGCCCGCTT GAACTGAGAA AGTCATTGAG CAGAGAAATGG	CTCGCAGCAG CGCCAACCAC TGTGCAGCGC GATTTTCTTA TCTCGAGTCA	TTTCGGCGGG GAGAAGCGCC CCGTTGCTCT AGCACTTTTC CTAGAGCCCA	TGTTCGTGCA TGCGCGTACA TCGCGTCCCG AGAGCGAGGC ACTCAGGCGC	GGTGCTGTGC TGCGCACTCC GCGCCAGTCC CGAGCCCCAG	1020 1080 1140 1200 1260 1320
10		40 Protein cession #: N 11		31	41	51	
	Ī	1	1	1	<u> </u>]	
15	KGYLQKEVTD ATLLHVLTLS VNVPSHRGLT MCWNMMQVLM IRRIMAAAKP	CSQIIDHSHV HMVSLACSDI FERYIAICHP CNRSSTRHHE KSQKGSLAGG KHDWTRSYFR EKRLRVHAHS	LVFLIGMPME FRYKAVSGPC QPETSNMSIC TRPPQLRKSE AYMILLPFSE	FYSIIWNPLT QVKLLIGFVW TNLSSRWTVP SEESRTARRQ TFFYLSSVIN	TSSYTLSCKL VTSALVALPL QSSIFGAFVV TIIFLRLIVV PLLYTVSSQQ	HTFLFEACSY LFAMGTEYPL YLVVLLSVAF TLAVCWMPNQ FRRVFVQVLC	60 120 180 240 300 360 420
20		LEPNSGAKPA					
	Nucleic Ac	41 DNA sequid Accession	1 #: NM_022	358			
25	1	11	21	31	41	51	
	CGCCATGCGG	GTCCGGGCAC AGGCCGAGCG GCTGCTGTCT	TGCGCGCGGC	CGGGCTGGTC	CTGTGCACCC	TGTGTTACCT	60 120 180
30	ACTGCTGGTC CCGCGAGCTG GTTCCCCGGC CGCGCCGGGT	CAGAAGCGGG GAGCGCCTGG TCCTTCTACT ACGGACTCCG GTCACTTTCC	GCGCTCTCCG CGCTCCAGGC TCGCCATCAC GCAAGGTCTT	GAGGAAGTTC TGAGCCCCAC CGTCATCACT CTGCATGTTC	GGCTTCTCGG CGCGCCGGCC ACCATCGGGT TACGCGCTCC	CCGAGGACTA GCCAGTGGAA ACGGCCACGC TGGGCATCCC	240 300 360 420 480
35	CCTGTTGGCG GGTGGTGGCC GCACTTCGAG CATCGGCTTC	GCCAAGTGCT GGGCTGCTGG GGCTGGACCT GGCGACTTCG TTCAGCTTCC	GCCTGGGCCT CGTGTGCCGC TCTTCCACGC TGGCACTGCA	GCGGTGGACG CACCCTGGCC CTACTACTAC GAGCGGCGAG	TGCGTGTCCA CTCGGGGCCG TGCTTCATCA GCGCTGCAGA	CGGAGAACCT TCGCCTTCTC CCCTCACCAC GGAAGCTCCC	540 600 660 720 780
40	CAACCTGGTG CCCCCCAGC CCCGGCCCGC CGCCGCGAC	GTCCTGCGCT CCGCGCCCCC TCCGTGGGCT	TCCTCGTTGC CGGGGGGCGCC CCGCCTCTGT TTTCGCCCCC	CAGCGCCGAC CGAGAGCCGT CTTCTGCCAC CTCGAGCCCG	TGGCCCGAGC GGCCTCTGC GTGCACAAGC GGGGTCGTGC	GCGCTGCCCG TGCCCCGCCG TGGAGAGGTG GTGGCGGGCA	840 900 960 1020 1080
45	AATCTGGAAT GGATGACGGG AAGTCCCCTC	GGGAGGGTCT CCTCTAGGCG	GGCTTCAGCT GTCTTCTGCC AAAAATATAT	ATCAGGGCAC ACGAGCAGTT	CCTCCCCAGG TCTCATTACT	GATTGGAAAC	1140 1200 1260
50		42 Protein cession #: 1		31	41 .	51	
	ī	ī	ī	Ĩ	ī ·	ĩ	
55	ELERLALQAE TLVTFQSLGE FEGWTFFHAY LVVLRFLVAS	PHRAGRQWKF RLNAVVRRLL YYCFITLTTI ADWPERAARP	PGSFYFAITV LAAKCCLGLR GFGDFVALQS PSPRPPGAPE	ITTIGYGHAA WTCVSTENLV GEALQRKLPY SRGLWLPRRP	PGTDSGKVFC VAGLLACAAT VAFSFLYILL	KFGFSAEDYR MFYALLGIPL LALGAVAFSH GLTVIGAFLN CHVHKLERCA	60 120 180 240 300
60	KUNIAGESPES	SPGVVRGGQA	PRPGARMASI				
	Nucleic Ac Coding seq	43 DNA seq id Accessio uence: 220.	n #: №M_000 .1656				
65	ì	11 	21 	31 	41 	51 } .	
	TGGCCCAGGG	AGTGTGAGGC ACATGAGGTT	TGCAGCCTCA GGCAGAGGGC	GAAGGTGTGA AGGCAAGCTG	GCAGTGGCCA GCCCTTGGTG	CCAACCTTGG CGAGAGGCAG GGCCTCGCCC GGTCCAGCAG	60 120 180 240
70	GCGCTGCTCG AACACCACCA GGTGTGCGCC	CCTTGCTCCT GGCCCGCTCT CCGTGAGGGA	CCCCACACTO GCTGAGGCTG CTGGAGGAAG	CTGGCACAGG TCGGATTACC CCAACCACCG	GAGAAGCCAG TTTTGACCAA TATCCATTGA	GAGGAGCCGA CTACAGGAAG CGTCATTGTC CTGGTACCGG	300 360 420 480
75	TTGTCCATCO GTGGGGAAGT TACAAGCCCO	CCACGGACAG CTCCAAATAT TTCAGGTGGT	CATCTGGGTC CCCGTACGTC GACTGCCTGT	CCGGACATTC TATATTCGGC AGCCTCGACA	TCATCAATGA ATCAAGGOGA ATCTACAACTT	CATCACCAAG GTTCGTGGAT AGTTCAGAAC CCCCTTCGAT	540 600 660 720 780
80	TCTTTGTGGC GAGTGGGAGT TACTATGCAG	GCTTGCCAGA TGCTGGGGGT AAATGAAGTT	AAAGGTGAAA GCTGCCCTAC CTATGTGGTC	TCCGACAGGA TTTCGGGAGT ATCCGCCGG	GTGTCTTCAT TCAGCATGGA GGCCCCTCTT	CATCAACATC GAACCAGGGA AAGCAGTAAC CTATGTGGTC CTACCTGCCC	900 960 1020
85	CCCAACAGTO	GCGAGAGGG1 TTTCTGACAC	CTCTTTCAAC GCTGCCGGCC	ATTACACTO	C TOCTGGGCTA GCACTCCTCT	CTCGGTCTTC CATTGGTGTC CTTCATTGTG	1080 1140 1200

	000000000					MAI company	
		ACAAGCAAGA					1260
		TCGCCTGGCT					1320
		AAGCCACCAA					1380
5		CCCAGGACTT					1440
,		CCTCGCTGGC					1500
		AGCGGGATGA					1560
		AGCTGCTATT					1620 1680
		TCTGGTCCAT					
10		CTGGTTAGGT					1740
10		GACATTTTCA AATCACAAGC					1800 1860
							1920
	DECACCACA	CTTGTCCCAC ACTCGGGCAC	TCCCTAGCAGC	CACCAIGGC	CTCCACTOTT	CCCCATTGAC	1980
		ATAAGGGACT					2040
15		CCAACTCTCT					2100
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	ATCAGATGAT	GGGAGIGGGA	NONNIANNI	GCAGIGADAC			
	Sea ID NO:	44 Protein	seguence				
20	•	ession #: N					
	1		21	31	41	51	
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	MLLWVOOALL	ALLLPTLLAQ	GEARRSRNTT	RPALLRLSDY	LLTNYRKGVR	PVRDWRKPTT	60
		LNVDEKNOVL					120
25		SPNIPYVYIR					180
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		GCCTCGGCCA					60
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40		GGAGGACCCG					180
40		GGCGCCCTCC					240
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55		ATTCTGTGAA					1080
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		GAGGCGGGAA				AGAGGAGCGA	1320
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50	GPCAGGGGGG	TCAATCATGG	GATCTGTGAG	TGGADACATA	ATAGAGAAGA	TGATTTTGAC	1500
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65						GGATGAAAAG	
						CATCATTTTT	1800
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		AATTCTTTGT					
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80	1	11	21	31	41	51	
	1	1		1	1	1	
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0.5						DCLDIDECAS	180
85 _.	GKVICPYNRR	CVNTFGSYYC	KCHIGFELOY	ISGRYDCIDI	NECTMDSHTC	SHHANCFNTQ	240
•					20	10	

5	PEPTRTPTPK SLRGDVFFPK WNPADRDNAI	VNLQPPNYEE VNEAGEFGLI GFYMAVPALA WEKTTSEDEK	IVSRGGNSHG LVQRKALTSK GHKKDIGRLK	RAPGTIKORI GKKGNEEKMK LEHKOLNISV LLLPDLQPQS GTDATKSIIF	egledekree DCSFNHGICD NFCLLFDYRL	KALKNDIEER WKQDREDDFD AGDKVGKLRV	300 360 420 480 540
10	Nucleic Aci	47 DNA sequent of Accession tence: 167	#: NM_0050	946			
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	GGATTTCCGG	GCTCCATGGC	AAGATCCCTT	CTCCTGCCCC	TGCAGATCCT	ACTGCTATCC	60
1.5				CAGGGTGACA			120
15				GCCCTGCTCA			180 240
				GGCGACAGGA			300
				ACACAGACCC			360
20				TCCATGGTGA GTCTCCGGCT			420 480
	GATGTGACCT	TTCCCTCTGA	CCTCATGTGC	GTGGATGTCA	AGCTCATCTC	CCCCCAGGAC	540
				AATTCCATGC			600
				GGGGGACCGT TGCGGCCAAC			660 720
25	ACTCAAGTGT	GCAAGTTCAC	CAAGTGGATA	AATGACACCA	TGAAAAAGCA	TCGCTAACGC	780
				ACAGAAAATG TTCCTCAAAG			840 900
				CCTAAAACCA			960
20	AACCCTCAA						
30	Sea ID NO:	48 Protein	semience				
		ession #: 1					
	1	11	21	31	41	51	
35	MARSILLAPLO	ILLISTATET	AGEEAOGDKI	 IDGAPCARGS	HPWOVALLSG	NOLHCGGVLV	60
55				QRIKASKSFR			120
				TTTSPDVTFP			180 240
	FTKWINDTMK		CNGDSGGFLV	CRGTLQGLVS	WGIFFCGQFN	DEGVIIQVCK	240
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		49 DNA sequid Accession		466.1			
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45	1	11	21	31	41	51 I	
73	GAATTCGGCG	ATGCCTCACA	ACTCCATCAG	ATCTGGCCAT	GGAGGGCTGA	ACCAGCTGGG	60
				GGAAGTGGTC			120
		GGTGTAAGGC		CTCTCGCCAG			180 240
	CGTCAGCAAG	ATCCTTGGCA					
50	GGGCTCCAAG		CCACCCCAA	GGTGGTGGAĞ	AAGATTGGGG	ACTACAAACG	300
50	GGGCTCCAAG CCAGAACCCT	CCCAAGGTGG ACCATGTTTG	CCACCCCAA CCTGGGAGAT	GGTGGTGGAĞ CCGAGACCGG	AAGATTGGGG CTCCTGGCTG	ACTACAAACG AGGGCGTCTG	360
50	GGGCTCCAAG CCAGAACCCT TGACAATGAC	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA	CCACCCCAA CCTGGGAGAT GTGTCAGCTC	GGTGGTGGAĞ CCGAGACCGG CATTAATAGA	AAGATTGGGG CTCCTGGCTG ATCATCCGGA	ACTACAAACG AGGGCGTCTG CCAAAGTGCA	
	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC	GGTGGTGGAĞ CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA	AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG	ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG	360 420 480 540
50 55	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG	GGTGGTGGAĞ CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG	AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG CCTGGCAGCG	ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGAGAA	360 420 480 540 600
	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AGTGATCAGG AAGCACCTTC	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCCG GCACGGATGC	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG ACTAAGCATT CTTCAGCCAG	AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG CCTGGCAGCG GACTCACAGA CACCACCTCG	ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCCGCTCGA	360 420 480 540 600 660 720
	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA GTGCCCATTT	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AGGATCAGG AAGCACCTTC GAGCGGCAGC	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCCG ACTACCCAGA	GGTGGTGGAĞ CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG ACTAAGCATT CTTCAGCCAG GGCCTATGCC	AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG CCCTGGCAGCG GACTCACAGA CACCACCTCG TCCCCCAGCC	ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG	360 420 480 540 600 660 720 780
	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC GGGCCCCGG GTGCCCCATT CGAGCAGGGC	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA ACCTCCCTA CCCAGCTCAG TCCATCAATG AGTGATCAGG AAGCACCTTC GAGCGGCAGG CTCTACCCGC	CCACCCCAA CCTGGGAGAT GTGTCAGCTG TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCC ACTACCCAGA TGCCCTTGCT	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG ACTAAGCATT CTTCAGCCAG	AAGATTGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG CCTGGCAGCG GACTCACAGGA CACCACCTCG TCCCCCAGCC CTGGACGACG	ACTACAAACG AGGGCETCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCAC	360 420 480 540 600 660 720
55	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC GGGACCCCGA GTGCCCATTT CGAGCAGGGC CCTGACCCC GGTGCCAGAT GGTGCCAGAT	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AGGACCCTTC GAGCGGCAGC CTCTACCCGC TCCAACACGC CCTCACTCAC	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG GCACGGATGC ACTACCCAGA TGCCCTTGCT CACTGGGGC CCTTCGCCAT	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTCGCTCAG ACTTAGCCAG GGCCTATGCC CAACAGCACC AAAGCAGGAAC AAAGCAGGAACA	AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG CCTGGCAGCG GACTCACGAG CACCACCTCG TCCCCCAGCC CTGGACGACGACA ACCCCCGAGGG	ACTACAAACG AGGGCTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTTC	360 420 480 540 600 660 720 780 840 900 960
55	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC CAGGACCCCGA GTGCCCATTT CGAGCAGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCACCC TAGCTCCACCT TAGCTCCACCC	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATAG AAGGACCATTC GAGCGGCAGC CTTACCCGC TCCAACACG CCTCACTCAC CCTTCCTCTT	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCG ACTACCCAGA TGCCCTTGCT CACTGGGCC CCTTGCCCAT TATCTAGCTCC	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTCGCTCAG ACTAGCATT CTTCAGCCAG GGCCTATGCC CAACACCACC CAACACCACC AAAGCAGGAA CGCCTTTTG	AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG TCCCCCAGCC CTGGACGACA ACTCACCAGA ACCCCCGAGGG GATCTCCCGAGGG GATCTGCAGG	ACTACAAACG AGGGCTTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTTC AAGTCGGCTC	360 420 480 540 600 660 720 780 840 900 960 1020
55 60	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCG GTGCCCATTT CGAGCAGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCACC CGGGGTCCCG	CCCAAGGTGG ACCATGTTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGCAGC TCCAACACGC CCTCACTCAC CCTTCCTCTTC	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CGGTCCTGGG ATAGCTGCG ACTACCCAGG ACTACCCAGG CCCTTGCCT CACTGGGGCG CCTTCGCCAT TATCTAGCTC	GGTGGTGGAG CCGAGACCGG CATTANATAGA CGTGGCCACC CCCGGAGTCA ACTAAGCATT CTTCAGCCAG GGCCTATGGC CAACAGCACC CAACAGCACC CAACAGCACC AAAGCAGGAA CGCCTTTTG TGCTGCCTCCC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTGG TCCCCAGCC CTGGACGACG ACTCACAGA ACCCCCAGGA GACTCACAGA GCCCCAGGA GCTCACCAGG GTGTACCAGG	ACTACAAACG AGGGCTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTTC	360 420 480 540 600 660 720 780 840 900 960
55	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC GGGACCCCGA GTGCCCATTT CGAGCAGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCACC CGGGGTTCCCG CCAGGCCCTC CCATCCCCCC	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AGGCGCAGC CTCTACCCGC CCTCACTCAC CCTTCCTCT CCCTTCAATG CCTTCCAATG CCTTCAATG CCTTCAATG AGCGGACAGC AGCGGACAGG	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG GGCTCCTGGG ATAGCTGCG ACTACCCAGA TGCCCTTGCC CCTTCGCCAT TATCTAGCTG CCTTTCCCCAT TATCTAGCTG GGAGATGGT GGAGATGGT	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTCGCTCAG GGCCTATGCC CAACAGCACC CAACAGCACC AAAGCAGGAA CGCCTTTTTG TGCTGCCTCCC GGGGCCCACC CTCCTCTGCCC	AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG GACTCACGA CACCACCTCG TCCCCCAGCC CTGACGACC ACCCCCGAGG GATCTCCCAGGC GTTCCCCGAGG GTTTCCGGC CTGCCCGGAT ACCCCCGAGG	ACTACAAACG AGGGCTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAA ACCCCCCCCCC	360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140
55 60	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA GTGCCCATTT CGAGCAGGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCACC CGGGGTCCCG CCAGGCCCTC CATCCCCAC AAGTGAATAC	CCCAAGGTGG ACCATGTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGCAGC TCCAACACGC CCTCACTCAC CCTTCTCATCAC CCTTCTCATCAC CCTTCTCATGG TCCACAGGC TCCACAGGC TCCACAGGC TCCACAGGC TCCACAGGC TCCACAGGC TCCACAGGC TCCACAGGC TCTCACAGGC TCTCAC	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CGGACCCCTGGG ATAGCTGCG GCACGGATGC ACTACCCAGG CCATTGCCTTGCT CACTGGGGCG CCTTCGCCAC CCTTTCCCCAC GAGAGATGGT GCAGCTATGCC CCTTTCCCCAC GAGAGATGGT CCTTTCCCAC	GGTGGTGGAG CCGAGACCGG CATTANATAGA CGTGGCCACC CCCGGAGTCA ACTAAGCATT CTTCAGCCAG GGCCTATGCC CAACAGCACC CAACAGCACC GAGCTCTGG TGCTGCCCCGGGGCCCACC CGCGGGCCCACC CGCGCCCCCCCC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTGG TCCCCAGCG CTGGACGACG ACTCACAGA ACCCCCGGAGG GATTCACCAGA ACCCCCGAGG CTCACCAGG CTGCCGAGG CTGCCCGGAC ATTCCCTACA CTCCCTACA	ACTACAAACG AGGGGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAGGAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCCAC CCTACCCGT TGTCCAGTTC AGTTCCAGTTC AGTTCACGCG ACCCACCCCA ACGCGCCCG ACCCACCCCG ACGCGCCGG GCGAGGCCTG	360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140
55 60	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CCCGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA GTGCCCATTT CGACGAGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCAC CGGGGTCCGG CCAGGCCCTC CATCCCCACC AAGTGAATAC GCGCTTCCCCC	CCCAAGGTGG ACCATGTTTG ACTGTCACTA ACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGGCAGC CCTCAACCCGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG CTCTCACGCG AGCGGACAGG TCCACTCAC CTTCCTCACT CCTTCAATG CTCTCACTCAC AGCGACAGGG AGCGACAGG	CCACCCCAA CCTGGGAGAT TGTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCCG ACTACCCAGA TGCCCTTGCCAT TATCTAGCTG CCTTTCCCCA GAGAGATGGT GCAGTTCCCCA GAGAGATGGT CCTTTCCCCA TATCTAGCT CCTTTCCCCA TATCTAGCT CCTTTCCCCA TATCTAGCT TATCTAGCT CCTTTCCCCA TGCTGAGTTC TGTGGCCA	GGTGGTGGAG CCGAGACCGG CATTANATAGA CGTGGCCACC CCCGGAGTCA ACTAAGCATT CTTCAGCCAG GGCCTATGCC CAACAGCACC CAACAGCACC GAGCTCTGG TGCTGCCCCGGGGCCCACC CGCGGGCCCACC CGCGCCCCCCCC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG CTGGAGGGG ACTCACAGA ACCCCCAGCC GATTCACAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC GTGTACGGGC TTCGCAGGAC ATCGCAGGA ATCCCCAGGA ATCTCCAGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA	ACTACAAACG AGGGGTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAA ACTCCCGAACA AGCCGCTCGA ACACCAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTTC AAGTCGGCTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGGCAGG ACCCACCCCA TGGTGGCAGG CCAACGCCGC CATCAAGGCCT	360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
556065	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC CAGGCCCCGA GTGCCCATTT CGACCACGGCCCCT GGTGGCAGAT TAGCTCCACC CGGGGTCCCC CATCCCCACC AAGTGAATAC GCGCTTCCCCC GGTGCACCCC GGTGCCCCCC CATCCCCACC AAGTGAATAC GCGCTTCCCCC GAGTGCACCC	CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGGCAGC CTCAACACGC CCTCACTCAC CCTTCCTCTT CCCTTCAGGGC AGCGGACAGG TCTCAGGGC AGCGGACAGG TCTGGCAATG ACTCCAGCT CCCTCAGGGC CCCACCACTGCT CCCACCACTG	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG GGCTCCTGGG ATAGCTGCG ACTACCCAGA TGCCCTTGCC CCTTCGCCAT TATCTAGCTC CCTTTCCCCAT GGAGATGGT GCAGGATGGT GCAGGATGGT CCTTTCCCCAT CCTTTCCCCAT CCTTTCCCCAT CCTTTCCCCAT CCTTTCCCCAT CCTTTCCCCAT CCACGGCTTCCCCAT CCACGGCCTTCCCCAT CCACGGCCTT	GGTGGTGGAG CCGAGACCGG CATTANAGAG CGTGGCCACC CCCGGAGTCA ACTAGCCAG CATCGCTCAG ACTAGCATC CAACGCACC CAACGCACC CAACGCTCTCG AAAGCAGGAA CGCCTTTTG TGCTGCCTCC GGGGCCCACC CACCCCCTACC CCACCACCCCCACC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG CTGGAGGGG ACTCACAGA ACCCCCAGCC GATTCACAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC GTGTACGGGC TTCGCAGGAC ATCGCAGGA ATCCCCAGGA ATCTCCAGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA	ACTACAAACG AGGGGTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAA ACTCCCGAACA AGCCGCTCGA ACACCAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTTC AAGTCGGCTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGGCAGG ACCCACCCCA TGGTGGCAGG CCAACGCCGC CATCAAGGCCT	360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
55 60	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA GTGCCCATTT CGAGCAGGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCACC CCAGGCCCTC CATCCCCACC CAGGCCCTC CATCCCCACC GGTGGAATAC GCGCTTCCCC GGGTGCACCC Seq ID NO:	CCCAAGGTGG ACCATGTTTG ACTGTCACTA ACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGGCAGC CCTCAACCCGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG CTCTCACGCG AGCGGACAGG TCCACTCAC CTTCCTCACT CCTTCAATG CTCTCACTCAC AGCGACAGGG AGCGACAGG	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CGGACTCCTGGG ATAGCTGCG ACTACCCAGG CCACTGGGCC CCTTCGCCAT TATCTAGCTC CCTTTCCCCA GGAGATGGT CCTTTCCCCA GGAGATGGT CCTTTCCCCA GCAGCTATGGC CCTTTCCCCA TGCAGCTTC CCTTTCCCCA TGCAGCTTC CCACGCCTT CCCACGCCTT	GGTGGTGGAG CCGAGACCGG CATTANAGAG CGTGGCCACC CCCGGAGTCA ACTAGCCAG CATCGCTCAG ACTAGCATC CAACGCACC CAACGCACC CAACGCTCTCG AAAGCAGGAA CGCCTTTTG TGCTGCCTCC GGGGCCCACC CACCCCCTACC CCACCACCCCCACC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTGG CTGGAGGGG GATTCACAGA ACCCCGAGCG ACTCACCAGA ACCCCGAGGG GATTGCAGGA CTGGCCGGAGG ATCTGCAGG ATCTGCAGG ATTGCAGGC ATTGCAGGC ATTGCAGGC ATTGCAGGC ATTGCAGGCA ATCGCAGGAGA ATCGCAGGCA ATCGCAGGAGA ATCGCAGGCA ATCGCAGGCAG ATCGCAGGCA ATCGCAGGCA ATCGCAGGCAGA ATCGCAGGCA ATCGCAGGCAGA ATCGCAGGCAGA ATCGCAGGCAGA ATCGCAGGCAGA ATCGCAGGCAGA ATCGCAGGCAGA ATCGCAGGCAG	ACTACAAACG AGGGCTCTG CCAAAGTGCA ATTCCCTGGG ACACAGGGACA ACTCCCGACAGGACA AGCCGCTCGA AGCCGCTCGA ACACCAAAGG CCTACCCGT TGTCCAGTTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGGCAGG CCTACCCCCT TGTGCAGGCTG CATCAAGGCCTG CATCAAGGCCTG CATCAAGGCCT	360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
556065	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA GTGCCCATTT CGAGCAGGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCACC CCAGGCCCTC CATCCCCACC CAGGCCCTC CATCCCCACC GGTGGAATAC GCGCTTCCCC GGGTGCACCC Seq ID NO:	CCCAAGGTGG ACCATGTTG ACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGCAGC TCCAACACGC CCTCACTCAC CCTTCCTCTTC CCTTCAATG AGCGACAGGC TCCACTCAC CCTCTCAATG CCCTCACTCAT CCCTCACTCATG CCCACCACTG TCCACCACCGC TCCACCACCGCT SO Protein	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CGGACTCCTGGG ATAGCTGCG ACTACCCAGG CCACTGGGCC CCTTCGCCAT TATCTAGCTC CCTTTCCCCA GGAGATGGT CCTTTCCCCA GGAGATGGT CCTTTCCCCA GCAGCTATGGC CCTTTCCCCA TGCAGCTTC CCTTTCCCCA TGCAGCTTC CCACGCCTT CCCACGCCTT	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG ACTAAGCATT CTTCAGCCAG GGCTATGCC CAACCTCTCG AAAGCAGGAC TGCTGCTCGCCCACCCCCACCCCCACCCCTACC CCCCTATTATGCCCCCCTACCCCCACACCCCTACCCCCTACCCCCTACCCCCTACCCCCTACCCCCC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG CTGGAGGGG ACTCACAGA ACCCCCAGCC GATTCACAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC GTGTACGGGC TTCGCAGGAC ATCGCAGGA ATCCCCAGGA ATCTCCAGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGA ATCGCAGGAC ATCGCAGGAC ATCGCAGGAC ATCGCAGGAC ATCGCAGGAC ATCACACATCCA	ACTACAAACG AGGGCTCTG CCCAAAGTGCA ATTCCCTGGG ACTCCCGGACA ACTCCCGGACA AGCCGCTCGA AGCCGCTCGA AGCCGCTCGA ACACCAAAGG CCTACCCGGT TGTCCAGTTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGGCAGG CCTACCGGT TT	360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
55 60 65 70	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCTA CGACCCCTT GGTGCCAGTT TAGCTCCACC CCAGGCCCTC CATCCCCACC CAGGCCCTC CATCCCCACC GGTGCAATA GCGCTTCCCC GGTGCAGT CAGGCCTCC CATCCCCACC GAGTGCACCC Seq ID NO: Protein Ac 1	CCCAAGGTGG ACCATGTTG ACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGCAGC TCCAACACGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG AGCGACAGGC TCCACCAGGC TCCACCAGGC TCCACCAGGC TCCACCAGGC TCCACCAGGC TCCACCACCGC TCCACCACGCT TCCACCAGGC TCCACCACGGC TCCACCACGGC TCCACCACGGC TCCACCACGGC TCCACCACGGC TCCACCACGGC TCCACCACGGC TCCACCACGGC TCCACCACGGCC TCCACCACGGCC TCCACCACGGCCC TCCACCACGGCCCCCCCCCC	CCACCCCAA CCTGGGAGAT GTGTCAGGTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCG ACTACCCAGG CCTTCGCCAT TATCTAGCTC CCTTTCCCCA GAGAGATGGT CCTTTCCCCA GAGAGATGGT CCTTTCCCCA GAGAGATGGT CCTTTCCCCA TGCTGGGCCA TGCTGAGTTC CCACGGCCTT Sequence NP_003457 21	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTAGCCAG ACTAGCCAG GGCCTATCCC CAACAGCACC CAACAGCACC GGGGCCCACC CTCCTCTGCCCC CCACCACCTCCC CCACCACCCCCACC CCACCCCTACC CCACCCCTACC CCACCCCTACC CCACCCCTACC CCCCATATTAT	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCGG TCCCCAGCG CTGGACGACG ACTCACAGA ACCCCCGAGG GATTCACCAGA ACCCCCGAGG GTTACCGGC GTGTACGGGC CTGCCCGAGG ATCCCCTACA TACAGTTCAC TACAGTACA	ACTACAAAAG AGGGGTCTG CCAAAGTGCA ATTCCCTGGG ACTCCCGGACA ACTCCCCGGCACA ACACGACACA ACCCCACCCC	360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1260
556065	GGGCTCCAAG CCAGAACCCT TGACACTAC GCAACCATTC CTCCACCTAC CTCCACCTAC CGGACCCCGA GTGCCCATTC GGTGCCATTC GAGCAGGGC CCTGACCCCT GGTGCAGAT TAGCTCCACC CAGCCCTC CATCCCCAC AAGTGAATAC GCGCTTCCC GAGTGCACCC GAGTGCACCC Seq ID NO: Protein AC 1 MPHNSIRSGE ILGRYYETGS	CCCAAGGTGG ACCATGTTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGGCAGC CTCACCAGC CCTCACTCAC CCTTCCCTTC	CCACCCCAA CCTGGGAGAT GTGTCAGCTG TGGACAGCTG CTGTAACTCC GGCTCCTTGG ACTACCCAGA TGCCCTTGCCAT CCACTGGGCGG CCTTCGCCAT GAGAGATGGT GCACTTGCCAT GCACTTGCCAT GCACTTGCCAT GCACTTGCCAT GCACTTGCCAT CCACTGGCCAT CCACTGGCCAT GCACGCCTT SEQUENCE NP_003457 21 VVNGRPLPEVV	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG CATCGCTCAG CAACAGCACC CAACCTCTCG AAAGCAGGAC CGCCTTTTTG CGGGGCCCACG CACCCCTAC CCCCATATAT TGACCATCTG ATTACCATCTGCC CACCCCTAC CCCCTACTGCC CCCTACTGCC CCCCTACTGCC CCCCTACTCC CCCCTACTGCC CCCCTACTGCC CCCCTACTGCC CCCCTACTGCC CCCCTACTGCC CCCCTACTGCC CCCCTACTGCC CCCCTACTGCC CCCCTACTGCC CCCCTACTCC CC	AAGATTGGGG CTCCTGGCTGA AAGTCCCTGA AAGTCCCTGA ACCCCAGTCGG GACTCACAGA CACCACCTCG TCCCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCGAGCG ACTCACCAGA ACCCCCGAGCG ATCTGCAGCA TCCCCCTGCAGC TCCCCCTGCACGAC TCCCCTGCACGAC TTACAGTACAG	ACTACAAACG AGGGGTCTG CCCAAAGTGCA ATTCCCTGGG ACTCCCGGACA ACTCCCGGACA AGCCGCTCGA AGCCGCTCGA AGCCGACCCCC CCTACCCGGT TGTCCAGTTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGGCAGC CTTACAGGCC TT 51 LRVSHGCVSK LLAEGVCDND	360 420 480 540 600 660 720 780 840 960 1020 1080 1140 1200 1320
55 60 65 70	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA GTGCCCATTT CGAGCAGGGC CCTGACCCCT GGTGCCAGT CATGCCACC CAGGCCCTC CATCCCACC CAGGCCCTC CATCCCCACC GGTGCAGAT Seq ID NO: Protein Ac 1 MPHNSIRSGE ILGRYYETGS TVPSVSSINF	CCCAAGGTGG ACCATGTTTG ACTGTCCCTA CCCAGCTCAG ACCTCCCTA CCCAGCTCAG AGCACCTTC GAGCGCAGC TCCAACACGC CCTCACTCAC CCTTCACTCAG CCTTCACTCAGGC AGCGGACAGG TCCACCACTG CCCACCACTG CCCACCACTG SO Protein CCGSION #: 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCG ACTACCCAG CCACGGATGC CCTTCGCCA CACTGGGGCG CCTTCGCCA CCTTTCCCCA CAGAGATGGT CCACTGGGCCA TGCTGAGTTC CCACTGGCCA TGCTGAGTTC CCACGGCCTT Sequence NP_003457 21 VNGRPLPEVV PVVATPKVVE NLPMDSCVAT	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTAAGCATT CTTCAGCCAG GGCCTATGCC CAACAGCACC CAACACTCTCG AAAGCAGGAA CGCCTTTTG CTCCTCTGCC CACCCCTACC CCACACTCTCG AAGCAGCACC CCCATATTAT TGACCATCTG KGGIVDLAHC KGLBYKRQNE KSLSPGHTLI	AAGATTGGGE CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTGG TCCCCAGCG CTGGAGACGACG ACTCACCAGA ACCCCCGGAGG GATTCACCAGA ACCCCCGAGG GTTACGGGC CTGCCCGAGT ATCACCAGA TACAGTTCCA TACAGTTCCA TACAGTTCCA TAGTTGAAGC TMFAWEIRDR PSSAVTPPES	ACTACAAAAG AGGGGTCTG CCAAAGTGCA ATTCCCTGGG ACTCCCGGACA ACTCCCCTGGA ACACGACAG ACCCCCACCCCA	360 420 480 540 600 660 720 780 840 900 1020 1020 1140 1200 1320
55 60 65 70	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CCACCTAC AATGACAGAC GTGCCCATTC CGACCCCT GGTGCCAGTT TAGCTCCACC CATCCCACC AAGTGACACC CAGGCCCTC CATCCCCACC AAGTGACACC Seq ID NO: Protein Ac I MPHNSIRSGE ILGRYYETGS TVPSVSSIME SINGLLGIAC ERQHYPEAYA	CCCAAGGTGG ACCATGTTTG ACCTCACTA ACCTCCCTA CCCAGCTCAG TCCATCAATG AAGCACCTTC GAGCGGCAGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG ACCGCACACGC AGCGGACAGG TCCAACACGC TCCACTCACT CCCTCCACTCACT CCCTCCACTCACT	CCACCCCAA CCTGGAGAT GTGTCAGCTG GGGTCAGCTG GGCTCCTGGG ATAGCTGCG ACTACCCAG ACTACCCAGA TGCCCTTGCT CACTGGGGGG CCTTCGCCAT TATCTAGCT GCATTCTCCCA GAGAGATGGT CCATTGCCAT TGCTATGCCAT TGCTATGCCAT TATCTAGCT CCATTGCCAT TATCTAGCT CCATTGCCAT TATCTAGCT CCATTGCCAT TATCTAGCT CCATTGCCAT TGCTGAGTTC CCACGGCCTT VNGRPLPEVV PKVATPKVVE NLPMDSCVAT SDQDSCRLST CLYPLPLLINST	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTCGCTCAG ACTCAGCCAG GGCCTATGCC CAACACCACC AAAGCAGGA CGCCTTTTTG GGGGCCCACC CACCCCTACC CACCACTTAGCCAG CCCCCTACC CACCACTTAGC CCCATATTAG TGACCATCTG CCCATATTAG TGACCATCTG CCCATAGTAG CCCATAGTAGACC CACCACTACCCCTACC CACCACCTACC CACCACCTACC CACCATAGTAG TGACCATCTG CCCATAGTAGACC CCCATAGTAGACC CCCATAGTAGACC CCCATAGTAGACC CCCATAGTAGACC CCCATAGTAGACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACC CCCATAGTAGACCACTACACTACACACTACACTACACACTACACTACACACTACACACTACACACTACACTACACACTACACTACACACTACACTACACACTACACACTACACACTACACACTACACACACACTAC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG TCCCCAGCC CTGGACGACGA ACTCACCAGA ACCCCCGAGC GATTGCAGG ATTGCAGG ATTGCAGG ATTGCAGG ATTGCAGGC TCCCCGAGC TCCCCGAGC TTGCCCGAGC TTGCCCGAGC TTGCCCGGAT TTGCAGGCA TCCTCCTACA TAGTTGAAGC TTAGTTGAAGC TMFAWEIRDR CFSSAVTPPES KHLRTDAFSC SNTPLGRNLS	ACTACAAACG AGGGCTCTG CCCAAAGTGCA ATTCCCTGGG ACACAGGGACA ACTCCCGGACA AGCCGCTCGA AGCCGCTCGA ACACCAAAGG GGGAAGGCCAC CCTACCCCGT TGTCCAGTTC AAGTCGCCTC AGTTCACGGG ACCCACCCCA TGTGGCAGG CCTACCCCCT TGTCACGGC TGTGCAGGCCT CATTCACGGG ACCCACCCCA TGTGGCAGG CCACCCCA TGTGGCAGG CCACCCCA TGTGGCAGG CCACCCCA TGTTGCCAGG CATCAAGGCC TT LLAEGVCDND CCACCCCA TGTTGCCAGG TGTTGCCAGG TGTTGCCAGG TGTTGCCAGG TT TI	360 420 480 540 600 660 720 780 840 960 1020 1080 1140 1200 1320
55 60 65 70	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CCCCCCTACCACCTAC AATGGATGAC CCGACCCCTAC GTGCCCACTTAC GCTGCCCCTC GCTGCCCCTC GCTGCCCCTC CATCCCCACC AAGTGAATAC GCGCTTCCCACC AAGTGAATAC GCGCTTCCCACC Seq ID NO: Protein AC 1 MPHNSIRSGE ILGRYYETGS TVPSVSSING SINGLLGIAG ERQHYPEAYAP PHSPFAIRQE	CCCAAGGTGG ACCATGTTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAGG TCCAATCAATG AAGCACCTTC GAGCGGCAGCC CTTCACCGCG CTCACTCAC CCTTCACTCAC CCTTCCATTCC AGCGGACAGG TCTCACTCAC CTTCACTCAC CTTCACTCAC CTCTCAATG CCCTCACTCAC SO Protein CCCACCACTG 11	CCACCCCAA CCTGGGAGAT GTGTCAGCTG GGGTCATGGCAGACTG GGACGGATGC ACTACCCAGA TGCCCTTGCCAT CCACTGGGCGG CCTTCGCCAT GAGAGATGGT GCAGGATGGCA GAGAGATGGT CCACTGGCCAT CCACTGGCAT CCACTGGCCAT CCACTGCAT CCACTGGCCAT CCACTGGCCAT CCACTGGCCAT CCACTGCAT CCACTGGCCAT CCACTGCCAT CCACTGCCAT CCACTGCCAT CCACTGCCAT CCACTGCCAT CCACTGC	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA CATCGCTCAG ACTCAGCCAG GGCTATGCC CAACCTCTCG AAAGCAGGAC CGCCTTTTTG GGGGCCCACG CACCCCTAC CCCCAATTAT TGACCATCT TGACCATCTGC CCCATATTAT TGACCATCTG KIGDYKRONE KSLSPGHTLI LDDGKATLTE LDLQVGSGVI LDUQVGSGVI	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG TCCCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCGAGCG ACTCACCAGA ACCCCCGAGCG ATCTGCAGCA TCCCCCAGACG TCCCCCAGACG TCTCCCCAGACG ATCTGCAGGC TTGCAGGCC TTGCAGGCC TTGCTCCTACAA TACAGTTGAAGC TTAGTTGAAGC TTAGTTGAAGC TTAGTTGAAGC TMFAWEIRDR PSSAVTPPES KHLRTDAFS SNTPLGRNLS PFNAFPHAAS	ACTACAAACG AGGGCTCTG CCCAAAGTGCA ATTCCCTGGG ACTCCCGGACA ACTCCCGGACA ACCCCCCGA AGCCGCCCCCA AGGCCCAC CCTACCCGGT TGTCCAGTTC AAGTCGCCCCC AGTCCACCCCA TGTGGCAGG ACCCACCCCA TGTGGCAGG CCTACCGGG ACCCCCCA TGTGGCAGG CCTACCCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG TT 51 LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPP HTDTYPVVAD TVYGGFTGQAL	360 420 480 540 600 660 720 780 960 1020 1140 1200 1320 60 120 180 240 300 360
55 60 65 70	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCTA CGGCCCCTT CGAGCAGGGC CCTGACCCCT CATGCCCCT CATGCCCACT CAGGCCCTC CATGCCCACC CAGGCCCTC CATCCCCACC GAGTGCAGAT GCGCTTCCCC AGTGGATAAC GCGCTTCCCC AGTGGATAAC GCGCTTCCCC TCCCACC Seq ID NO: Protein Ac I MPHNSIRSGE ILGRYYETS SINGLEGIAC ERQHYPEAYA PHSPFAIKQE LSGREMVGFI	CCCAAGGTGG ACCATGTTTG ACTGTCAACA AACCTCCTA CCCAGCTCAG AAGCACCTTC GAGCGCAGC TCCAACACGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG AGCGCACGC AGCGGCAGC TCCACCACGC TCCACCACTG CCCACCACTG SO Protein CCGGCACCACTG III GGLNQLGGAE IIRTKVQQPF PGSDKRKMDI SPSHTKGEQC TPEVSSSSST LPGYPPHIP	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCG ACTACCCAGG CCTTCGCCAT TATCTAGCTC CCTTTCCCCA GGAGATGGT CCTTCGCAT TATCTAGCTC CCTTTCCCCA GGAGATGGT CCTTTCCCCA GGAGATGGT CCTTTCCCCA TGCTGAGTTC CCACGGCCTT Sequence NP_003457 21 VNGRPLPEVV PKVATPKVVT NLPMDSCVAT SDQDSCRLST LYPLPLINTST PSSLSSSAFI TSGQGSYASSI	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTAGCCAG ACTAGCCAG GGCCTATCGC CAACAGCACC CAACAGCACC CAACAGCACC CCACTATTAT TGCCTAGC CCCCTACC CCACCTCTCG CCACCCCTACC CCACCTCTCG CCACCCCTACC CCACCCCTACC CCCCTACTCG CCCCCTACTCG CCCCTACTCG CCCCTACTCG CCCCCTACCC CCCCTACTCG CCCCCTACC CCCCTACTCG CCCCTACTCG CCCCTACTCG CCCCTACTCG CCCCCTACC CCCCTACTCG CCCCCTACTCG CCCCCTACTCG CCCCCTACTCG CCCCTACTCG CCCCCTACTCG CCCCCTACTCG CCCCCTACTCG CCCCCTACTCG CCCCCTACTCG CCCCCTACTCG CCCCTACTCG CCCCCTACTCG CCCCTACTCG CCCCCTACTCG CCCCCCTACTCG CCCCCTACTCG CCCCCCTACTCG CCCCCCTACTCG CCCCCTACTCG CCCCTACTCG CCCCTACTCCCCCT	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG TCCCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCGAGCG ACTCACCAGA ACCCCCGAGCG ATCTGCAGCA TCCCCCAGACG TCCCCCAGACG TCTCCCCAGACG ATCTGCAGGC TTGCAGGCC TTGCAGGCC TTGCTCCTACAA TACAGTTGAAGC TTAGTTGAAGC TTAGTTGAAGC TTAGTTGAAGC TMFAWEIRDR PSSAVTPPES KHLRTDAFS SNTPLGRNLS PFNAFPHAAS	ACTACAAACG AGGGCTCTG CCCAAAGTGCA ATTCCCTGGG ACACAGGGACA ACTCCCGGACA AGCCGCTCGA AGCCGCTCGA ACACCAAAGG GGGAAGGCCAC CCTACCCCGT TGTCCAGTTC AAGTCGCCTC AGTTCACGGG ACCCACCCCA TGTGGCAGG CCTACCCCCT TGTCACGGC TGTGCAGGCCT CATTCACGGG ACCCACCCCA TGTGGCAGG CCACCCCA TGTGGCAGG CCACCCCA TGTGGCAGG CCACCCCA TGTTGCCAGG CATCAAGGCC TT LLAEGVCDND CCACCCCA TGTTGCCAGG TGTTGCCAGG TGTTGCCAGG TGTTGCCAGG TT TI	360 420 480 540 600 660 720 780 960 1020 1140 1260 1320 60 120 180 240 300
55 60 65 70	GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC CGGACCCCTA CGGCCCCTT CGAGCAGGGC CCTGACCCCT CATGCCCCT CATGCCCACT CAGGCCCTC CATGCCCACC CAGGCCCTC CATCCCCACC GAGTGCAGAT GCGCTTCCCC AGTGGATAAC GCGCTTCCCC AGTGGATAAC GCGCTTCCCC TCCCACC Seq ID NO: Protein Ac I MPHNSIRSGE ILGRYYETS SINGLEGIAC ERQHYPEAYA PHSPFAIKQE LSGREMVGFI	CCCAAGGTGG ACCATGTTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAGG TCCAATCAATG AAGCACCTTC GAGCGGCAGCC CTTCACCGCG CTCACTCAC CCTTCACTCAC CCTTCCATTCC AGCGGACAGG TCTCACTCAC CTTCACTCAC CTTCACTCAC CTCTCAATG CCCTCACTCAC SO Protein CCCACCACTG 11	CCACCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCG ACTACCCAGG CCTTCGCCAT TATCTAGCTC CCTTTCCCCA GGAGATGGT CCTTCGCAT TATCTAGCTC CCTTTCCCCA GGAGATGGT CCTTTCCCCA GGAGATGGT CCTTTCCCCA TGCTGAGTTC CCACGGCCTT Sequence NP_003457 21 VNGRPLPEVV PKVATPKVVT NLPMDSCVAT SDQDSCRLST LYPLPLINTST PSSLSSSAFI TSGQGSYASSI	GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGAGTCA ACTAGCCAG ACTAGCCAG GGCCTATCGC CAACAGCACC CAACAGCACC CAACAGCACC CCACTATTAT TGCCTAGC CCCCTACC CCACCTCTCG CCCCTACC CCACCTCTCG CCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCTACC CCCCCTACC CCCCTACC CCCCCTACC CCCCCTACC CCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCCTACC CCCCTACC CCCCCTACC CCCCCCCC	AAGATTGGGG CTCCTGGCTG AAGTCCCTGA AAGTCCCTGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACCTCG TCCCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCGAGCG ACTCACCAGA ACCCCCGAGCG ATCTGCAGCA TCCCCCAGACG TCCCCCAGACG TCTCCCCAGACG ATCTGCAGGC TTGCAGGCC TTGCAGGCC TTGCTCCTACAA TACAGTTGAAGC TTAGTTGAAGC TTAGTTGAAGC TTAGTTGAAGC TMFAWEIRDR PSSAVTPPES KHLRTDAFS SNTPLGRNLS PFNAFPHAAS	ACTACAAACG AGGGCTCTG CCCAAAGTGCA ATTCCCTGGG ACTCCCGGACA ACTCCCGGACA ACCCCCCGA AGCCGCCCCCA AGGCCCAC CCTACCCGGT TGTCCAGTTC AAGTCGCCCCC AGTCCACCCCA TGTGGCAGG ACCCACCCCA TGTGGCAGG CCTACCGGG ACCCCCCA TGTGGCAGG CCTACCCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG ACCCACCCCA TGTGCCAGG TT 51 LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPP HTDTYPVVAD TVYGGFTGQAL	360 420 480 540 600 660 720 780 960 1020 1140 1200 1320 60 120 180 240 300 360
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45	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC	 GGTGCAGCGG ACAGCCTTGC CACCCCTCTA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC	120 180
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	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA GGCCGGGGAA CGATATGCAC CGGGGCGGTG TTTCAGAGTC	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGCT GTCACCAGTT	120 180 240 300 360 420
	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCA AACCAGGACC ATCATCAATG AGGCCCAACG GCCCACTGCA TATGAATCTG	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT GGCAGCAGAT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC GTTCCAGGGG	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA	CCATGGCTAC TTCTGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC	120 180 240 300 360 420 480
50	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG CACCCTGGCC	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGGT TTTCAGAGTG CTTTCAGGGG CCTCATGCTC	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTAGATCCA ATCAAATCCA	CCATGGCTAC TTCTGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGCT TGGCTACTCC TCGTCCCACT	120 180 240 300 360 420 480 540
	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT GGCAGCAGAT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGTG TTTCAGGGTG GTTCCAGGGG CCTCATGCTC CGTCTCCTCT	GGTGCAGCGG ACAGCCTTGC ACACCCCTCTA GACGCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC ATCAAATCGA ATCAAATCGA CATTGTCCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAGAAAAA CTGCTGGGAC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGTC TCGCTACCAGTC TCGTCCCACT AAAGTGCTTG	120 180 240 300 360 420 480
50	I CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACTGCA TATGBATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GGGGGGACAAC GCGTGCTAACGA GCGTGCTAACGA	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGTCCAGGG CCTCATGCTC CGTCTCCTCT CAAGAGCCCC TCAGAAAAGG	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCGAGGATG	CCATGGCTAC TCTTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCGAG	AGCAAGACCC CACAGAGCAC CACAGAGCAC CAGCAGCCGC GCTGTTGGTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT	120 180 240 300 360 420 480 540 600 660 720
50	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT	11 GGTGCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GGGGGACAAC TCTGCGCCGG TCTGCGCCGG	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATGTCAGGTC CTTCCAGGGG CCTCATGCTC CGTCTCCTCT CAGAGAGCCCC TCAGAAAAGG TGACAAAAGG	GTTGCAGCGG ACAGCCTTGA ACAGCCTGTA ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCAAACTGA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGCAGGATG GGTAGAGCACT GGTAGAGCACT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCACCCC ACAGAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAGG CCTGCCAGGC	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGTACCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG	120 180 240 300 360 420 480 540 600 660 720 780
50	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCA AACCAGGACC ATCATCAACG GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACATGT GGGCCTGTGG	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG GGCAGCAGAAA ACTCTAACGA GACCCATCAA GGGGGACAAC GCGTGCTAAG TCTGCGCCGG TCTGCGCCGG	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGTG TTTCAGGGGG CCTCATGCTC CGTCTCCTCT CAAGAGCCCC TCAGAAAAGG TGACAAAAGCA CTCCCTGCAG	GTTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCGAGGATG GGTAGAGACT GGACTCGTGT	CCATGGGTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCGGC CACAGTGGCT ACTACTCCCT TCCCCACCC ACAGAGAAT ACAGAAGAAT ACTACTGCTGGGAC TCCCTAAGGT CTTACCCAGG CCTGCCAGGAG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGGCC GTCACCAGTT TGGCTACTCCT TGGCTACTCCT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT	120 180 240 300 360 420 480 540 600 660 720
50 55	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAACG GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACCACATGT GGGCCTGTGG GCCCGGCCCA	11 GGTGCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GGGGGACAAC TCTGCGCCGG TCTGCGCCGG	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGGGGG	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCGAGGATG GGTAGAGACT AGCACGTGTAGAGACT AGCACGTGTAGAGACT AACCTCTGCAGA	CCATGGCTAC TCTTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCGCC CACAGTGGCT TCCCCCACCC ACAGAGAAT TCTGCTGGGAC TCCCTAAGGT CTTACCCAG CCTGCAGGAGAAAAAA CCTCCCAGAGAAAAAAA CCTCCCAAGGAAAAAAA AGTTCACCAAGAAAAAAA AGTTCACCAAAAAAAAAA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT CCTCCACTGC CACAGTAGAT TGATTCTGC ACAGATAGAT TGATTCTGGT TTACCCTTGT TTACCCTTGT TGGTTCCAG	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	TOTAL	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA GGGGGACAAC TCTCGCCGGG TCTGCAATGG ACAGACCGGG TCTGCAATGG ACAGACCGGG ACAGACCGGG ACAGACCGGG ACAGACCGGG ACGCCCAACTC CAGCCCTGAC	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATGGAG CTTCCAGGGG CTTCCAGGGG CCTCATGCTC CAAGAGCCCC TCAGAAAAGG TGACAAAAGCA CTCCCTGCAG CTGCTCTCACAG CTCCCTGCAG CTGCTCACACAAAACCA CTCCCTGCAG CTGCAGCACAAAACCA CTCCCTTCACACAAAACCA CTCCCTTCCAACACACAC	GTTGCAGCGG ACACCCTCTA ACACCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGCCT TGCGAGGATT TGCGAGGATG ACACTCTGGCC GTCAGCTGT TGCGAGGATG ACCTCTGGCA GACCTCATT	CCATGGGTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCCGC CACAGTGGGCTAC ACTACTCCCT TCCCCACCCC ACAGAAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAAG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTCCCAGGA CCTCCCAGGA CCTCCCAGGA CCTCCCAGGA CCTCCCAGGA	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAG ATGCTCAGCA GATGGTTCAGGATCCAG ATGCTCAGCA GATGTTCAGGATCCAG	120 180 240 300 360 420 480 540 600 660 720 840 900 960 1020
50 55	CTTGTGGTTC CCCTGGATGT GTTCTCGCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGGCCTGTGG GCCGGCCCA AAACCATCT GCTGCAGGGA ATGTTCATCT	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGAAGAAAGT GGCAGCAGAAA GACCCATCAAA GGGGGACAAC GCGTGCTAAGG TCTGCAATGG ACAGACCGGG ACGACCACCAC CAGCCCATCAAC CCCACCACCACCACCACCACCACCACCACCACCAC	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGAA CGATATGCAC CGGGGGTG TTTCAGGGG CCTCATGCTC CAAGAGCCC TCAGAAAGCA CTCCCTGCAG TGTCCTGCAG TGACAAAGCA CTCCCTGCAG CTGAGTCATC CAAGACCAC CTCCTGCAG TGTCTACACG TGTCTACACG TGTCTACACG TGTCTACACG TGTCTACACG TGTCTACACG TGTCTTCA TGACCCCATG	GTTGCAGCGG ACAGCCTTTA GACGCCCGGT ACCCAGCCGT TTGGTGCATCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCCAGGATG GGTAGAGACT GGACTCGTGT ACCTCTGCA CCAGGACTCAT TCTCCTGCA	CCATGGGTAC TCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCGCC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAAG CCTGCCAGGG CCTGCGAGGA AGTTCACCAA TCACCAAC TCACGGGTCT	AGCAAGACCC CACAGAGCCT CACAGAGCCGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAC ATCCCACCT GTGGATCCAC TCGCCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACTGCA ATCATGAATCT CACCCTGGCC AAAGATGTCA GTGTCTGGGT TTGAATATCA GACACCATGT GCCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCT ATTGGGCTGAA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCOGACTG GGAAGAAAGT GGCAGCAGAAA GACCCATCAAA GGGGGACAAC GCGTGCTAAGG TCTGCAATGG ACAGACCGGG ACGACCACCAC CAGCCCATCAAC CCCACCACCACCACCACCACCACCACCACCACCAC	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCC TCAGAAAAGCA CTCCTGCAC TGTCCCTGCAC CTGCCTGCAC CTGCCTGCAC CTGCCTGCAC CTGCCTGCAC CTGCTCCTCTCCT	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCGAGGATG GGTAGAGACT ACCTCTGTGC CCAGGACTCA CCAGGACTCA TCTCTGGAC CCAGGACTCA CCAGGACTCA CCTCGGGAC CCTCGGGAC CCTCGGGACC	CCATGGCTAC TCTTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC ACACAGTGGCT TCCCCCACCC ACACAAGAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCGAG CCTGCAGGGAGA AGTTCACCAA GCACACCGGC CCTTCCCAAAA TCAGGGTCTG ATTTCCCAAAA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT CAGTCCCACT CAGTCCCACT TGATTCTGG TTACCCTTGT TTACCCTTGT GTGGATCCAG ATCCCCACCT GATGTTTCAGG ATCCCCCACC CTGTCCCAGGG CTTCCCCCAC	120 180 240 300 360 420 480 540 600 660 720 840 900 960 1020
50 55 60	TOTAL	11	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATGAGTC CGTCCATGCTC CGTCTCCTCT CAAGAGCCCC TCAGAAAGGA TGACAAAGCA CTCCTTGCAG TGTCTACACG CTGCTTCTACACG CTGCATGCTC CTGCTGCAG TGTCTACACG CTGCTTCACACG CTGCATGTCACC CTGCATGACC CTGCTTTCA ACTCCTTTCA CCTCTTTCA CCCTTGGAGC CTAGTTGAAC CCCTGGGGCA	GTTGCAGCGG ACAGCCTTTA GACGCCCGTT ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGACTGTGT AACCTCTGGC GTCAGGCACTCA GCCCTCATT TCTCCTGGACA CCTGTGAGACA CCAGGACTCA GCCTCATT TCTCCTGGACA CCTTCATCCT	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCT ACTACTCCT TCCCCACCC TCTCCCACCC CTTACGGAC CTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTCCCAGG CCACCCGC CCTTCCCAGA TCACGGGTCT CAGGGTCTA CAAGCTCAAA CAAGCTCAAG	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC TACCCTTTTCTGGTATCCTGTCCCCACT GATGTTCTGGTTCCCCACCT GATGTTGATCCCCACCT GATGTTGAGA CTTCCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACTGCC AAAGATGTGC CACCCTGGCC AAAGATGTCA GTGTCTGGT TTGAATATCA GACACCATGT GCCCTGTGG GCCCTGTGG GCCTGTGG GCCTGTGG GCCTGTGGG CCGGCCCA AAGATCATCC GCTGCAGGGA ATGTTCATCT ATTGGGTTGC CGGGGTTGC CGGGGGTTGC TCTCTGCAGGC	11	21 GGGGAAATCA TECTCTGTGAC GTCCGGGGAA CGATATGCAC GGCCGGGGAA CGTTCCAGGGG CCTCATGCTC CAAGAGCCC TCAGAAAAGGA CTCCCTGCAG TGTCTCCTCT CTAGAGTCCCTCCAGGGCAC CTCCCTGCAG CTGCCTGCAG CTGCCTCCACA CTCCCTGCAG CTGAGTCATC CTGAGTCATC CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC	GTTGCAGCGG ACAGCCTTTA GACGCCCGTT ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGACTGTGT AACCTCTGGC GTCAGGCACTCA GCCCTCATT TCTCCTGGACA CCTGTGAGACA CCAGGACTCA GCCTCATT TCTCCTGGACA CCTTCATCCT	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCT ACTACTCCT TCCCCACCC TCTCCCACCC CTTACGGAC CTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTCCCAGG CCACCCGC CCTTCCCAGA TCACGGGTCT CAGGGTCTA CAAGCTCAAA CAAGCTCAAG	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC TACCCTTTTCTGGTATCCTGTCCCCACT GATGTTCTGGTTCCCCACCT GATGTTGATCCCCACCT GATGTTGAGA CTTCCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50556065	TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR GRANTATCA GRANTATCA GRANTATCA GRANTATCA GRANCATGCA GRANCCATGT GRANCCATGT GRANCCATGC GRANCC	11 GGTGCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGTCCGACTG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA GGGGGACAAC TCTGCGCCGG TCTGCAATGG ACAGACCGGG ACAGACCGGG ACAGACCGGC CCGCGCTCCCCCCCCCC	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTCC CGTCTCCTCT CAAGAGCCCC TCACAAAGCA CTCCCTGCAG TGTCTACACG CTGACATCACC CTGACATCACC CTGCAGT TGTCTACACG CTGACTCATC ACTCCTTCAC TGACCCCATG CTAGTGAAA CCCCTGCAGG CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC sequence	GTTGCAGCGG ACAGCCTTTA GACGCCCGTT ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGACTGTGT AACCTCTGGC GTCAGGCACTCA GCCCTCATT TCTCCTGGACA CCTGTGAGACA CCAGGACTCA GCCTCATT TCTCCTGGACA CCTTCATCCT	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCT ACTACTCCT TCCCCACCC TCTCCCACCC CTTACGGAC CTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTCCCAGG CCACCCGC CCTTCCCAGA TCACGGGTCT CAGGGTCTA CAAGCTCAAA CAAGCTCAAG	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC TACCCTTTTCTGGTATCCTGTCCCCACT GATGTTCTGGTTCCCCACCT GATGTTGATCCCCACCT GATGTTGAGA CTTCCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR TOTOTICACTOR GRANTATCA GRANTATCA GRANTATCA GRANTATCA GRANCATGCA GRANCCATGT GRANCCATGT GRANCCATGC GRANCC	11	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTCC CGTCTCCTCT CAAGAGCCCC TCACAAAGCA CTCCCTGCAG TGTCTACACG CTGACATCACC CTGACATCACC CTGCAGT TGTCTACACG CTGACTCATC ACTCCTTCAC TGACCCCATG CTAGTGAAA CCCCTGCAGG CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC sequence	GTTGCAGCGG ACAGCCTTTA GACGCCCGTT ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGACTGTGT AACCTCTGGC GTCAGGCACTCA GCCCTCATT TCTCCTGGACA CCTGTGAGACA CCAGGACTCA GCCTCATT TCTCCTGGACA CCTTCATCCT	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCT ACTACTCCT TCCCCACCC TCTCCCACCC CTTACGGAC CTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTCCCAGG CCACCCGC CCTTCCCAGA TCACGGGTCT CAGGGTCTA CAAGCTCAAA CAAGCTCAAG	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC TACCCTTTGTTCCTCAGTGC TTACCCTTCT GTGATCCAGT TGGATCCAGT TGGATCCAGT TTACCCTTGT GTGGATCAGA TTCCCCACCT GATGTTGAGA CTTCCCCACC CTGTCCCAGGG GCCCATCCCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50556065	CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA ATATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GACACCATGT ATATGAATATCA GCCTGTCGG GCCTGCTGGG GAAACCATCC GCTGCAGGGA ATGTTCATCT ATTGGGCTGA CGGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1	TI CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GGCGGCAGAT ACTCTAACGA GGGGGCAACAC GCGTGCTAAG TCTGCAGCGG ACAAACCGGG ACAAACCGGG ACGCCCTGAC CTCCAGCCCT CTCCAGCCCC CTCTCATCT TCTGACCCAA 54 Protein cession #: 11 11	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCC TCACAAAAGCA CTCCCTGCAG TGTCTCATCAC CTGAGTCACTC CGTGCTCCTCT CAGTGCCCC TCACAAAGCA CTCCTTCACAG CTGCTCTCTCACAG CTGCTCTCTCACAG CTGCTTCACACG CTGAGTCATC ACTCCTTTCAA TGACCCCATG CCCTGGGGCA ATTTAGTCCC Bequence NP_036559 21	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA ACATTGTCCCT CGAGTGCACT GGACTGCTGGACT GGACTCGTG ACCCTCATT TCTCCTGGAC CCTGGGAACA CCTTTCATCCT AGAATAAAC CCTTCTGCA CCTGGGAACA CTTTCATCCT AGAATAAAC	CCATGGGTAC CCATGGGTAC CGGATGACAG GGCAGGCGGC CACAGTGGCT TCCCCCACCC ACACAAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAGG CCTGCCAGGAGAAAAT CACACCACAC	AGCAAGACCC CACAGAGCCT CACAGAGCCCC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT CCTCCAGTGC AAAGTACAT TGATTCTGG TTACCCTTGT GTGGATCCAG ATCCCCACCT GATGTTGAGA CTTCCCCCAC CTGCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1080 1140 1200
50556065	TOTOTOGAGE TOTOTOGAGE TOTOTOGAGE ANCAGGACC ANCATCANTG AGGCCCACTGCA TATGAATCTA GCCACTGGCC ANAGATGTCA GTGCTCTGGCT TTGAATTCA GACACCATGT GGGCCTTGGG GCCGGCCCA GAAACCATCT GCTGCAGGGA ATGTTCATCT ATTGGCTTA ATTGGCTGA CGGGGGTTGC TCTCTGCAGG Seq ID NO: Protein Ac I MATARPPWMW	11	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCCC TCAGAAAGCA TGACAAAGCA TGTCTACACG CTCCTTGCAG TGTCTACACG CTGCTTCACACG CTGCTTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA CCCTGGGGCA ATTTAGTCCC sequence NP_036559 21 LGVTEHVLAN	GTTGCAGCGG ACACCCTCTA ACACCAGCCGT TTGGTGCATCC CGTCTAGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGGGAGGATG GGACTCGTGT ACCCTCGGCAC CCTGGGACA CCAGCACTA TCTCCTGGACA CCTTCCTGGACA CCTTCCTGGACA CCTTCATCCT AGAAATAAAC	CCATGGGTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCGGC CACAGTGGGT ACTACTCCCT TCCCCACCC CTGCTAAGGT CTTACCCAAGG CCTGCCAGGG CCTGCAGGG CCTCCCAGGG CCACCCGCC CCTTCCCAGA TCACCGAGG TCACGGTCTA TCACCAA CAAGCTCAGG TCAGGGTCTA CAAGCTCAGG TGAGAAGTGG 41 TVPSGSNQDL	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATACTCTGGTACCCACT GATGTTCTGGG TTACCCTTAT GTGGATCCGA TTACCCTACT GATGTTGAGA CTTCCCCACC CTCTCCAGGG GCCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 840 960 1020 1020 1140 1200
5055606570	TOTAL	TI CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGCTCTACTG GGATCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GGGGGACAAC TCTGCGCCGG TCTGCAATGG ACAGACCGGG TCTGCAATGG ACAGCCCTGAC CTCCAGCCC CCGTTCTCT TCTGACCCAA 54 Protein cession #: 11 VLCALITALL SDCDMHTQPW	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATGTCCAGGGC GTTCCAGGGC GTTCCAGGGC CCTCATGCTC CAAGAGCCCC TCAGAAAGG TGACAAAGCA CTCCCTGCAG TGACCCCATG CTGAGTCATC ACTCCTTCA ACTCCTTCA ACTCCTTCA GACCCCATG CTAGTTGAC CCCTGGGGCA ATTTAGTCCC Bequence NP_036559 21 LGVTEHVLAN QAALLLRPNQ	GTTGCAGCGG ACAGCCTTGC CACCCCTCTA GAGGCCCGGT ACCCAGCCGT TTGGTGGAT CGTCTCGGCC GTCAAACTGA ACAAACTGA CATTGTCCCT CAAGTGCACT GGGAGACT GGACTCGTGT ACCCTCGGAC TCCCGGAACA TCCCTCGGAC TCTCCTGGAC CCTCGGAACA TCTCCTGGAC CTTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHP	CCATGGGTAC TCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCGGC CACAGTGGGT ACTACTCCT TCCCCACCCC ACAGAAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGGTCTG ATTTCCAAAA ATTCCAAAA TCAGGGTCTG TGAGAAGTGG TGAGAAGTGG TGAGAAGTGG TTPSGSNQDL QWLLTAAHCR	AGCAAGACCC CACAGAGCCT CACAGAGCCCC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT CCTCCAGTGC AAAGTACAT TGATTCTGG TTACCCTTGT GTGGATCCAG ATCCCCACCT GATGTTGAGA CTTCCCCCAC CTGCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1080 1140 1200
50556065	TOTOTOGATO CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA AAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GACACCATGT GACACCATGT GACACCATGT GACACCATGT TTGAATATCA GACACCATGT GAGCCTTGGG CCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCC ATTGGGCTGA CGGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1 MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW	TI GGGTGCTCTG GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGCTCTACTG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GGCGAGAT ACTCTAACGA GGGGGACAAC GCGTGCTAAG TCTGCGCCGG TCTGCAATGG ACAGCCCATCAA CCTCCAGCCCT GTCTCAATCT TCTGACCCAA 54 PIOLEIN CESBION #: 11 VLCALITALL SDCDMHTQPW QQMPQGVKSI GTTKSPQVHF	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCCC TCAGAAAAGCA CTCCTTGCAG TGTCTACACG CTGAGTCACC CTGAGTCACC ACTCCTTCA ACTCCTTCA ACTCCTTCA CTGCTGCAG CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC Bequence NP_036559 21 LGVTEHVLAN QAALLLRPNQ PHPGYSHPGB PKVLQCLNIS	GTTGCAGCGG ACACCCTCTA ACACCCCTCTA GACGCCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT CGTCTCGGCC GTCAAATCCA CATTGTCCCT CAAGTGCACT GGACTCGTGT ACCTCTGGAC CCAGCGACTCA CCTCGGAACA CCTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVIVHPS SNDLMLIKLN VLSQKRCEDA	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCTAC ACTACTCCT TCCCCACCC CTTCCCAGGC CTTCCCAGG CCTGCCAGG CCTCCAGG CCTCCAGG CCTCCAGG TCACGGGAGA AGTTCACAAA CAAGCTCAGG TCAGGGTCTG TATTCCAAAA CAAGCTCAGG TGAGAAGTGG 41 TVPSGSNQDL QWLLTAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT AAAAAAAAAA	120 180 240 300 360 420 660 660 720 780 840 900 1020 1080 1140 1200
5055606570	TOTOTOGATO CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA AAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GACACCATGT GACACCATGT GACACCATGT GACACCATGT TTGAATATCA GACACCATGT GAGCCTTGGG CCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCC ATTGGGCTGA CGGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1 MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW	TI CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA ACTCTAACGA GCGTGCTAAG TCTGCGCCGG TCTGCAATCG ACAGACCGGG AGGCCAACTC CTCCAGCCC CCGTGTCTCT TCTGACCCAA 54 Protein Cession #: 11 VLCALITALL SDCDMHTQPWSI	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCCC TCAGAAAAGCA CTCCTTGCAG TGTCTACACG CTGAGTCACC CTGAGTCACC ACTCCTTCA ACTCCTTCA ACTCCTTCA CTGCTGCAG CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC Bequence NP_036559 21 LGVTEHVLAN QAALLLRPNQ PHPGYSHPGB PKVLQCLNIS	GTTGCAGCGG ACACCCTCTA ACACCCCTCTA GACGCCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT CGTCTCGGCC GTCAAATCCA CATTGTCCCT CAAGTGCACT GGACTCGTGT ACCTCTGGAC CCAGCGACTCA CCTCGGAACA CCTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVIVHPS SNDLMLIKLN VLSQKRCEDA	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCTAC ACTACTCCT TCCCCACCC CTTCCCAGGC CTTCCCAGG CCTGCCAGG CCTCCAGG CCTCCAGG CCTCCAGG TCACGGGAGA AGTTCACAAA CAAGCTCAGG TCAGGGTCTG TATTCCAAAA CAAGCTCAGG TGAGAAGTGG 41 TVPSGSNQDL QWLLTAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200
5055606570	CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAATGC GCCCACTGGC AAAGATGTGC GCCCTGGCC AAAGATGTCA GTGTCTGGT TTGAATATCA GACACCATGT GCCCTGTGG GCCTGTGG GCCTGTGGG CCCAGCCCA GAAACCATCC GCTGCAGGGC ATTGGGTTGA TTGGGTTGA TTGGGTTGA TTGGGTTGA TTGGGTTGA TTGGGTTGA CGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1 MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV	TI GGGTGCTCTG GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGCTCTACTG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GGCGAGAT ACTCTAACGA GGGGGACAAC GCGTGCTAAG TCTGCGCCGG TCTGCAATGG ACAGCCCATCAA CCTCCAGCCCT GTCTCAATCT TCTGACCCAA 54 PIOLEIN CESBION #: 11 VLCALITALL SDCDMHTQPW QQMPQGVKSI GTTKSPQVHF	21 GGGGAAATCA TECTCTGTGAC GGCCGGGGAA CGATATGCAC GGCCGGGGAA CGATATGCAC CGGGCGGGTGT TTCAGAGTC GTTCCAGGG CCTCATGCTC TCAGAAAAGGA TGACAAAAGCA CTCCTGCAG CTGAGTCATC CTAGTTGAAC CCCTGGGGCA ATTTAGTCCC BEQUENCE	GTTGCAGCGG ACACCCTCTA ACACCCCTCTA GACGCCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT CGTCTCGGCC GTCAAATCCA CATTGTCCCT CAAGTGCACT GGACTCGTGT ACCTCTGGAC CCAGCGACTCA CCTCGGAACA CCTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVIVHPS SNDLMLIKLN VLSQKRCEDA	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCTAC ACTACTCCT TCCCCACCC CTTCCCAGGC CTTCCCAGG CCTGCCAGG CCTCCAGG CCTCCAGG CCTCCAGG TCACGGGAGA AGTTCACAAA CAAGCTCAGG TCAGGGTCTG TATTCCAAAA CAAGCTCAGG TGAGAAGTGG 41 TVPSGSNQDL QWLLTAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200
505560657075	TOTOTOGATO COCTOGATOT COCTOGATOT GTTCTCGCCA AACACGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTC CACCCTGGCC AAAGATGTCA GTGCTCTGCT TTGAATATCA GACACCATGT GGGCCTTGGG GCCGGCCCA GAAACCATCT CTGCAGGGA ATGTTCATCT ATTGGCTTA TTTGGCTTA TTTGGCTTA TTTCTTCTGCAGC Seq ID NO: PIOTE IN AC I MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV Seq ID NO: Nucleic Ac	TI CTCTCTACTT GGGTGCTCTG GCAGCAGTT GGAGCAGG GATCCGACTG GGACCAGAT ACTCTAACGA GGCCCATCAA GGGGGCAAC TCTGCGCCGG TCTGCAATGG ACAGCAGTG ACAGCCGTGAC CTCCAGCCC CCGGTGTCTC GTCTCAATCT TCTGACCCAA 54 Protein Cession #: 11 VLCALITALL SDCDMHTQPW GQMFQGVKSI GTTSPQVHF CNGSLQGLVS 55 DNA sequid Accession	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATATGCAC CGGGCGGGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCCC TCAGAAAGCA TGACAAAGCA CTCCTTGCAG TGTCTACACG CTGCTTCTACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTGCAG ATTTAGTCCC Bequence NP_036559 21 LGVTEHVLAN QAALLLRPNQ PHPGYSHPGB PKVLQCLNIS WGDYPCARPN uence n #: NM_002	GGTGCAGCGG ACACCCTCTA ACACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGACTCGTGT ACCTCTGGAC GTTCGGACT GGACTCGTGT ACCTCTGGAC CCTGGGACTCA CCTCGGAACA CCTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVIVHP SNDLMLIKIN VLSQKRCEDA	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCTAC ACTACTCCT TCCCCACCC CTTCCCAGGC CTTCCCAGG CCTGCCAGG CCTCCAGG CCTCCAGG CCTCCAGG TCACGGGAGA AGTTCACAAA CAAGCTCAGG TCAGGGTCTG TATTCCAAAA CAAGCTCAGG TGAGAAGTGG 41 TVPSGSNQDL QWLLTAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200
5055606570	TOTAL	TI CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAGCAGAT ACTCTAACGA GACCCATCAA GGGGGACAACA TCTGGCCGG TCTGCAATGG ACGCCTGAC CTCCAGCCC CCGTGTCTCT TCTGACCCA 54 Protein cession #: 1 VLCALITALL SDCDMHTQPW QQMFQGVKSI GTTKSPQVHF CNGSLQGLVS 55 DNA seq id Accessio quence: 681.	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCCC TCAGAAAGG TGACAAAGCA CTCCCTGCAG TGTCTCACGGG CTGAGTCATC ACTCCTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA CCCTGGGGCA ATTTAGTCCC Bequence NP_036559 21 LGVTEHVLAN QAALLLRPNQ PHPGYSHPGB PKVLQCLNIS WGDYPCARPN UENCe UE	GGTGCAGCGG ACACCCTCTA ACACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCAGCCG GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGCAGGATG GGCAGACTCA GCCTCTGGC GTCAGGACT ACCTCTGCA TCCCAGCAGT TCCCAGGACT ACCTCTGCA TCTCCTGCA TCTCCTGCA TCTCCTGCA TCTCCTGCAACA CCTTCATCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA RPGVYTNLCK	CCATGGGTAC TCTCTGGGGT ACACCGTGCC GGATGACAG GGCAGGCGCC CCACAGTGGCT ACTACTCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCAG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGGTCTG ATTTCCAAAA ACAGCTCAGG TGAGAAGAT TTYPSGSNQDL QWLLTAAHCR RRIRPTKDVR YPRQIDDTMF FTKMIQETIQ	AGCAAGACCC CACAGAGACCT CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAG ATCCCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200
505560657075	TOTOTOGATO COCTOGATOT COCTOGATOT GTTCTCGCCA AACACGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTC CACCCTGGCC AAAGATGTCA GTGCTCTGCT TTGAATATCA GACACCATGT GGGCCTTGGG GCCGGCCCA GAAACCATCT CTGCAGGGA ATGTTCATCT ATTGGCTTA TTTGGCTTA TTTGGCTTA TTTCTTCTGCAGC Seq ID NO: PIOTE IN AC I MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV Seq ID NO: Nucleic Ac	TI CTCTCTACTT GGGTGCTCTG GCAGCAGTT GGAGCAGG GATCCGACTG GGACCAGAT ACTCTAACGA GGCCCATCAA GGGGGCAAC TCTGCGCCGG TCTGCAATGG ACAGCAGTG ACAGCCGTGAC CTCCAGCCC CCGGTGTCTC GTCTCAATCT TCTGACCCAA 54 Protein Cession #: 11 VLCALITALL SDCDMHTQPW GQMFQGVKSI GTTSPQVHF CNGSLQGLVS 55 DNA sequid Accession	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATATGCAC CGGGCGGGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCCC TCAGAAAGCA TGACAAAGCA CTCCTTGCAG TGTCTACACG CTGCTTCTACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTTCACACG CTGCTTGCAG ATTTAGTCCC Bequence NP_036559 21 LGVTEHVLAN QAALLLRPNQ PHPGYSHPGB PKVLQCLNIS WGDYPCARPN uence n #: NM_002	GGTGCAGCGG ACACCCTCTA ACACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGACTCGTGT ACCTCTGGAC GTTCGGACT GGACTCGTGT ACCTCTGGAC CCTGGGACTCA CCTCGGAACA CCTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVIVHP SNDLMLIKIN VLSQKRCEDA	CCATGGGTAC TTCTGGGGGT ACACGTGCC GGATGACAG GGCAGGCGGC GCACAGTGGCTAC ACTACTCCT TCCCCACCC CTTCCCAGGC CTTCCCAGG CCTGCCAGG CCTCCAGG CCTCCAGG CCTCCAGG TCACGGGAGA AGTTCACAAA CAAGCTCAGG TCAGGGTCTG TATTCCAAAA CAAGCTCAGG TGAGAAGTGG 41 TVPSGSNQDL QWLLTAAHCR RRIRPTKDVR YPRQIDDTMF	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCAGC CAGCAGCAGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTCT GATGTTCAGA ATCCCCACCT GATGTTGAGA CTTCCCCACC CTGTCCAGGG GCCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200
505560657075	TOTATION TO THE PROPERTY OF TH	TI CTCTCTACTT GGGTGCTCTG GCAATGATGT TGGGAGCTGG GATCGACTG AGCTCTACTG GGATCGACTG AGCTCTACTG GGAGCAGAT ACTCTAACGA GACCATCAA GGGGGACAACA TCTGCACCGG TCTGCAATGG ACAGCCCTGAC CTCCAGCCCT CCGTGTCTCT TCTGACCCAA 54 Protein Cession #: 11 CTTKSPQVHF CNGSLOGLVS 55 DNA seq id Accassio quence: 681. 11 ; CCCTCCCCCTG	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCCC TCAGAAAGG TGACAAAGCA CTCCCTGCAG TGTCTCACAG TGTCTACAC ACTCCTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA ACTCCTTCA CCCTGGGGCA ATTTAGTCCC BeQUENCE NP_036559 21 LGVTEHVLAN QAALLLRPNQ PHPGYSHPGH PKVLQCLNIS WGDYPCARPN URENCE n #: NM_002 .2990 21 TTGCTGGCAT	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGGTAGAGACT GGACTCGTGT ACCCTCTGGAC CCTGGGACT TCTCCTGGAC CCTGGGACT ACCTCTAGCA TCTCCTGGAC CCTTGCAATCCAT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA RPGVYTNLCK 214 31 CCCCGAGCTTC	CCATGGCTAC CCATGGGTAC CCATGGGTAC ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCCC ACAGTGGCT CCTCACGGAC CCTCCCAGGG CCTGCCAGGG CCTCCCAGGG CCTTCCCAGA CCACCGGC CCTTCCCAGA TCAGGGTCTG ATTTCCAAGA TCAGGGTCTG ATTTCCAAGA TCAGGGTCTG ATTTCCAAGA CAAGCTCAGG TGAGAAGTGG TVPSGSNQDL QWLLTAAHCR RRIRFTKDVT YPRQIDDTMF FTKMIQETIQ 41 CCTCCCTTGCC	AGCAAGACCC CACAGAGCCT CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CTCACGGCC ACAGATAGAT TGATTCTGGG ATCCCCACT ATCCCCACC ATGCTTGATCCAGTC ATCCCACCT ATCCCCACC ATGTTGATCCAG ATCCCACCT AAAAAAAAAA	120 180 240 300 360 480 540 660 660 720 780 840 900 960 1020 1140 1200
505560657075	TOTAL SERVICE	TI CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGACCAGAT ACTCTAACGA GACCCATCAA GGCGGCAGAT ACTCTAACGA TCTGCACTGG ACAGACCGGG ACAGACCGGG ACAGACCGGG ACGCCTCACT CTCCAGCCC CCGTGTCTCT GTCTCAATCT TCTGACCCAA 54 Protein cession #: 11 VLCALITALL SDCDMHTQPW QQMPQGVKSI GTTKSPQVHF CNGSLQGLVS 55 DNA seq id Accession puence: 681. 11 CCCTCCCCCTG CCTCCCCCTG CCTCTCCCCCTG CCTCTCCCCCTG CCTCTCCCCCTG CCTCTCCCCCTG CCTCTCCCCCTG CCTCTCCCCCTG CTCTTTTGCCCC CTCTTTTTGCCCC CTCTTTTGCCCC ACCTCCCCCTG CTCTCCCCCTG CTCTTTTGCCCC CTCTCTCT	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTTCCAGGG CCTCATGCTC CAAGAGCCC TCAGAAAAGCA CTCCTTCACA CTCCTGCAG TGTTCACAG CTGAGTCATC CAGAGCCC CTAGATACC CCCTGCAG ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA CCCTGGGGCA ATTTAGTCCC sequence NP_036559 21 LGVTEHVLAN QAALLLRPNQ PHPGYSHPGE PKVLQCLNIS WGDYPCARPN uence n #: NM_002 .2990 21 TTGCTGGCAT TTGCTGCCAT GGCTGCTCCGC	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCAGCGT CGTCTCGGCC GTCAAACTGA ACTAAACTGA CATTGTCCCT CAAGTGCACT GGACTCGTGCAGACTG ACCAGCGTT TCCCAGGACTG ACCTCTGCA CCAGGACTG ACCTCTGCA CCAGGACTA TCTCCTGGAC CCTGGGAACA CTTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHP SNDLMLIKLN VLSQKRCEDA RPGVYTNLCK 214 31 CCCGAGGCTTC AGACCGGGCT	CCATGGGTAC TCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCGGC CACAGTGGGT ACTACTCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC CCTCCCAAGGC CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGTTTTCCAAGA TCAGGTCTG TTACCAGG TGAGAGAGAT TCACCAGG CCTTCCAGGA TCAGGGTCTG ATTTCCAAGA TCAGGGTCTG ATTTCCAAGA CAAGCTCAGG GGAAAGTGG 41 TVPSGSNQDL VPRQIDDTMF FTKMIQETIQ 41 CTCCCTTGCC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC GCAAAGCTGC	AGCAAGACCC CACAGAGCAT CTCTGGAGC CAGCAGCGC CAGCAGCGC GCTGTTGCTA GCTCACCGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTCT GTGGATCCAC GATGTTGATCCCACC TAAACAAAAAAAAAA	120 180 240 300 360 420 600 720 780 840 900 960 1080 1140 1200

		CTCGCCGGCG					240
		TCCCCCCCAG					300
		TTATGCAGCA					360
5		CAGGCTGCGG AGGAGGTGCT					420 480
•		GCCCTGAGAT					540
		GGGTCCGCCT					600
		TCGCCCCGGGA					660
10		GTTTTGCATT					720
10		AAACGACCGG					780 840
		TGGACTGGGC GTGCCTTGCG					900
		ATCAAGAAGT					960
		TTCAATAGAA					1020
15		GGTGACACCA					1080
		GAAAGTTCAT					1140
		ATCAATGCAC					1200
		GGCATTTTTC					1260 1320
20		ACCATACATT CTGCATGCCT					1380
		TGAGAAAGCA					1440
		TGACGCCATG					1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
25		AGGCATAGTG					1620
25		GACAACCATG					1680
		TAATGTCATC					1740 1800
		AGTGGAAGCC					1860
		AGGCATCTAT					1920
30	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
		AAAATGTGAT					2040
		AACCGCTAAA					2100
		TAAAGGAAAG					2160 2220
35		TAAATGTCAT					2280
-		GCTTGGAAAA					2340
		TGGAAATCTG					2400
		CTGGGAAGGT					2460
40		GGGCCAAGTG					2520
40		CAGGAGCATC CTGGAATTGT					2580 2640
		CAAAACCTCA					2700
	CAGAATGTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTTT	CATCATTTTC	ATAGTTACAT	2760
4.5		GTTGCTTAAA					2820
45		GTCCTCATCA					2880
		TTGCACAAGA					2940
		CAAATTAAAT					3000 3060
		AGGAGACAAA					3120
50		AAGTATCCTC					3180
	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCACTTTACT	GTAATATATA	3240
		ATCAGCATAG					3300
		CCCTACGCTT					3360
55		GTACAGTAAT GGTTGCCAAA					3420 3480
55		GATTCGTGTT					3540
		GCTTTTTAAA					3600
		GGATACTAAT					3660
60		ATAAGTTTAT					3720
60		AAAAACTAAT	AATACAATGT	CACTITATCA	GAATACTAGT	TTTAAAAGCT	3780
	GAATGTTAA						
	Sea ID NO.	56 Protein	semiance				
		cession #:					
65	1	11	21	31	41	51	
	1	1	1		1	1	
						NAASCARCLA	60
						ENBINTOVTP	120 180
70						ndlsrkmapp Tenitepeka	240
						ALDSKLAGIV	300
						YKDLLPLLPG	360
						SRKPGMEGCR	420
75						CEDNRGPKGK	480
75						CSCHKIKLGK	
						QHCVNSKGQV QAILDQCKTS	
						WNSNKIKSSS	
00		KLILQSVCTR					
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	Coding sec	puence: 123. 11	.1418	31	41	51	
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	GGGCGCAGCG	GGGCCCGTCT	GCAGCAAGTG	ACCGACGGCC	GGGACGGCCG	CCTGCCCCCT	60
	CTGCCACCTG	CCCCCCTCCC	GGCCCGGAGC	CCCGAGCCCC	GGTAGCGCGT	AGAGCCGGCG	120
	CGATGCACGT						180
-	CCCTGTTCCT						240
5	GCTTCATCCA	CCGGCGCCTC	CGCAGCCAGG	AGCGGCGGGA	GATGCAGCGC	GAGATCCTCT	300
_	CCATTTTGGG						360
	CCATGTTCAT	GCTGGACCTG	TACAACGCCA	TGGCGGTGGA	GGAGGGCGGC	GGGCCCGGCG	420
	GCCAGGGCTT	CTCCTACCCC	TACAAGGCCG	TCTTCAGTAC	CCAGGGCCCC	CCTCTGGCCA	480
	GCCTGCAAGA						540
10							
10	TGGAACATGA						600
	TTTCCAAGAT	CCCAGAAGGG	GAAGCTGTCA	CGGCAGCCGA	ATTCCGGATC	TACAAGGACT	660
	ACATCCGGGA						720
	AGCACTTGGG						780
	AGGAGGGCTG	GCTGGTGTTT	GACATCACAG	CCACCAGCAA	CCACTGGGTG	GTCAATCCGC	840
15	GGCACAACCT	CCCCCTCCAC	CTCTCCCTCC	AGACGCTCGA	TGGGCAGAGC	ATCAACCCCA	900
							960
	AGTTGGCGGG						
	TCTTCAAGGC	CACGGAGGTC	CACTTCCGCA	GCATCCGGTC	CACGGGGAGC	AAACAGCGCA	1020
•	GCCAGAACCG	CTCCAAGACG	CCCAAGAACC	AGGAAGCCCT	GCGGATGGCC	AACGTGGCAG	1080
	AGAACAGCAG						1140
20							
20	GAGACCTGGG						1200
	AGGGGGAGTG	TGCCTTCCCT	CTGAACTCCT	ACATGAACGC	CACCAACCAC	GCCATCGTGC	1260
	AGACGCTGGT						1320
	AGCTCAATGC						1380
	ACAGAAACAT	GGTGGTCCGG	GCCTGTGGCT	GCCACTAGCT	CCTCCGAGAA	TTCAGACCCT	1440
25	TTGGGGCCAA						1500
23							
	CTGCCTTTTG	TGAGACCTTC	CCCTCCCTAT	CCCCAACTTT	AAAGGTGTGA	GAGTATTAGG	1560
	AAACATGAGC	AGCATATGGC	TTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAAGA	1620
							1680
						AAGAAAAATG	
	GCCGGGCCAG	GTCATTGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
30	TTATCACCC	CTACCACCCA	CCCCACCCAG	CCCTGGGAGG	AAGGGGGGGT	GGCAAGGGGT	1800
-							
	GGGCACATTG	GTGTCTGTGC	GAAAGGAAAA	TIGACCCGGA	AGTTCCTGTA	ATAAATGTCA	1860
	CAATAAAACG	AATGAATG					
	0 TD 110	50 B					
25	Seq ID NO:	58 Protein	sedneuce				
35	Protein Acc	ession #: N	TP_001710				
	1	11	21	31	41	51	
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	1	1	1	1	1	1	
	MHVRSLRAAA	PHSFVALWAP	LFLLRSALAD	PSLDNEVHSS	FIHRRLRSQE	RREMOREILS	60
		HLQGKHNSAP					120
40							
4 0	LQDSHFLTDA	DMVMSFVNLV	EHDKEFFHPR	YHHREFRFDL	SKIPEGEAVT	AAEFRIIKDI	180
	IRERFONETF	RISVYQVLQE	HLGRESDLFL	LDSRTLWASE	EGWLVFDITA	TSNHWVVNPR	240
							200
						IRSTGSKQRS	300
	QNRSKTPKNQ	EALRMANVAE	NSSSDQRQAC	KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
	QNRSKTPKNQ	EALRMANVAE	NSSSDQRQAC	KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	
45	QNRSKTPKNQ GECAFPLNSY	EALRMANVAE MNATNHAIVQ	NSSSDQRQAC	KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ	EALRMANVAE MNATNHAIVQ	NSSSDQRQAC	KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC	EALRMANVAE MNATNHAIVQ H	NSSSDQRQAC TLVHFINPBT	KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC	EALRMANVAE MNATNHAIVQ	NSSSDQRQAC TLVHFINPBT	KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO:	EALRMANVAE MNATNHAIVQ H 59 DNA seq	NSSSDQRQAC TLVHPINPET	KKHELYVSFR VPKPCCAPTQ	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act	EALRMANVAE MNATNHAIVQ H 59 DNA sequid accession	NSSSDQRQAC TLVHFINPET Hence 1 #: NM_002	KKHELYVSFR VPKPCCAPTQ	DLGWQDWIIA	PEGYAAYYCE	360
	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150.	NSSSDQRQAC TLVHFINPET Mence 1 #: NM_002	KKHELYVSPR VPKPCCAPTQ	DLGWQDWIIA LNAISVLYFD	PEGYAAYYCE DSSNVILKKY	360
45 50	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act	EALRMANVAE MNATNHAIVQ H 59 DNA sequid accession	NSSSDQRQAC TLVHFINPET Hence 1 #: NM_002	KKHELYVSFR VPKPCCAPTQ	DLGWQDWIIA	PEGYAAYYCE	360
	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150.	NSSSDQRQAC TLVHFINPET Mence 1 #: NM_002	KKHELYVSPR VPKPCCAPTQ	DLGWQDWIIA LNAISVLYFD	PEGYAAYYCE DSSNVILKKY	360
	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequil	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11	NSSSDQRQAC TLVHFINPET Hence 1 #: NM_002: .3362 21	KKHELYVSFR VPKPCCAPTQ 321 31	DLGWQDWIIA LNAISVLYFD 41	PEGYAAYYCE DSSNVILKKY	360 420
	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ 1 1 AACTCCCGCC	EALRMANVAE MNATNHAIVO H 59 DNA sequence: 150. 11 TCGGGACGCC	NSSDQRQAC TLVHFINPET Hence 1 #: NM_002 .3362 21 1 TCGGGGTCGG	KKHELYVSPR VPKPCCAPTQ 921 31 GCTCCGGCTG	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC	PEGYAAYYCE DSSNVILKKY 51] TGCGGCGCCC	360 420 60
	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ 1 1 AACTCCCGCC GCGCTCCGGT	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC GCGTCCGCCT	NSSDQRQAC TLVHFINPET Hence 1 #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCCG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA	DLGWQDWIIA LNAISVLYPD 41 CGGCTGCTGC GTCTGCGGCC	PEGYAAYYCE DSSNVILKKY 51 } TGGGGGGCCC CGCCGTGGCC	360 420
50	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ 1 1 AACTCCCGCC GCGCTCCGGT	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC GCGTCCGCCT	NSSDQRQAC TLVHFINPET Hence 1 #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCCG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA	DLGWQDWIIA LNAISVLYPD 41 CGGCTGCTGC GTCTGCGGCC	PEGYAAYYCE DSSNVILKKY 51 } TGGGGGGCCC CGCCGTGGCC	360 420 60
50	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ 1 i AACTCCCGCC GCGCTCCGGT CCTCAGCTCC	EALRMANVAE MNATNHAIVQ H 59 DNA sected dence: 150. 11 TCGGGACGCC TTTTCCTGAG	NSSDQRQAC TLVHFINPET Lence 1 %: NM_002: .3362 21 1 TCGGGGTCGG CCTGTGCCGG CCGCCGCGGA	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC	PEGYAAYYCE DSSNVILKKY 51] TGCGGCGCCC CGCGTGCGC CCGGCCAGAC	360 420 60 120 180
	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequit AACTCCCGCC GCGCTCCCGCC CCCGCCTCCGCC CCCCCCGCTC	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTTCCTGAG GCCTCTGCTC	NSSDQRQAC TLVHFINPET Lence 1 #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCGG AGGGTCCTGC	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGCGAGCTGC TGCTGCCGCT	DLGWQDWIIA LNAISVLYFD 41 CGCTGCTGC GTCTGCGGC GCGGGGATCC GCTGGGCGGT	PEGYAAYYCE DSSNVILKKY 51] TGGGGGGGCCC CGGCCAGAC ACCCAGACAG	60 120 180 240
50	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequi AACTCCGGCC GCGCTCCGGT CCTCAGCTCC CCCCGCGTT CCATTGTCTT	EALRMANVAE MNATNHAIVQ H 59 DNA sequitence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG	NSSDQRQAC TLVHFINPET Hence H: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGCGTCCTGC	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGCGGT GCACGGCGCG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGACAG CCCGGCAGCAGC CGGCGCCCCGC	60 120 180 240 300
50	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequi AACTCCGGCC GCGCTCCGGT CCTCAGCTCC CCCCGCGTT CCATTGTCTT	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTTCCTGAG GCCTCTGCTC	NSSDQRQAC TLVHFINPET Hence H: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGCGTCCTGC	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGCGGT GCACGGCGCG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGACAG CCCGGCAGCAGC CGGCGCCCCGC	60 120 180 240
50	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding seqt 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT CCATTGTCTT TTCCCTGTGA	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGGCC GGTTGAGGCC	NSSDQRQAC TLVHPINPET Lence 1 \$: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCGG CCGGCGGA AGGTCCTGC CCGGGCCCGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT ATACATGTGTA	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCAGGGCGC GCTGGCCGC CTGGCTGCTCT	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CCGGCCCTGC CGGCCCTGC	60 120 180 240 300 360
50	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequ 1 AACTCCCGCC GCGCTCCGGTT CCCTCAGCTCC CCCGCCGGTT TTCCCTGTGT CTGTCCAGGA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TCTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGGCT CACGGAGCGG CACGAGCGGG CACGAGCGGG	NSSDQRQAC TLVHFINPET Lence 1 #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCGG AGCGTCCTGC CCGGGCCGGA AGCGTCTTGCCGG CGGGCCGGG CGTTTGGCCG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT AGGATGCACT AGGCAGCAGCAG	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GCTGGGGGC GCTGGGGGGTCC GCTGGGCGGTCC CTGGCTGCTCC CCTGAGCTTT	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CGGGCGCTGCGC GATGGGGCCC GATGGGGCCC	60 120 180 240 300 360 420
50 55	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCGCGGTT CCATTGTCTT TTCGCTGTGA ACCGGCTGCA ACCGGCTGCA	EALRMANVAE MNATNHAIVQ H 59 DNA sequidance: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTTGCTC CATCAAGCAG GGTTGAGGCT GGACGCGGGGGGGGGG	NSSDQRQAC TLVHFINPET HENCE HENM_002 3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGCGTCCTGC CCGGGCCCGG AGCGTCTCCCC CCGGGCCCGG AGCGTCTCCCC CCGGGCCCGG AGCTTCCAGT	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TCGGGACTGC TACATGTATA AGGCCAGCAA GTGTGGCTA	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGCGGT GCAGGGGTC CCTGGCGGCC CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACAG CCGGCGCAGACAG CGGGCGCTGC GAACTGCGG ACTGGAGAAG	360 420 60 120 180 240 300 360 420 480
50	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ 1 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCGGTT TCGCTGTGA CTGTCCAGGA ACCGCTGGA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TCTCTCGCT TTTCCTGAG GCCTCTGCTC CATCAGCAG GGTTGAGGC CACGGAGGGG GGACTCTGGC TGCCAACGCG	NSSDQRQAC TLVHPINPET Lence 1 #: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCGG CCGGCGGGA AGGGTCCTGC CCGGCCGGGA AGGTTCTGCC CCGGCCCGG ACCTTCCAGT TCCTTCAACA	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TCGCGGCT TACATGTGTA AGGGCAGCAG GTGTGGCTCG TCAAATGGAT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGCGGT GCAGGGGTCC CCTGGCCGCT CCTGAGCTTT GGATGATGTC TGAGGCAGGT TGAGGCAGGT	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CCGGCGCTGCG GATGGGCCC GCAGCTGTGG ACTGGAGAAG CCTGTGGGTCC	60 120 180 240 300 360 420
50 55	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ 1 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCGGTT TCGCTGTGA CTGTCCAGGA ACCGCTGGA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TCTCTCGCT TTTCCTGAG GCCTCTGCTC CATCAGCAG GGTTGAGGC CACGGAGGGG GGACTCTGGC TGCCAACGCG	NSSDQRQAC TLVHPINPET Lence 1 #: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCGG CCGGCGGGA AGGGTCCTGC CCGGCCGGGA AGGTTCTGCC CCGGCCCGG ACCTTCCAGT TCCTTCAACA	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TCGCGGCT TACATGTGTA AGGGCAGCAG GTGTGGCTCG TCAAATGGAT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGCGGT GCAGGGGTCC CCTGGCCGCT CCTGAGCTTT GGATGATGTC TGAGGCAGGT TGAGGCAGGT	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CCGGCGCTGCG GATGGGCCC GCAGCTGTGG ACTGGAGAAG CCTGTGGGTCC	60 120 180 240 300 360 420 480 540
50 55	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TTCCGTGTGA CTGTCCAGGA ACCGCTGCA AAGCCCGCAG TGAAGCATCC	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TCTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGGCT CACGGACGCG GGACTCTGGGC TGCCACGGCG TGCCACGCC TGCCACGCA	NSSDQRQAC TLVHPINPET Lence 1 \$1 NM_002: 3362 21 1 TCSGGGTCGG CCTGCCGGA AGCGTCCTGC CCGGGCCGGA CGTTCTCAC ACCTTCCAGT TCCTTCAAGT TCCTTCAAGT GCTAGAGATCG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACA AGGCAGCAG TCAAATGGAT AGCCACAGAC	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTTGGGGCC GCTGGCGGT GCAGGGGCGC CTGGCTGCTC CCTGAGCTTT GGATGATGT TCAGGCAGGT CCAGGTCACA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CCGGCCGTGC GATGGGCCC GCAGCTGTGG ACTGGAGAAG CCTGTGGTCC CTTCGTTGCC	360 420 60 120 180 240 300 360 420 480 540 600
50 55	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequ 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TTCGCTGTGA CTGTCCAGGA ACCGCTGCA AAGCCCGCAG TGAAGCATCC ACATTGATGG	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGGTTGAGGCT CACGAGCGG GGACTCTGGC TGCCAACGCC AGCCTCGGC AGCCTCGGG	NSSDQRQAC TLVHFINPET Jence 1 #: NM_002: .3362 21 TCGGGGTCGG CCGCCGGA AGCGTCCTGC CCGGGCCGG CGTTCGCGC ACCTTCACAGT TCCTTCAACA GCTAGAGATCG CCCACCTACC	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCACT TACATGTTA AGGCAGCAG GTGTGGCTCG TCAAATGGAT AGCCACAGAC AATGGTTCCG	A1 CGGCTGCTGC GCTGGGGGCC GCTGGGGGTCC CCTGGGCGTTT GGATGATGT CCAGGTGGT CCAGGTGGT AGATGATGC AGATGACA AGATGGACA LGATGGACA AGATGGACA AGATGGACA LGATGGACA AGATGGACA AGATGGACA AGATGGACA AGATGGACA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGGCCAGAC ACCCAGACAG CGGCGCTGCGC GCAGCTGTGGC GCAGCTGTGGC CCTTGTTGCC CCCCTTTCTG	60 120 180 240 300 420 480 540 600 660
50 55	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequ 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TTCGCTGTGA CTGTCCAGGA ACCGCTGCA AAGCCCGCAG TGAAGCATCC ACATTGATGG	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGGTTGAGGCT CACGAGCGG GGACTCTGGC TGCCAACGCC AGCCTCGGC AGCCTCGGG	NSSDQRQAC TLVHFINPET Jence 1 #: NM_002: .3362 21 TCGGGGTCGG CCGCCGGA AGCGTCCTGC CCGGGCCGG CGTTCGCGC ACCTTCACAGT TCCTTCAACA GCTAGAGATCG CCCACCTACC	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCACT TACATGTTA AGGCAGCAG GTGTGGCTCG TCAAATGGAT AGCCACAGAC AATGGTTCCG	A1 CGGCTGCTGC GCTGGGGGCC GCTGGGGGTCC CCTGGGCGTTT GGATGATGT CCAGGTGGT CCAGGTGGT AGATGATGC AGATGACA AGATGGACA LGATGGACA AGATGGACA AGATGGACA LGATGGACA AGATGGACA AGATGGACA AGATGGACA AGATGGACA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CCGGCCGTGC GATGGGCCC GCAGCTGTGG ACTGGAGAAG CCTGTGGTCC CTTCGTTGCC	360 420 60 120 180 240 300 360 420 480 540 600
50 55 60	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TCGCTGTGA ACCCGCTGGA ACCCGCTGCA AAGCCCGCAG TGAAGCATCC ACATTGATGG ATGGTCAGAGA	EALRMANVAE MNATNHAIVQ H 59 DNA sequitence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGATGAGGCT CACGGACGGG TGGCACGCC TGCCACGGGACGGC TGCCACGCG TGCCACGCG AGCCTCGGG AGCCTCGGG CAACCACACACACACACACACACACACACACACAC	NSSDQRQAC TLVHPINPET ience if: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGGGTCTGC CCGTCTCCC CGGGCCGG TCTCCTCCAC TCCTCCAC TCCTTCAACA GCTGAGATCC CCCACCTACC GTCAGCAGCA GTTAGCAGCA	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGCCAGCAC TCAATGGAT AGCCACAGAC AATGGTTCCG AGCAGCAGAC AATGGTTCA	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGT GCAGGGGGTCC CCTGAGCTT TGATGATGTC TGAGCAGGC CCGGTAGCC CCTGAGCTC CCAGGTCACC CCTGACCCC CCTGACCCC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGACAG CCGGCCAGACAG CCGGCGCTGC GATGGGGCCC GCAGCTGTG ACTGGAGAAG CCTGTGGTCC CTTCGTTGCT CCGCCAGCTG	60 120 180 240 360 420 540 600 660 720
50 55 60	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ AACTCCCGCC GCGCTCCGGGT CCTCAGCTCC CCCGCCGGTT TTCCCTGTGA CTGTCCAGGA ACCCGCTGCA ACCCGCTGCA TGAAGCATCC ACATTGATGG ATGGTCAGGA GTCCTGAAGCA GTCCTGAAGCA TGAAGCATCC ACATTGATGG ATGGTCAGGG ATGGTCAGGG ATGGTCAGGCA GTCCTGAAGCA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAGCAG GGTTAGGCC TGCTAGGCC TGCTAGGCC AGCTCTGGC TGCCAACGCC AGCCTCGGA GCACCCCCGAA TAGTGGGCT TAGTGGCT TAGTGGCT TGCCAACGCC TGCCAACGCC TGCCAACGCC TGCCAACGCC TAGTGGGCT TAGTGGGCT TAGTGGGCT	NSSDQRQAC TLVHPINPET Lence 1 #: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCGG CCGCCGCGA AGGGTCCTGC CCGGCCCGGA AGGTCCTGC CCGGCCCGGA AGGTCCTGC CCGGCCCGGA CGTTTCACC ACCTTCCAGC GCTAGAACA GCTGAGATCC CCCACCTACC ATATTCCTGCT	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGGGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGGCAGCAG GTGTGGCTCG TCAAATGGAT AGCCACAGAC AATGGTTCGA AGGCAGAGAC AATGGTTCGA	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GCGGGGATCC GCTGGCGGG CTGGCTGTC CCTGAGCTT GGATGATGT TGAGGCAGGT CCAGGTCACA AGATGGGACC TCGCTCC TGCTTTTGGC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCAGACA ACCCAGACAG ACCCAGACAG CGGCGCTTGCG GATGGGCCC CTTCGTTGCC CCCCTTTCTG CCGCCAGCTG CAGCCTTCCAGCCAGCTGC CCCCTTTCTCAGCCAGCTTCCAGCCAGCTGCCAGCTTCCAGCCAG	60 120 180 240 360 420 480 540 660 660 720 780
50 55	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TTCCCTGTGA ACCCGCCGG AAGCCCGCA AAGCCCGCA ACATTGATGC ACATTGATGC ACATTGATGG ACGCTCAGAGA ACGCCCAGGAGA ACGCCCAGAGA ACGCCCAGAGA ACCCCCGCAGAAGCAGCAGAA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAC GGGTTAGGCC TGCTCACCACGCA GCACCCCCACCACACA TAGTGGGCTG TAGTGGCTGCTCTGCC TCACCTTGG	NSSDQRQAC TLVHFINPET Lence 1 #: NM_002: 3362 21 TCSGGSTCGG CCTGCCGGA AGCSTCCTGC CCGGCCGGA AGCTCCTGC CCGGCCGGG CGTTCGCC ACCTTCAGCA AGCTAGATAC GCTAGCAGCA TATTCCTGGT TAGCAGCAGCA TATTCCTGGT AGCATTGCTG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGGGAGCA TGGGAGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCACA AGGCACAGAC AATGGTTCCG AGGAGCGGAA AATGGTTCCG AGGAGCGGAA ATGAAAGCTT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTTGGGGCC GCTGGCGGT GCAGGGGCGC CTGGCTGTC CCTGAGCTTT GGATGATGTC CCAGGTCACA AGATGGGACC TCTGACGTTC TCTGACGTTTTGGC TGCTTTTTGGC TGCTTTTTGGC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCAGAC ACCCAGACA ACCCAGACAG CGGCCTGC GCAGCTGCG CCTGGTGCC CCTTGGTCC CCTTCTTGCC CCCCTTTCTG CAGCCTTCCA GTGCTGCAC GTGCTGCAC GTGCTGCAC GTGCTGCAC GTGCTGCAC GTGCTGCAC GTGCTGCAC GTGCTGCAC	360 420 120 180 240 480 540 660 720 780 840
50 55 60	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCTTCAGCTCC CCCCGGTT TCGCTGGA ACCGCAGA ACCGCTGCA AAGCCCGCAG AAGCCATCC ACATTCATGG GTCTCAGGA GCCGCAGG GCCGCAGA GCAGCAGAA CCCAGGAA	EALRMANVAE MNATNHAIVQ H 59 DNA sequidence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGCG TGCACCAC AGCCTCGGA AGCCTCGGA AGCCTCGGA TAGTGGCT CATCACTTG CATCACTTG CATCACTTG CATCACTTGGC GCACCACAC TAGTGGGCT GCTACCTTGG CTTCACCTTG GGTAGTAGCG GGTTTACCTTG	NSSDQRQAC TLVHPINPET #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGA AGCGTCCTCC CCGGGCCGG ATTCGCG GTTAGACA GCTTAGACA GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTCGGC AGCATTAGAGA	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TCGGGAGCTGC TCACATGTGTA AGGCAGCAG TCAATGGAT AGCCACAGA ATGATCAC AGGAGCGCACAGA AGGAGCGGAA AGGAGCGGAA AGGAGCGGAA AGGAGCGGAA AGGAGCGGAA AGGACCACAGA AGGAGCGCACAGA AGGAAGCTT AGGCCACAGTT AGGCCACAGTT	A1	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGACAG CCGGCCAGACAG CCGGCCGCC GCAGCTGCG CAGCTGCG CAGCTGCG CAGCTGCG CATGGGCCC CTTCTGTTGCC CCCCTTTCTG CCGCCAGCTG CAGGCTTGCA CAGGCTTGCA CTGCTGCAC TTCTCAGCCC CTTCTTGCC	60 120 180 240 360 420 480 540 660 660 720 780
50 55 60	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCTTCAGCTCC CCCCGGTT TCGCTGGA ACCGCAGA ACCGCTGCA AAGCCCGCAG AAGCCATCC ACATTCATGG GTCTCAGGA GCCGCAGG GCCGCAGA GCAGCAGAA CCCAGGAA	EALRMANVAE MNATNHAIVQ H 59 DNA sequidence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGCG TGCACCAC AGCCTCGGA AGCCTCGGA AGCCTCGGA TAGTGGCT CATCACTTG CATCACTTG CATCACTTG CATCACTTGGC GCACCACAC TAGTGGGCT GCTACCTTGG CTTCACCTTG GGTAGTAGCG GGTTTACCTTG	NSSDQRQAC TLVHPINPET #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGA AGCGTCCTCC CCGGGCCGG ATTCGCG GTTAGACA GCTTAGACA GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTCGGC AGCATTAGAGA	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TCGGGAGCTGC TCACATGTGTA AGGCAGCAG TCAATGGAT AGCCACAGA ATGATCAC AGGAGCGCACAGA AGGAGCGGAA AGGAGCGGAA AGGAGCGGAA AGGAGCGGAA AGGAGCGGAA AGGACCACAGA AGGAGCGCACAGA AGGAAGCTT AGGCCACAGTT AGGCCACAGTT	A1	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGACAG CCGGCCAGACAG CCGGCCGCC GCAGCTGCG CAGCTGCG CAGCTGCG CAGCTGCG CATGGGCCC CTTCTGTTGCC CCCCTTTCTG CCGCCAGCTG CAGGCTTGCA CAGGCTTGCA CTGCTGCAC TTCTCAGCCC CTTCTTGCC	60 120 180 240 300 360 420 480 540 600 720 780 840 900
50 55 60	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac; Coding sequit AACTCCCGCC GCGCTCCGGT CCTCAGGTC CCCCGCCGGTT TCGCTGTGA ACCCGCTGA ACCGCTGGA ACCGCTGGA ACCGCTGGA ACGGCTGCA AGGCCTGCAGGA CCGCTGAGCA CCAGGAGGT GAGCCAGGA CCCAGGAGGT AGCCACCCCC	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TCTTCCGAG GCCTCTGCTC CATCAAGCAG GGATCAGCG GGACTCTGCT CACCAACGCC AGCCTCGCC AGCCTCGCC AGCCTCGCA TAGTGGCT CACCACACA CAACCACACA TAGTGGCTG CAACCACACA TAGTGGCTG CATCACTCCCTTCCCT	NSSDQRQAC TLVHPINPET #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGGTCCTGC CCGTCAGC AGCTCTCACC ACCTTCAACA GCTAGAGATCC CCTACCTACC GTCAGCAGGA TATTCCTGCT AGGATTGGGA TGGCTCTTGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TACATGTGTA AGGCAGAGCA GTGTGCCTC TACATGTGTA AGGCAGAGCA GTGTGCCTC GTCAGATGGAT AGCCACAGAC AATGGATCA AGGCACAGAC AATGGTTCA AGGCCACAGA AGGAGCGGA AGGAGCGGA AGGAGCGGA AGGAGCGGA AGGAGCGGA AGGAGCGAA AGGACGGAA AGGACGATGAGAC	ALIGNODWIIA LINAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC CCTGAGCTTT TGAGGCAGGT CCAGGTCACC CCTGACGCTC TGCTTTTGGC TGCTTTTGGC TGCTTTTTGGC TGCATTGCCAGGTTCCCAGGTTCCCAGGTTCCCAGGTTCCCAGGTTCCCAGGTTCCCAGGTTCCCACACTCCCCTCCCT	PEGYAAYYCE DSSNVILKKY 51 TGGGGGGCCC CGCCGTGCGC CGGCCAGAC ACCCAGACAG ACCGAGCAGAC CCTGTGGTCC CTTCGTTGCC CCCCTTTCTG CGGCAGCTGCAGCTGCAGCTTGCAGCTTGCAGCTTGCAGCAGCTTGCAACCGCAGTTCCAACCCCCTTCCAGCCCCCCTTCCAGCCCCCCCC	360 420 60 120 180 240 360 420 660 660 720 780 840 900 960
50 55 60	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ AACTCCCGCC GCGCTCCGGGT CCTCAGCTCC CCCGCCGGTT TTCGCTGTGA ACCGCTGCA ACCGCTGCA ACCGCCGGAGT TGAAGCATCC ACATTGATGG ATGTCAGGA GTCTCAGGA GTCTCAGGA GCCCCCAGAA CCCAGGACGT AGCACCCCC GCCCCCCCACA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTAGAGCG GGACTCTGGCA GGCTCAGGCG AGCCTCGGAA GCACCACAG TAGTGGCT GCAACGCC AGCCTCGGA GCACCACTGG CAACCACCAC CATCAGGA GCACCTCGGA GCACCTCGGA GCACCTCGGA GCACCTCGGA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGCAGA CCTCGCAGA CCTCGGAGA CCTCCGCAGA	NSSDQRQAC TLVHPINPET LENCE 1 #: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCGG CCGGCGGA AGGGTCTGC CCGGGCCGGA CGTTTCACC ACCTTCAGC GCTAGACAC GTCAGCACC GTCAGCACC GTCAGCACC GTCAGCACC GTCAGCACC GTCACCTACC GTCAGCACC GTCAGCACC ACCTTCT AGGTATTGCTG AGGTTATGGG GGCACCATGT GGCACAGTGT	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGGCAGCAG GTGTGGCTCG TCAAATGGAT AGCACAGAC AATGGTTCG AGGAGCGGA AATGGTTCGAC AGGAGCGGA ATGAAAGCTT AGGCCACAG ATGAAAGCTT AGGCCACAGG TTGCCCACGG TTGCCCACGG	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GCGGGGATCC GCTGGCGGCT GCATGGCGGCT TGGATGATGTT TGAATGATGTC TCAGGCAGGTCACA AGATGGGACC CCTGACGTTC TGCTTTTTGGC TGCCAGGGTG CCATTGCCAG TCCCATCACT TGCTTCTGCTG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCAGACA ACCCAGACAG ACTCAGACAG ACTGGAGAAG CCTGTGGTCC CTTCGTTGCC CCCCTTTCTG CAGCCTTCCAG CAGCCAGCTG CAGCCTTCCAG CTTCCAGCCAGCTG CAGCCTTCCAGCCAGCTG CAGCCTTCCAGCCAGCTG CAGCCTTCCAGCCAGCTG CAGCCTGCAGCTC CTGACCCAGG	360 420 60 120 180 240 360 420 480 540 660 720 780 840 900 960 1020
50556065	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ AACTCCCGCC GCGCTCCGGGT CCTCAGCTCC CCCGCCGGTT TTCGCTGTGA ACCGCTGCA ACCGCTGCA ACCGCCGGAGT TGAAGCATCC ACATTGATGG ATGTCAGGA GTCTCAGGA GTCTCAGGA GCCCCCAGAA CCCAGGACGT AGCACCCCC GCCCCCCCACA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTAGAGCG GGACTCTGGCA GGCTCAGGCG AGCCTCGGAA GCACCACAG TAGTGGCT GCAACGCC AGCCTCGGA GCACCACTGG CAACCACCAC CATCAGGA GCACCTCGGA GCACCTCGGA GCACCTCGGA GCACCTCGGA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGGAA CCTCGCAGA CCTCGCAGA CCTCGGAGA CCTCCGCAGA	NSSDQRQAC TLVHPINPET LENCE 1 #: NM_002: 3362 21 TCGGGGTCGG CCTGTGCCGG CCGGCGGA AGGGTCTGC CCGGGCCGGA CGTTTCACC ACCTTCAGC GCTAGACAC GTCAGCACC GTCAGCACC GTCAGCACC GTCAGCACC GTCAGCACC GTCACCTACC GTCAGCACC GTCAGCACC ACCTTCT AGGTATTGCTG AGGTTATGGG GGCACCATGT GGCACAGTGT	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGGCAGCAG GTGTGGCTCG TCAAATGGAT AGCACAGAC AATGGTTCG AGGAGCGGA AATGGTTCGAC AGGAGCGGA ATGAAAGCTT AGGCCACAG ATGAAAGCTT AGGCCACAGG TTGCCCACGG TTGCCCACGG	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GCGGGGATCC GCTGGCGGCT GCATGGCGGCT TGGATGATGTT TGAATGATGTC TCAGGCAGGTCACA AGATGGGACC CCTGACGTTC TGCTTTTTGGC TGCCAGGGTG CCATTGCCAG TCCCATCACT TGCTTCTGCTG	PEGYAAYYCE DSSNVILKKY 51 TGGGGGGCCC CGCCGTGCGC CGGCCAGAC ACCCAGACAG ACCGAGCAGAC CCTGTGGTCC CTTCGTTGCC CCCCTTTCTG CGGCAGCTGCAGCTGCAGCTTGCAGCTTGCAGCTTGCAGCAGCTTGCAACCGCAGTTCCAACCCCCTTCCAGCCCCCCTTCCAGCCCCCCCC	360 420 60 120 180 240 360 420 660 660 720 780 840 900 960
50556065	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequi AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCCGCGGTT TTCGCTGTGA ACCGCTGCA AAGCCCGCAG AAGCCCGCAG ACATTGATGA ATGGTCAGAG ATGGTCAGAG ACGGCAGAA CCCAGGACGT AGCACCCCCC GCCCCCACA TCCGGCCACA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession Lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTTCGCTC CATCAGCAG GGATTCAGGGG GGACTCTGGC TACCAACGCC AGCCTCGGG CAACCACCA TACTGGGCT CTTACTAGGCT GCTACTTGGC GGACCTCGGAG CTTCACTGGC CTTACTGCC GGAGCCTGCAG CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCAATGCAGGG CCTCCGCAGA CCATCCGCAGA CCATCCGCAGA	NSSDQRQAC TLVHFINPET ##: NM_002: .3362 21 TCGGGGTCGG CCGCGCGGA AGCGTCCTGC CCGGCCCGGA AGCGTCTTCCACT GCTTCCACT GCTTCACAG GCTAGAGAT CCCACCTACC GTCAGCAGCA GTTAGCCG AGCTTCTGCT GCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGCTATTGCTG AGCTATTGCTG AGCTATTCACAGT TGCACAGTGT AGCATTGCTG AGCTATTCACAGT TGCACAGTGT ATCTACCGCT	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGGGAGCA TGGGAGCTGC TGCTGCGCT AGGATGCACT AGGATGCACT AGGCAGCAG GTGTGGCTCG TCAAATGGAT AGCCACAGAC AATGGTTCCG AGGAGCGGAA AGGCCCACAG GGGAGCGCACAGAC TGAGACT AGGAGAGCT TGCCAACGC TGCCACAGC TGCCACAGC TGCCACAGC TGCCACAGC GGGATGAGCAC TTGCCAACGG GCATTGGCCA	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCCC GCTGGGGGTCCT GCTGGCTG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACA ACCCAGACAG CGGCCGCGC GAACTGGGCCC CTTCGTTGGCC CCTTTCTG CGGCCAGCTG CAGGCTTGCA CTGGCAGCTGC ACCCAGCAG TTCTCAGCC AACCGCAGTC CTGACCCAGGCG GGCCCACCCA	360 420 120 180 240 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TCGCTGGA ACCGCCGGT AAGCCCGCA AAGCCCGCA AAGCCCGCA GCAGCCAGAA CCCAGCAGCA GCAGCCACA AGCCACCACA TCCGCCACA TCGGCCACG TCATCCTGGA	EALRMANVAE MNATNHAIVO H 59 DNA sequitence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGATGAGGCT TGCCAACGAG GGACTCTGGC TGCCAACGCC AGCCTCGGA AGCACACACA TAGTGGGCT CTTACCTTG CGTAGTAGGCG GGACTGCAG CATCACCTGG CAACCACACAC AGCTCGGAGA TAGTGGGCTG CTTCACCTTG CGTAGTAGGCG GAGCCTGCAGA AGCACACACAC AGCACACACACACACACACACA	NSSDQRQAC TLVHPINPET #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGGTCTGC CCGTCTCCC CGGGCCGG ATTTCGCC TCCTTCAACA GCTGAGATCC GTCAGCAGGA TATTCCTGCT AGCATTGCTG AGGTATTAGGG TGGCTCTTG AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT CCCCACAGTGT TGGCTCTTTG GCCACAGTGT ATCTACCGCT CACCTAGCAG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TCACATGTGTA AGGCAGCAC TCACATGTGTA AGGCACCAGAC ATGGTTCCG AATGGTTCCG AATGGTTCCG AATGGTTCACAGAC TCACAGAC TCACAGAC TCACAGAC TCACAGAC ATGAAAGCTT AGGCCACAGA TGAAAGCTT AGGCACACAG ATGAAAGCT TTGCCAACAG ATGAAAGCT TTGCCAACAG ATGAAAGCT TTGCCAACAG AGATTGAAGAC AGATTGAAGAC AGATTGAAGAC AGATTGAAGAC AGATTGAAGAC	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC CCTGGCGGT CCTGGCGGT CCTGGCGGT TGAGGCAGGT TGAGGCAGGT TGAGGCAGGT TGAGGCAGGT TGAGTCACA TGAGCAGGT TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGCTG TCCAGGGCAGGG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CGGCCAGACAG CGGCCAGACAG CGGCGCTGCG GAAGCTGCG GAAGCTGTGG CCTTCGTTGCC CCCCTTTCTG CAGCCAGCAG TTCTGAGCAC TTCTAGCCCC AACCGCAGTC CTAACCCAGG GGCCCACCAC TTTGAGCCAC	360 420 60 120 180 240 360 420 540 600 720 780 840 900 960 1020 1080
50556065	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ AACTCCCGCC GCGCTCCGGT CCTCAGCTC CCCCCGGTT TTCGCTGGA ACCGCTCGGA ACCGCTGGA ACGGCTGCA AGGCCGCAGA TGAAGCATCC ACATTGATGG ATGGTCAGGA ACGCCGCAGA TGAAGCACCC GCCCCACA TCCGGCCACA TCACGGCCGT TCATCCTGGA AGGGTGTTTAC	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGATCTGGC GGACTCTGGC TGCCAACGCC AGCCTCGGAA GCACCACCAC TAGTGGCT CATCAGCTGGC AGCCTCGGA GCACCACCAC TAGTGGCT CTTCACCTGGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA AGCCACACTT AGCTGGCAGC AGCCACACTT AGCTGGCAGC	NSSDQRQAC TLVHPINPET IENCE I #: NM_002: 3362 21 TCGGGGTCGG CCGGCGGA AGGTCCTGC CCGTCCTCCC CCGGCCGGA AGGTCTTGCCG ACCTTCCAGT TCCTTCAACA GCTGAGATCC GCTCAGCT AGCATTGCTG AGGTATGAGA TATTCCTGCT AGCATTGTG AGGTATGAGA GCTAGAGA TATTCCTGCT AGCATTGTG AGGTATGAGG AGGTAGAGG AGGTAGAGGAGG AGGTAGAGG AGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TACATGTGTA AGGCAGCAG GTGTGCCTC TACATGTGTA AGGCAGCAG GTGTGCTCG TCAAATGGAT AGCCACAGAC AATGATTCCG AGGAAGCGAA AGGATGAAGCT TGCCACAG ATGAAAGCT AGGCCATTGCCAA AGATTGAAGA TTGCCAACGG GCATTGGCCA AGATTGAAGA TGACCTGCCT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC CCTGAGCTTT GGATGATGTC CCTGAGCTT TGAGGCAGGT CCAGGTCACA AGATGGGACC CTGAGCTCT TGCTTTTGGC TGCCAGGGGT TCCCATCACT GCATTGCCAGT TCCCCCAAG TCCCCCAAG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CCGGCGCTGCGC GATGGGGCCC GCAGCTGTGG ACTGGAGAAG CCTGTGGTCC CTTCGTTGCC CCCCTTTCTG CAGCCTGCAGCTGCA GTGCTGGCAC TTCTCAGCCC AACCGCAGTTC CTGACCCAGG GGCCCACCCA TTTGAGCCAC GTTTGCCAG	360 420 120 180 240 360 420 480 540 6600 6600 900 900 1020 1020 1140 1200
50556065	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCGGTT TTCGCTGGA ACCGCCGGG ACCGCCGGG TGAAGCATCC ACATTGATGG ATGGTCAGGA AGGCCGCAGA CCCAGGACGT AGCCACACA CCCAGGACGT AGCCACCCC GCCCCCACA TCCGGCCACA TCATCCTGGA AGGGTGTTTAC	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGATCTGGC GGACTCTGGC TGCCAACGCC AGCCTCGGAA GCACCACCAC TAGTGGCT CATCAGCTGGC AGCCTCGGA GCACCACCAC TAGTGGCT CTTCACCTGGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA AGCCACACTT AGCTGGCAGC AGCCACACTT AGCTGGCAGC	NSSDQRQAC TLVHPINPET IENCE I #: NM_002: 3362 21 TCGGGGTCGG CCGGCGGA AGGTCCTGC CCGTCCTCCC CCGGCCGGA AGGTCTTGCCG ACCTTCCAGT TCCTTCAACA GCTGAGATCC GCTCAGCT AGCATTGCTG AGGTATGAGA TATTCCTGCT AGCATTGTG AGGTATGAGA GCTAGAGA TATTCCTGCT AGCATTGTG AGGTATGAGG AGGTAGAGG AGGTAGAGGAGG AGGTAGAGG AGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TACATGTGTA AGGCAGCAG GTGTGCCTC TACATGTGTA AGGCAGCAG GTGTGCTCG TCAAATGGAT AGCCACAGAC AATGATTCCG AGGAAGCGAA AGGATGAAGCT TGCCACAG ATGAAAGCT AGGCCATTGCCAA AGATTGAAGA TTGCCAACGG GCATTGGCCA AGATTGAAGA TGACCTGCCT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC CCTGAGCTTT GGATGATGTC CCTGAGCTT TGAGGCAGGT CCAGGTCACA AGATGGGACC CTGAGCTCT TGCTTTTGGC TGCCAGGGGT TCCCATCACT GCATTGCCAGT TCCCCCAAG TCCCCCAAG	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC ACCCAGACAG CCGGCGCTGCGC GATGGGGCCC GCAGCTGTGG ACTGGAGAAG CCTGTGGTCC CTTCGTTGCC CCCCTTTCTG CAGCCTGCAGCTGCA GTGCTGGCAC TTCTCAGCCC AACCGCAGTTC CTGACCCAGG GGCCCACCCA TTTGAGCCAC GTTTGCCAG	360 420 60 120 180 240 360 420 540 600 720 780 840 900 960 1020 1080
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50556065	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCATTGTCTT TTCGCTGGA ACCCGCAG ACCCGCAG ACCCCAGA ACCCGCAG ACCCAGA ACCCGCAG ACCCAGA ACCCCCCCACA ACCCCCCCACA ACCCCCCCACA TCACCCCGG TCATCCTGGA ACCCCCCCACA ACCCCCCCACA ACCCCCCCACA ACCCCCC	EALRMANVAE MNATNHAIVO H 59 DNA sequida Accession lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCTTCAGCTG CATCAAGCAG GGTTGAGCG TGCACCGCA AGCCTCGGCA TAGTGGGCT GCTACCTCG CATCACCTGG CATCACCTGG CACCACACA TAGTGGGCT GCTACCTGG GAGCCTCGAG AGCCTCGAG AGCCTCGAG CCTCCGCAG AGCCTGCAG CCTCCGCAG AGCCTGCAG CAACCACTT AGCTGCAGG AGCCACACTT AGCTGCAGG AGCCACACTT AGCTGCAGG AGCCACACTT AGCTGCAGG AGCCACACTT AGCTGCAGG CGTGCTGGCAGG CGTGCTGGCAGG CGTGCTGCAGG AGCCACACTT AGCTGCAGG CGTGCTGGCAGG CGTGCTGGGAG CCACCTCGCAGGA CCACCTCGCAGGA CCACCTCGCAGGA AGCCACACTT AGCTGCAGGC CGTGCTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGGAG CCACCTCGTGGCAGC CCACCTCGTGGCAGC CCACCTCGTGGCAGC CCACCTCGTGGAGG CCACCTCGTGGCAGC CCACCTCGTGGCAGC CCACCTCGTGGCAGC CCACCTCGTGGAGG CCACCTCGTGGCACC CCACCTCGTGCACC CCACCTCCCCCACC CCACCTCCCCCACC CCACCTCCCCCACC CCACCTCCCCCACC CCACCTCCCCCACC CCACCTCCCCCACC CCACCCCCCCC	NSSDQRQAC TLVHPINPET #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGA AGCGTCCTCC CCGGGCCGGG	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TACATGTGTA AGGCAGCAG ATGGATGCAC AGGATGCAC AGGAGCAGCA AGGAGCAGCA AGGACCACAGA AGGACCACAGA TCAAATGGAT AGCCACAGA ATGAAAGCTT AGGATGAGC ATGAAAGCTT AGGATGAGAC TTGCCAACGG GCATTGGCA AGATTGCAACG TTGCCACTGCCT TCCGCTGCCC TTCGCTGAAAG	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGGATC GCAGGGGGT CCTGAGCTT GGATGATGTC TGAGCAGT TGAGCAGGT TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCCAGGTC TGCTTTTGGC CCATCACT TCCCATCACT TCCCCCCAAG CATCCCCAAGG CATCCCCATGC TCCCCCAAGG CACCCATGC TTGCCCATGGC TTGCCCCAAGG CACCCATGGC TGATGCTGGT TCCCCCAAGG CACCCATGGC TGATGCTGGT	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGACA ACCCAGACAG CGGGCCAGCA GATGGGGCCC GCAGCTGCG CAGCTGCG CAGCTGCG CATGGTGCC CTCTTCTG CGCCAGCTG CAGCTTGCA ACCCAGCT CAGCCAGCC AACCGCAGTC CTCACCCAG GGCCCACCCA TTTGAGCCAC GGTCTGCCAG AGGGTCTACC AGGGTCTACC GGTCTACCC GGTCTACC GTCTACC GGTCTACC GTCTACC GGTCTACC GTCTACC GTCTA	60 120 180 240 360 420 540 600 720 780 840 900 960 1020 1140 1260 1320
5055606570	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac; Coding sequit AACTCCCGCC GCGCTCCGGT CCTCAGGTC CCCGCCGGTT TCGCTGTGA ACCCGCAGA ACCCGCAGA ACCCGCAGA TGAAGCATCC ACATTGATCC GCAGCAGAA CCCAGGAGT AGCCACACA TCCGCCACA TCCGCCACA TCACGCAGAG TCATCCTGGA GCGCTCCACA TCAGGAGT AGCCACACA AGCCCACACA TCAGGAGT AGCACCCCC GCCCCCACA TCCGGCCACA TCAGGAGT AGCACCCCC ACACACGGGTTTTAC AGCCAGGGT AGCACGCGCACA AGCCACGGGCCA AGCCACGGGCCA AGCCACGGGCCA AGCCACGGGCCA AGCCACGCGCCACA AGCCACGGGCCA AGCCACGCGCCACA AGCCACGCGCCACA AGCCACGCGCCACA AGCCACGCGCCACACACGCGT AGCACGCGCCACACGCGT AGCACGCGGCCA AGCCACGCGGCCACACGCGT AGCACGCGGCCA	EALRMANVAE MNATNHAIVO H 59 DNA sequitence: 150. 11 TCGGGACGCC TTTTCCTGAG GCTCCGCCT TTTTCCTAG GCTTCGCT CATCAAGCAG GGATCTGGC TGCCAACGCC AGCCTCGGCA GCACCCTCGCA TAGTGGGCT CATCAGCAG CAACCACACAC TAGTGGGCT GCAACCACACAC TAGTGGCTG CAACCACACAC TAGTGGGCTG CAACCACACAC TAGTGGGCTG CAACCACACAC TAGTGGGCTG CAACCACACAC CATCCACACAC TAGTGGGCTG CAACCACAC CATCCACACAC CATCCACACAC CATCCACACAC CATCCACACAC TAGTGGGCTGCAG CCACCTGCAGA CCACCTGCAGA CCACCTGCAGA CCACCTGCACAC TAGCTGGCAGC CGACCTGCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCACAC CCACCTGCACAC CCACCTGCACAC CCACCTGCACAC CCACCTGCAC CCACCTCCAC CCACCTCAC	NSSDQRQAC TLVHPINPET # NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGGTCCTGC CCGTCTGCCG AGGTCTGC CGGGCCGG ACTTCCAGT TCCTTCACA GCTAGATACA GCTAGATACA GTAGAGATG AGGTATGAGA TATTCCTGCT AGGATATGAGA TATTCCTGCT AGGATATGAGA TATTCCTGGT AGGTATGAGA TATTCCTGGT AGGTATGAGA TGGCCACAGTGT ATTACCGGT CACCTAGCAG GAGGAGGTG CACGCGGGAAG TTGGCCAAT TTGCCAGTAGGAGAG TTGGCCAAT GGTCAGGGGAAG TTGGCCAAGGGAAG TTGGCCAAGGGAGAGAGGGGGAAGA TTGGCCAAGGGAGAGAGGGGGAAGA TTGGCCAAGGGAGAGAGGGGGGAAGAGGGGGGAAGAGGGGGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGGCAGCAG TCAAATGGAT AGCCACAGAC AATGGATCAC AATGGTTCA AGGCAGCAGA TGAAAGCTT AGGATGAAGCT TCCAACGG TTGCCAACGG ATGAAGCT TTGCCAACGG TTGCCTGACCT TCCGGCTGCC TTGCTGAACG TTGCTGAACG GGACAGGATGT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGGCGGT GCAGGGGTCCTC CCTGAGCTTT TGAGCAGGT TCAGGCAGGT CCAGGTCACA AGATGGGACC TGCTTTTGGC TGCTTTTGGC TGCTTCTGCT GCATTGCCAG TCCCATCACT TCCCCCAAG CATCCCACT TCCCCCAAG CACCCATGGC	PEGYAAYYCE DSSNVILKKY 51 TGGGGGGCCC CGCCGTGCGC CGCGGCAGAC ACCCAGACAG CCGGGCCTGCG GATGGGCCC GCAGCTGTG CATGGGCCC CTTCTGTTGCC CTTCTTGTTGCA GTGCTGGCAC TTCTAGCCC AACCGCAGTC CTTCTAGCCC AACCGCAGTC CTTCTAGCCC AACCGCAGTC CTTTAGCCAG GGCCCACCCA GGTCTGCCAG GGCCCACCCA GGTCTGCCAG GGCTTGCCAG GGCTCTACCCCAG GGTCTACCACCT GTGGCCACTG GTGGCCACCTG	360 420 120 180 240 360 420 540 660 720 780 840 960 1020 1080 1140 1200 1140 1210 1320 1380
5055606570	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac; Coding sequit AACTCCCGCC GCGCTCCGGT CCTCAGGTC CCCGCCGGTT TCGCTGTGA ACCCGCAGA ACCCGCAGA ACCCGCAGA TGAAGCATCC ACATTGATCC GCAGCAGAA CCCAGGAGT AGCCACACA TCCGCCACA TCCGCCACA TCACGCAGAG TCATCCTGGA GCGCTCCACA TCAGGAGT AGCCACACA AGCCCACACA TCAGGAGT AGCACCCCC GCCCCCACA TCCGGCCACA TCAGGAGT AGCACCCCC ACACACGGGTTTTAC AGCCAGGGT AGCACGCGCACA AGCCACGGGCCA AGCCACGGGCCA AGCCACGGGCCA AGCCACGGGCCA AGCCACGCGCCACA AGCCACGGGCCA AGCCACGCGCCACA AGCCACGCGCCACA AGCCACGCGCCACA AGCCACGCGCCACACACGCGT AGCACGCGCCACACGCGT AGCACGCGGCCA AGCCACGCGGCCACACGCGT AGCACGCGGCCA	EALRMANVAE MNATNHAIVO H 59 DNA sequitence: 150. 11 TCGGGACGCC TTTTCCTGAG GCTCCGCCT TTTTCCTAG GCTTCGCT CATCAAGCAG GGATCTGGC TGCCAACGCC AGCCTCGGCA GCACCCTCGCA TAGTGGGCT CATCAGCAG CAACCACACAC TAGTGGGCT GCAACCACACAC TAGTGGCTG CAACCACACAC TAGTGGGCTG CAACCACACAC TAGTGGGCTG CAACCACACAC TAGTGGGCTG CAACCACACAC CATCCACACAC TAGTGGGCTG CAACCACAC CATCCACACAC CATCCACACAC CATCCACACAC CATCCACACAC TAGTGGGCTGCAG CCACCTGCAGA CCACCTGCAGA CCACCTGCAGA CCACCTGCACAC TAGCTGGCAGC CGACCTGCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCAGAC CCACCTGCACAC CCACCTGCACAC CCACCTGCACAC CCACCTGCACAC CCACCTGCAC CCACCTCCAC CCACCTCAC	NSSDQRQAC TLVHPINPET # NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGGTCCTGC CCGTCTGCCG AGGTCTGC CGGGCCGG ACTTCCAGT TCCTTCACA GCTAGATACA GCTAGATACA GTAGAGATG AGGTATGAGA TATTCCTGCT AGGATATGAGA TATTCCTGCT AGGATATGAGA TATTCCTGGT AGGTATGAGA TATTCCTGGT AGGTATGAGA TGGCCACAGTGT ATTACCGGT CACCTAGCAG GAGGAGGTG CACGCGGGAAG TTGGCCAAT TTGCCAGTAGGAGAG TTGGCCAAT GGTCAGGGGAAG TTGGCCAAGGGAAG TTGGCCAAGGGAGAGAGGGGGAAGA TTGGCCAAGGGAGAGAGGGGGAAGA TTGGCCAAGGGAGAGAGGGGGGAAGAGGGGGGAAGAGGGGGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGGCAGCAG TCAAATGGAT AGCCACAGAC AATGGATCAC AATGGTTCA AGGCAGCAGA TGAAAGCTT AGGATGAAGCT TCCAACGG TTGCCAACGG ATGAAGCT TTGCCAACGG TTGCCTGACCT TCCGGCTGCC TTGCTGAACG TTGCTGAACG GGACAGGATGT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGGCGGT GCAGGGGTCCTC CCTGAGCTTT TGAGCAGGT TCAGGCAGGT CCAGGTCACA AGATGGGACC TGCTTTTGGC TGCTTTTGGC TGCTTCTGCT GCATTGCCAG TCCCATCACT TCCCCCAAG CATCCCACT TCCCCCAAG CACCCATGGC	PEGYAAYYCE DSSNVILKKY 51 TGGGGGGCCC CGCCGTGCGC CGCGGCAGAC ACCCAGACAG CCGGGCCTGCG GATGGGCCC GCAGCTGTG CATGGGCCC CTTCTGTTGCC CTTCTTGTTGCA GTGCTGGCAC TTCTAGCCC AACCGCAGTC CTTCTAGCCC AACCGCAGTC CTTCTAGCCC AACCGCAGTC CTTTAGCCAG GGCCCACCCA GGTCTGCCAG GGCCCACCCA GGTCTGCCAG GGCTTGCCAG GGCTCTACCCCAG GGTCTACCACCT GTGGCCACTG GTGGCCACCTG	60 120 180 240 360 420 540 600 720 780 840 900 960 1020 1140 1260 1320
50556065	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Act Coding sequ AACTCCCGCC CCGCGGTT CCTCAGCTC CCCGCGGTT TTCGCTGTGA ACGCTCCAGGA ACGCCGCAGA ACGCCGCAGA TGAAGCATCC ACATTGATGG ATGGTCAGGA GTCCTGAGCA GCACCCCC GCCCCACA TCCGGCCACA TCCGGCCACA TCAGCCAGGAGT TCATCCTGG AGGGTGTTTAC AGCCACGGT AGAAGGGCCAGG GCCCCCACG TCACCCCC TCACCTCTGAGCA TCCAGCAGT TCACCTCG	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGATCTGGC TGCAAGCAC GGACTCTGGC TGCCAACGCC AGCCTCGGAA GCACCACAC ATACTAGGC CAACCACAC CATCAGGCG GAGCCTGGA GCACCTCGGA GCACCACGC GGAGCTGCGC GGAGCTGCGCAG CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA AGCACACTTGC GTGGTGGAG CGAGCTGGTG GTGGTGGAG CGACCTGGCT GCTAAGAAGAG	NSSDQRQAC TLVHPINPET IENCE 1 #: NM_002: 3362 21 TCGGGGTCGG CCGCGCGGA AGGTCCTGC CCGCCGCGGA AGGTCCTGC CGGCCCGGA AGGTCCTGC CGGCCCGGA AGGTCCTGC CGGCCCGGA AGGTTCCCGC ACCTTCCAGT TCCTTCAACA GCTAGGAGACC GTCAGCAGGA TATTCCTGCT AGGATTGCTG AGGTTATGGG GCACAGTGT ATCTACCGCT CACCTACCG CACCTAGCA CACCTAGCAG TGGCCACTAGCA CACGCGGGAG TTGCCAAGACA CCCCAAGACA	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGT TACATGTGTA AGGGCAGGAG ATGATGATTCAG AGGCAGGAG ATGATCAGA ATGATTCCG AGGAGGGAA ATGATAGGAT AGGCCATGT AGGCATGTC TCGAACG ATGAAAGCT TTGCCAACG GCATTGGCA AGATTGAAAG TTCCGGCTGCC TTCCGGCTGCC TTCCTGAAAG GACAGGATGT GCCAGGTGGA	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGCGGT CCTGAGCTGT GGATGATGTT GGATGATGTT TGAGCAGGT CCAGGTCACA AGATGGGACC TGCTTTTTGGC TGCAGGGT TCCCATCACT GTCTCTCTGT GGAGGCAGGG ACACCACTAC CACCCCAAG CACCCATAGCC GGAGGCAAA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCTGCGC CGGCCAGAC ACCCAGACAG ACCCAGACAG ACTGGAGAAG ACTGGAGAAG CCTTTCTG CCCCTTTCTG CAGCCTTCTG CAGCCTTCCAG GTGCTGGCAC TTCTAGCCAC TTCTAGCCAC GTCTTGACCAG GGCCCACCAA ACCGCAGTC CTGACCAG GGCCCACCCA ACCGCAGTC CTGACCCAG GGCCCACCCA ACCGCAGTC CTGACCCAG GGCCTACCCAG CGTCTGCCAG CGTCTGCCAG CGTCTGCCAG CGTCTGCCAC CGTCTACACCT CTGACCACTG CCCGGCTACT	360 420 120 180 240 360 420 540 660 660 660 720 780 840 900 1020 1020 1020 1140 1260 1380 1440
5055606570	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequi AACTCCCGCC GCGCTCCGGT CCATGGTC CCATGGTC CCATGGTGT AGCCCGCAG AGCCCGCAG AGCCCGCAG AGCCAGAA CCCAGGACGT AGCACCCCC GCCCCCACA TCAGCACGAC TCAGCACGAC AGCCACACA TCCGGCCACG TCATCCTGGA AGCACCCCC GCCCCCACA TCCGGCCACG TCATCCTGGA AGCCACCAC TCATCCTGGA AGCCACCAC TCATCCTGGA AGCCACCAC TCATCCTGGA AGCCACCGCT TCGCTCCTCT TGGATTGCCT	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTAGG GCCTCTGCTC CATCAAGCAG GGTTGAGCT TACCAGGAGGCG GGACTCTGGC TACCACACA AGCACCTCGGA GCACCCTCGGA CCTCCGCAG CCTCCGCAGA CCACCTCTGC GTGGTGGGAG CCTCCAGCAC CGAGCTGCTG CGAGCTGCTG CGAGCTGCTG CGACTGCTG CGACTGCTG CCTCAAGAGAG CGACCTGCAGA	NSSDQRQAC TLVHFINPET ##: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGA AGCGTCTCCC CCGGCCCGG ATTCGCC GTCAGCAGA TATTCCTGCT AGCATTGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCT AGCATTGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCGCACAGGC TATTCCGGT CACCGGGAGA CACCGAAAAC ACACCAAAAC	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGGGGCA CGGGGAGCA TGGGACTGC AGGATGCACT AGGATGCAC AGGATGAGAC TTGCCAACGG GCATTGCCA AGATTGAAGA TTGCCACGG TCCCGCTGCC TTCCTGAAAG GACAGCATGTA CCACCTGCAC CTCCCTGCAC CCACCTGCAC CCACCTCGCAC CCACCTCCAC CCACCTCGCAC CCACCTCCAC CCACCTCAC CCACCT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGGTCC GCTGGGCGGC GCAGGGGTCT GCATGAGCTTT GGATGATGTC TCAGGTAGTT TCAGGCAGGT TCCAGGTCAC TCCTTTTGGC TCCCATCAC TCCCATCAC TCCCCATCAC TCCCCCAAGG CATCCCATCAC TCCCCCAAGG CACCCATGAC TCCCCAAGG CACCCATGAC TCCCCAAGAG CACCCATGAC TGGAGGCAGAGG CACCCATGAC TGGAGGGCAAA CTGGTACAGA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGCA ACCCAGACAG CGGGCGCAGCA GATGGGGCC GCAGCTGTGG CCTTCGTTGCC CCCCTTTCTG CCGCCAGCTG CAGCCTAGCA ATTCAGCCC AACCGAGTTGCA CTTCCAGCCAGG GGCCCACCCA TTTGAGCCAC GTTTGCCC GTGGCCACCCA TTGAGCCAC GGTCTGCCCC AGGCTTGCCC GTGGCCACCT AGGGTTCTACCC GTTGCCACC GTTTAGCCACC GTTTACACCT GTGGCCACCT CCCGGCTACT AACCAGATGC	60 120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1220 1380 1440 1500
5055606570	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequi AACTCCCGCC GCGCTCCGGT CCATGGTC CCATGGTC CCATGGTGT AGCCCGCAG AGCCCGCAG AGCCCGCAG AGCCAGAA CCCAGGACGT AGCACCCCC GCCCCCACA TCAGCACGAC TCAGCACGAC AGCCACACA TCCGGCCACG TCATCCTGGA AGCACCCCC GCCCCCACA TCCGGCCACG TCATCCTGGA AGCCACCAC TCATCCTGGA AGCCACCAC TCATCCTGGA AGCCACCAC TCATCCTGGA AGCCACCGCT TCGCTCCTCT TGGATTGCCT	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTAGG GCCTCTGCTC CATCAAGCAG GGTTGAGCT TACCAGGAGGCG GGACTCTGGC TACCACACA AGCACCTCGGA GCACCCTCGGA CCTCCGCAG CCTCCGCAGA CCACCTCTGC GTGGTGGGAG CCTCCAGCAC CGAGCTGCTG CGAGCTGCTG CGAGCTGCTG CGACTGCTG CGACTGCTG CCTCAAGAGAG CGACCTGCAGA	NSSDQRQAC TLVHFINPET ##: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGA AGCGTCTCCC CCGGCCCGG ATTCGCC GTCAGCAGA TATTCCTGCT AGCATTGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCT AGCATTGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCTG AGCTATGCGCACAGGC TATTCCGGT CACCGGGAGA CACCGAAAAC ACACCAAAAC	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGGGGCA CGGGGAGCA TGGGACTGC AGGATGCACT AGGATGCAC AGGATGAGAC TTGCCAACGG GCATTGCCA AGATTGAAGA TTGCCACGG TCCCGCTGCC TTCCTGAAAG GACAGCATGTA CCACCTGCAC CTCCCTGCAC CCACCTGCAC CCACCTCGCAC CCACCTCCAC CCACCTCGCAC CCACCTCCAC CCACCTCAC CCACCT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGGTCC GCTGGGCGGC GCAGGGGTCT GCATGAGCTTT GGATGATGTC TCAGGTAGTT TCAGGCAGGT TCCAGGTCAC TCCTTTTGGC TCCCATCAC TCCCATCAC TCCCCATCAC TCCCCCAAGG CATCCCATCAC TCCCCCAAGG CACCCATGAC TCCCCAAGG CACCCATGAC TCCCCAAGAG CACCCATGAC TGGAGGCAGAGG CACCCATGAC TGGAGGGCAAA CTGGTACAGA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGCA ACCCAGACAG CGGGCGCAGCA GATGGGGCC GCAGCTGTGG CCTTCGTTGCC CCCCTTTCTG CCGCCAGCTG CAGCCTAGCA ATTCAGCCC AACCGAGTTGCA CTTCCAGCCAGG GGCCCACCCA TTTGAGCCAC GTTTGCCC GTGGCCACCCA TTGAGCCAC GGTCTGCCCC AGGCTTGCCC GTGGCCACCT AGGGTTCTACCC GTTGCCACC GTTTAGCCACC GTTTACACCT GTGGCCACCT CCCGGCTACT AACCAGATGC	360 420 120 180 240 360 420 540 660 660 660 720 780 840 900 1020 1020 1020 1140 1260 1380 1440
5055606570	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequilated according sequilated according sequilated according sequilated according sequilated according sequilated according accordi	EALRMANVAE MNATNHAIVO H 59 DNA sequitence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCTCTCGCCA CATCAAGCAG GGACTCTGC TAGCAAGCAG GGACTCTGGC TGCCAACGCC TAGCAGCGG GGACTCTGGC AGCCTCGGAA GCACCACACAC TAGTGGGCTG CTTCACCTGG GAGCCTGCAG AGCCTGCAGAG TAGTGGGCTG CTCCGCAGA TAGTGGGCTG CGACCACACAC TAGTGGGCTG CGACCACACAC TAGTGGGCTG CGACTGCAGG CAGCCTGCAGGA CATCCAGGGC AGCCTGCAGGA CAGCTGCAGGC CGACTTGACCTGGCAGCA CGACTGGCAGC CGACTGAGAGAG CGACCTGGCC GGACTCACGGC GGACTCACGGC	NSSDQRQAC TLVHPINPET #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGAA AGCGTCTGCC CCGGCGGAA AGCGTCTGCCG GTCAGCAC TCCTTCAACA GCTAGAGATCC GCACAGTGT AGCATTGCTG GCCACAGTGT ATCTACCAGT CACCTAGACAA ACACCAAAAAC ACACCAAAAAC TTCGAGGTCT TTCGAGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGGTCT TTCGAGTCT TTCGAGGTCT TTCGAGTCT TTCGAGGTCT TTCGAGTCT TTCGAGTCT TTCGAGTCT TTCGAGTCT TTCGAGTC	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGGCAGCAG TCAAATGGAT AGCCACAGAC ATGGATCCG AATGGTTCCG AGGATGGCA ATGAAGCTT AGGCCACAG TTCACAGAC TTGCCAACGG TCCGGCTGCA TGCCACGG TCCGGCTGCA TGCCACGG TCCGGCTGCA TGCCACGCT TCCCGCTGCA TTGCCAACGC TCCCGCTGCA TTGCCAACGC TCCCGCTGCA TTGCCAACGC TCCTCACAG TTCACAGTTGT TCACAGTTGT TCACAGTTGT TCACAGTTGT TCACAGTTGT	ALIGNODWIIA LINAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGGGGATCC GCTGGGGGGT CCGTGGCGGT TGGATGATGTC TGATGATGTC TGATGATGTC TGATGATGTC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TCCATGGTACACT TCCATCACT TCATCACT TGATGCTACAGA CACCTTGCCG GAAGGCCAAGA CTGGTACAGA GACCTTGCCGC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CGCGCCAGCCAGCCAGCCAGCCCGCCGCCGCCCCCCCTTCTGCCCCCCCC	50 420 120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560
5055606570	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac; Coding sequity AACTCCCGCC GCGCTCCGGT CCTCAGCTC CCCCGCGGT CCTCAGCTC CCCGCGGT TCCATGTCT TTCGCTGTGA ACCGCCGGG ACCGCCGGG TGAAGCATCC ACATTGATGG ATGGTCAGAG ATGGTCAGAG ATGGTCAGAG GTCCTGAGCA GCACCCCCC GCCCCACA TCCGGCCACA TCACCTGGA AGGCTGTTTAC AGCCCACGGT TCATCCTGGA AGGCCACGGT TCATCCTGGA AGCACGGCC TCACCCCCT TCATCTCAGA TCGACTGCT TGGATTGCT TCATCTCAGA	EALRMANVAE MNATNHAIVO H 59 DNA sequid Accession tence: 150. 11 TCGGGACGCC TCTTCCGAG GCCTCGCCT TTTCCTAAG GCCTCGCTC CATCAAGCAG GGATCTCGCC AGCCTCGGCA GGACCCTCGG TGCCAACGCC AGCCTCGGAA GCACCACACA TAGTGGGCT GGAGCTGGCG GAGCCTGCGAG CCTCCGCAGA CCACCTGGCT GGAGCTCGCG CGACCTGGCG CGACCTGGCG CGACCTGGCG CGACCTGGCG CGACCTGGCG GGACCCAGCC GGACTCACGG TGGTGAGAAAG GACCCAGGCC TGATGGGAC TGATGGAC TGATGGGAC TGATGGGAC TGATGGAC TGATGAC TGATGCAC TGATGAC TGATGCAC TGATGAC TGATGCAC TGATGAC TGATCAC TGATGAC TGATGAC TG	NSSDQRQAC TLVHPINPET ##: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGAA AGCGTCCTGC CCGTCTGCCC ACCTTCCACT ACCATTCCAGT TCCTTCAACA GCTGAGATCC CCCACCTACC ACCTTCCAGT TCCTTCACAGT TCCTTCAGT AGCATTGCTGC CACCAGTAGT ATTCCTGCT CACCTAGCAG GAGGAGCGTG CACCTAGCAG CACCTAGCAG CACCTAGCAG CACCTAGCAG CACCAGAGAC ACACCAAAAAC CCCCAAGACA ACACCAAAAC TTCGAGGTCT TGGGTCCTT TGGTCCCTT	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TECTGCCGCT TACATGTGTA AGGCAGCAG GTGTGGCTCG GTCAATGGAT AGCCACAGAC AATGGATCAG AGGATGCAC AGGATGCAC AGGATGCAC TCAATGGTT AGGCATGAGC TTGCCAACG TTGCCAACG GCATTGGCCA AGATTGAAGA TTGCTGAACG TTCCTGAACG GCACGTGCA CTACAGTTGA	ALIGNODWIIA LINAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGCGGT TGAGGCTT GGATGATGTT TGAGGCAGGT TCAGGCAGT TCAGGCAGT TCAGGCAGT TCAGGCAGT TCCAGGTCAC TGCTTTTGGC GCGGCAAG TCCCATCACT GTCTCTGCTG GGGGCAAGAG CACCCATGCC TGAGCTCA TCCCCCAAG CACCCATGCC GAGGCCAAA CAGCCCAAG CACCCATGCC CACCCCAGC CACCCTGCAC CACCCTCACC CACCCCAGC CACCCCAGCC CACCCCAGCC CACCCCAGCC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CGCGGCAGAC ACCCAGACAG CGGGCGCTGCG GATGGGGCC GATGGGGCC GCAGCTTGGT CCTTCGTTGCC CCCCTTTCTG CAGCCAGCTGCA TTCAGCCC TTCTCAGCCC TTCTCAGCC GGCCACCT CGGCTACT CGGCCACCT GTGGCCACT CGCCGCTACT AACCAGATGC ATCAACAGGG GGCAGCATCG	360 420 120 180 240 360 420 480 540 6600 6600 720 780 840 900 950 1020 1140 1200 11200 11200 11320 11380 1440 1560 1560 1620
505560657075	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequil AACTCCCGCC GCGCTCCGGT CCATCGTCT CCATGTCTT TTCGCTGTGA ACCCCCC AAGCCCCCA AAGCCCCCA AAGCCCCCA ACATTGATGA ATGGTCAGAG ACCGCAGA CCCAGGACGT AGCACCCCC GCCCCCACA TCATCCTGA AGCCACCCCC GCCCCCACA TCCGGCACG TCATCCTGA AGCCACCCCC TCATCCTGA AGCCACCCCC TCATCCTGA AGCCACCAC TCATCCTGA TCATCCTGA AGCCCACGGT TCATCTCAGA TGGAGTTTCATCAGA TGGAGTTTCATCAGA TGGAGTGTTA AGGCGCAAGGT TCATCTCAGA TGGAGTGTTA AGGCGCAAGGT TCATCTCAGA	EALRMANVAE MNATNHAIVO H 59 DNA sequida Accession Lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAGCAG GGATTCAGGG GGACTCTGGC TACCAACGCC AGCCTCGGG CAACCACAC AGCCTCGGG CAACCACCAC AGCCTCGGG CAACCACCAC AGCCTCGGAG CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCACACTT AGCTGCAGG GGACTACGG GGGCTGCAG CGAGCTGGGG GGGCTGCAG CGAGCTGGCG GGGCTGCAG GGACCACCT GCTGAGAGAG CCACCAGGC GGACTCACGG GGACTCACGG TGATGGGACA CCGTGTTCCAA	NSSDQRQAC TLVHFINPET ##: NM_002: .3362 21 TCGGGGTCGG CCGGCGGGA AGGCTCCTGC CCGGCCCGGA AGGCTCCTGC CCGGCCCGGA AGGCTCCTGC GTCACCAGT TCCTTCAACA GCTGAGATC GTCAGCAGCA TATTCCTGCT AGGATTGGTG AGGTATTGGTG AGGTATTGGTG AGGTATTGGTG AGGTATTGAGA TTGCAGAGAGCA TTGCAGAGAGCA TTGCAGGAGA TTGGCAAAAA TTCGAGGAGA TTGGAGAAAA TTCGAGGAAAA TTCGAGGAAAA TTCGAGGAAAA TTCGAGGAAAA TTCGAGGTATT TGGTACCGTT TGGTACCGTT TGGTACCGTT TGGTACCGTT	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGGGA CAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	LIGNODWIIA LINAISVLYFD 41 CGGCTGCTGC GTCTGCGGCCC GCGGGGATCC GCTGGGGGGCC GCTGGGGGCC CCTGAGCTTT GGATGATGTC CCAGGTCACA AGATGGGACC CCTGAGCTT TGCAGGTCACA AGATGGGACC CTGCAGGTC TGCTTTTTGGCT GCAGGTCACA TCCCATAGCC CACACCATGGC CACACCATGGC CACACCACCA CCACACCC CACACCCCC CACACCCCCC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACAG CGGCCGAGC ACCCAGACAG ACTGGAGAAG CCGGGCGCCC CTTCGTTGCC CCCCTTTCTG CGGCAGCTGCA ACCCAGCTG TTCTAGCAC TTCTAGCCC AACCGCACT TTTTAGCCAC GTCTTCCAG GGCCCACCCA TTTTAGCCAC CTGACTTCCAG GGCCACCCA TTTAGACCAC TTTAGACCAC TTTAGACCAC TTTAGACCAC CTGACCAGC ACCACCAC TTTAGACCAC TTTAGACCAC TTTAGACCAC CTGACCACCAC ACCAGCACC ACCAGCACC CCCCGCTACT AACCAGATGC ACCAGCATCG GGCAGCATCG CGCCAGCCAC CCCCAGCCAC	360 420 120 180 240 300 360 420 480 540 600 660 720 780 840 900 1020 1080 11200 1260 1320 1320 1320 1340 1500 1500 1620 1680
505560657075	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequil AACTCCCGCC GCGCTCCGGT CCATCGTCT CCATGTCTT TTCGCTGTGA ACCCCCC AAGCCCCCA AAGCCCCCA AAGCCCCCA ACATTGATGA ATGGTCAGAG ACCGCAGA CCCAGGACGT AGCACCCCC GCCCCCACA TCATCCTGA AGCCACCCCC GCCCCCACA TCCGGCACG TCATCCTGA AGCCACCCCC TCATCCTGA AGCCACCCCC TCATCCTGA AGCCACCAC TCATCCTGA TCATCCTGA AGCCCACGGT TCATCTCAGA TGGAGTTTCATCAGA TGGAGTTTCATCAGA TGGAGTGTTA AGGCGCAAGGT TCATCTCAGA TGGAGTGTTA AGGCGCAAGGT TCATCTCAGA	EALRMANVAE MNATNHAIVO H 59 DNA sequida Accession Lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAGCAG GGATTCAGGG GGACTCTGGC TACCAACGCC AGCCTCGGG CAACCACAC AGCCTCGGG CAACCACCAC AGCCTCGGG CAACCACCAC AGCCTCGGAG CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCTCGCAGA CCACACTT AGCTGCAGG GGACTACGG GGGCTGCAG CGAGCTGGGG GGGCTGCAG CGAGCTGGCG GGGCTGCAG GGACCACCT GCTGAGAGAG CCACCAGGC GGACTCACGG GGACTCACGG TGATGGGACA CCGTGTTCCAA	NSSDQRQAC TLVHFINPET ##: NM_002: .3362 21 TCGGGGTCGG CCGGCGGGA AGGCTCCTGC CCGGCCCGGA AGGCTCCTGC CCGGCCCGGA AGGCTCCTGC GTCACCAGT TCCTTCAACA GCTGAGATC GTCAGCAGCA TATTCCTGCT AGGATTGGTG AGGTATTGGTG AGGTATTGGTG AGGTATTGGTG AGGTATTGAGA TTGCAGAGAGCA TTGCAGAGAGCA TTGCAGGAGA TTGGCAAAAA TTCGAGGAGA TTGGAGAAAA TTCGAGGAAAA TTCGAGGAAAA TTCGAGGAAAA TTCGAGGAAAA TTCGAGGTATT TGGTACCGTT TGGTACCGTT TGGTACCGTT TGGTACCGTT	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGGGA CAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	LIGNODWIIA LINAISVLYFD 41 CGGCTGCTGC GTCTGCGGCCC GCGGGGATCC GCTGGGGGGCC GCTGGGGGCC CCTGAGCTTT GGATGATGTC CCAGGTCACA AGATGGGACC CCTGAGCTT TGCAGGTCACA AGATGGGACC CTGCAGGTC TGCTTTTTGGCT GCAGGTCACA TCCCATAGCC CACACCATGGC CACACCATGGC CACACCACCA CCACACCC CACACCCCC CACACCCCCC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACAG CGGCCGAGC ACCCAGACAG ACTGGAGAAG CCGGGCGCCC CTTCGTTGCC CCCCTTTCTG CGGCAGCTGCA ACCCAGCTG TTCTAGCAC TTCTAGCCC AACCGCACT TTTTAGCCAC GTCTTCCAG GGCCCACCCA TTTTAGCCAC CTGACTTCCAG GGCCACCCA TTTAGACCAC TTTAGACCAC TTTAGACCAC TTTAGACCAC CTGACCAGC ACCACCAC TTTAGACCAC TTTAGACCAC TTTAGACCAC CTGACCACCAC ACCAGCACC ACCAGCACC CCCCGCTACT AACCAGATGC ACCAGCATCG GGCAGCATCG CGCCAGCCAC CCCCAGCCAC	360 420 120 180 240 360 420 480 540 6600 6600 720 780 840 900 950 1020 1140 1200 11200 11200 11320 11380 1440 1560 1560 1620
5055606570	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCGGTT TCGCTGGA ACCGCGGG AAGCCCCCACA AAGCCCGCAG GCCCCCCACA TCCGGCAGG TGAAGCATCC GCCCCCCACA TCCGGCCAGG TCATCTTGTTAGC AGCCACGGT AGCCACGGT AGCCACGGT TCATCTGGA AGCCACGGT TCATCTCGGA AGCCACGGT TCATCTCAGA AGCCACGGT TCATCTCAGA AGCAGCGCAAG TCATCTCAGA AGCAGCGCAAG TCGCCACCGT TCATCTCAGA AGCAGGTGTA AGGGGCAAG TGGAGTGTA AGGGGCAAG TGGAGTGTA AGGGGCAAG AGCAGCGGC AGCACGGGC AGCAGGGGCAAG AGCAGTGCAT AGGAGGTGTAA	EALRMANVAE MNATNHAIVO H 59 DNA sequited accession lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCTTCGCCC CATCAAGCAG GGTTGAGGCT CACGAGCGC TGCCACGCC TGCCACGCC AGCCTCGGCA AGCCTCGGCA TAGTGGCT CTTCACCTTG CGTAGTAGCG GAGCTCCACAC AGCTGCAGC CACCACACC TAGTGGCT CGTAGTAGCG GAGCTGCAG CACTCCGCAGA CACTCCGCAGA CACTCCGCAGA CACTCCGCAGA CACTCCGCAGC GGACTCCACGC GGGACTCCGCG GGACTCACGG CGACCACCT GCTGAGGAG CGACCTGAGGAG CGACCTGAGGAG CGACCTGCCCA GGACTCACGG TGATGGGAC CGGGTTCCCACGC GGACTCCCACGC GGACTCCCACGC GGACTCCCACGC GGACTCCCCACGCC GGACTCCCACCC GGACTTCCCACCC GGACTTCCACCC GGACTCCCACCC GGACTCCCACCC GGACTCCACCC GGACTCCACC GCACCC GGACTCCACC GCACCCACC GGACTCCACC GGAC	NSSDQRQAC TLVHPINPET #: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGGTCTGCC CCGGCCGGA AGGTCTGC CCGTTGCTGC CGGGCCGG GTTTGGCG GTTAGACA GCTGAGATCC GTCAGCAGACA TATTCCTGCT AGCATTGTG GCCACAGTGT ACCATGCT CACCTAGG GAGGAGCGGG GAGGAGCGGG CCCACAGACA CACCCAAAAC TTCGAGGTCT TTGGAGGTCT TTGGAGGTCT TTGGAGGTCT TTGGAGGTCT TTGGAGATAC CCCAAAAAC TTCGAGGTCT TTGGAGGTCT TTGGAGGTCT TTGGAGGTCT TTGGAGGAGAAAAC TTCGAGGAAAA	KKHELYVSPR VPKPCCAPTQ 31 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGCAGCAG TGAAATGGAT AGCCACAGAC AGGAGCGGA AGGAGCGGA AGGAGCGCAAGA GCGCCAAGA GCGCCAAGA TTGCCAAGGA TTGCCAAGGT TCCGGCTGC AGGATGAGC TTCCGGCTGC TCCGGCTGCC TCCTGAAAG TCAACGGT TCAGCAGTGT TCAGCAGTGC GCAGCTGGA CTACAGTTGT TCAAGAATGG CTACAGTTGT CGGCTCCC GCTGCC CTACAGTTGT CAGCAGTTGT CAGCAGTTGT CAGCAGTTGT CAGCAGTTGT CGGCTCCCTGC GCTCCCTGCC GCTCCCCTGCCCCTGCCCCCCCC	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC CCTGAGCTT GGATGATGT TGAGGCAGGT TCAGGCAGGT TCAGGCAGGT TCAGGCAGGT TCAGGCAGGT TCAGGCAGGT TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTCTCTGCT TGCTTTTGGC TGCTCTCTGCT TGCTCTCTGCT GGATGAGGT CCATCACT TCCCCCAAG CACCACAGG CACCCACCACC TTCAGCCACACCACCACCACCACCACCACCACCACCACCACC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CGGCCAGCA ACCCAGACAG CGGCGCAGCA CGGCGCAGCA CTTCGTTGCC CCCCTTTCTG CAGCTTGCA CCCCCTTTCTG CAGCTAGCA CTTCGTTGCC CCCCTTTCTG CAGCTAGC ACCCAGCTG CTGCCAGCCA TTTCAGCCCC ACCGCAGTC CTGACCCAGC TTTGAGCCAC CGTCTACCC CGCTACC AGGCTCACCC ACCGGCTACC AGGCTCACCC AGGCTCACCC ACCGGCTACC CGCCACCCA CCCGGCTACC CCCGGCTACC CCCGGCTACC CCCCGCCACCC ATCAACAGGG CCCCAGCCAC CCCCAGCCAC CCCCAGCCAC	60 120 180 240 360 420 540 600 720 780 900 960 1020 1140 1260 1320 1380 1440 1560 1560 1560 1680 1740
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505560657075	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequil AACTCCCGCC GCGCTCCGGT CCATCGTCTC CCCCCCGCGGTT CCATTGTCTT TTCGCTGTGA ACCCGCCA AAGCCCGCAG AAGCCCGCAG ACATTGATGG ATGGTCAGGA ACCGCAGAG CCCACGAGAGGT CCACGCAGA CCCACGAGAGGT AGCACCCCC GCCCCCACA TCCGGCACG TCATCTGGA AGCCACCAC TCATCTCGGA AGCCACCAC TCATCTCAGA AGCCAGGAGGT TCATCTCAGA AGCCAGGAGG TGAGTTTAA AGCCGCAAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC AGCCCACTAC TCATCTCAGA AGCCACTAC AGCCCACTAC TCATCTCAGA AGCCACTAC AGCCCACTAC AGCCCCCCC AGCCCAC AGCCCACTAC AGCCCCCCC AGCCCCCCC AGCCCCCCAC AGCCCACTAC AGCCCACTAC AGCCCACTAC AGCCCCCCC AGCCCAC AGCCACTAC AGCCAC	EALRMANVAE MNATNHAIVO H 59 DNA seq ild Accession lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTTGGCC CATCAGGAG GGTTGAGCG GGACTCTGGC TACTAGGCG GGACTCTGGC TACTAGGCG CACCACACA TAGTGGGCT GCTACTGGC GAGCCTCGGA CCTCCGCAGA CCTCCGCAGA CCTCGCAGA CCTGAGGAG CCTCAAGGG GACCCACGCT GCTGAGGAGA CCTGAAGAGC CGAGCTGCAG CGACCTGCC GGACTCACG GGACTCACGG TGAAGGAGC CGAGCTGCC CGAGCTGCC CGACTGCC CGACTGCC CGAGCTCCCAA CGGACTCACGG CGACTCACGG CGACTCACGG CGACTCACGG CGACTCACGC CGACTCACGC CGACTCACGC CCGCCATTTCACC CCGCCATTTT CCTCCATTTT CCTCCATTT CCTCCATTTT CCTCCATTTT CCTCCATTTT CCTCCATTTT CCTCCATTTT CCTCCATTT CCTCCATT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATT CCTC	NSSDQRQAC TLVHFINPET ##: NM_002: .3362 21 TCGGGGTCGG CCGCGCGA AGGGTCTGCCC CCGGCCCGGA AGGGTCTTCGAC GTTTCGACA GCTTGACAG GTTAGCAG GTTAGCCG GTCAGCAGCA TATTCCTGCT AGCATTGGTC AGCATTGGTC AGCATTGGTC AGCATGGT AGCATTGGTC AGCATGGT AGCATTGGTC CACCGAGGAC AGCACAAAA CTCAGGGGAG TTGGCGAAA GGCGGGAG TTGGCGAAAA CCCAAAAA CCCAAAAA CCCAAAAA CCCGGGAAA ACACCAAAA CCCGGGAAA CCCGGGGAAA CCCGGGAAA CCCCAAAAC CCGGGCAAAA CCCCAAAAC CCGGGAAA CCCCAAAAC CCGGGCAAAA CCCCAACA CCGGGAAA CCCCAAAAC CCCGGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACACAAAAC CCCCACACACAAAAC CCCCACACACAAAAC CCCCACACAAAAC CCCCACACACACACACACACACACACACACACACACACAC	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGGGGCA CGGGGAGCA TGGGACTGCC AGGATGCACT AGGATGCACT AGGACGAG GTGTGGCTC AGGATGCACT AGGCAGCAG AGGATGACAC AGGATGACAC AGGATGACAC AGGATGACAC AGGATGACAC AGGATGAGAC TTGCCAACGG GCATTGACAC AGATTGACAC CTACCAGTTGCCA AGATTGACAC CTACAGTTGCCAC GGATTGACAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCCAC CTACAGTTGCCCAC CTACAGTTGCCCCCCCCCC	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGGGGGC GCAGGGGGTC CCTGAGCTTT GGATGATGTC CCAGGTCACA AGATGGGACC CTGACCTCT TGCTTTTGGC CATCCTCTGCTG GGGCCAGGG CACCCATGCC TGCTAGGCAGG CACCCATGGC CACACCACCA CCACAGCC CACACCACCA CCCAGAGGCAAC CCCAGAGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGGCGCAAC CCCAGGGCAAC CCCAGGGCAAC CCCCAGGCGCAAC CCCAGGGCAAC CCCAGGGCAAC CCCCAGGGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCCAC CCCCACCAC CCCCAGCCAC CCCCACCAC CCCCACCAC CCCCACCAC CCCCACCA	PEGYAAYYCE DSSNVILKKY 51 1 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACA ACCCAGACAG CGGGCGCAGAC ACTGGAGAAG CCTTCGTTGCC CCCCTTTCTG CGGCAGCTGCA TTCTAGCCC AACCGCAGTTGCA TTCTCAGCCC AACCGCAGTTG GGCCACCCA TTTGAGCCAC TTTGAGCCAC TTTGAGCCAC TTTGAGCCAC GTCTTCCCAG GGCCACCCA TTTAAGCCAC TTTAAGCCAC TTTAAGCCAC GTCTACACCT GTGGCACTAC CCCGGGTACT AACCAGATGC ATCAACAGCG GGCCAGCAC CCCCGGCTACT ACCAGATGC TCCCAGCCAC CGGCCACCAC TGTACACAGCA CCCCAGCCAC TGGCCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCAC TGCACCACCAC TGCACCAC TGCACCACCAC TTCACACTTGCA	360 420 120 180 240 360 420 540 600 720 780 900 960 1020 1140 1260 1320 1380 1440 1560 1560 1560 1680 1740
505560657075	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Aci Coding sequil AACTCCCGCC GCGCTCCGGT CCATCGTCTC CCCCCCGCGGTT CCATTGTCTT TTCGCTGTGA ACCCGCCA AAGCCCGCAG AAGCCCGCAG ACATTGATGG ATGGTCAGGA ACCGCAGAG CCCACGAGAGGT CCACGCAGA CCCACGAGAGGT AGCACCCCC GCCCCCACA TCCGGCACG TCATCTGGA AGCCACCAC TCATCTCGGA AGCCACCAC TCATCTCAGA AGCCAGGAGGT TCATCTCAGA AGCCAGGAGG TGAGTTTAA AGCCGCAAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC TCATCTCAGA AGCCACTAC AGCCCACTAC TCATCTCAGA AGCCACTAC AGCCCACTAC TCATCTCAGA AGCCACTAC AGCCCACTAC AGCCCCCCC AGCCCAC AGCCCACTAC AGCCCCCCC AGCCCCCCC AGCCCCCCAC AGCCCACTAC AGCCCACTAC AGCCCACTAC AGCCCCCCC AGCCCAC AGCCACTAC AGCCAC	EALRMANVAE MNATNHAIVO H 59 DNA seq ild Accession lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTTGGCC CATCAGGAG GGTTGAGCG GGACTCTGGC TACTAGGCG GGACTCTGGC TACTAGGCG CACCACACA TAGTGGGCT GCTACTGGC GAGCCTCGGA CCTCCGCAGA CCTCCGCAGA CCTCGCAGA CCTGAGGAG CCTCAAGGG GACCCACGCT GCTGAGGAGA CCTGAAGAGC CGAGCTGCAG CGACCTGCC GGACTCACG GGACTCACGG TGAAGGAGC CGAGCTGCC CGAGCTGCC CGACTGCC CGACTGCC CGAGCTCCCAA CGGACTCACGG CGACTCACGG CGACTCACGG CGACTCACGG CGACTCACGC CGACTCACGC CGACTCACGC CCGCCATTTCACC CCGCCATTTT CCTCCATTTT CCTCCATTT CCTCCATTTT CCTCCATTTT CCTCCATTTT CCTCCATTTT CCTCCATTTT CCTCCATTT CCTCCATT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATTT CCTCCATT CCTC	NSSDQRQAC TLVHFINPET ##: NM_002: .3362 21 TCGGGGTCGG CCGCGCGA AGGGTCTGCCC CCGGCCCGGA AGGGTCTTCGAC GTTTCGACA GCTTGACAG GTTAGCAG GTTAGCCG GTCAGCAGCA TATTCCTGCT AGCATTGGTC AGCATTGGTC AGCATTGGTC AGCATGGT AGCATTGGTC AGCATGGT AGCATTGGTC CACCGAGGAC AGCACAAAA CTCAGGGGAG TTGGCGAAA GGCGGGAG TTGGCGAAAA CCCAAAAA CCCAAAAA CCCAAAAA CCCGGGAAA ACACCAAAA CCCGGGAAA CCCGGGGAAA CCCGGGAAA CCCCAAAAC CCGGGCAAAA CCCCAAAAC CCGGGAAA CCCCAAAAC CCGGGCAAAA CCCCAACA CCGGGAAA CCCCAAAAC CCCGGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCAAAAC CCCCACGGAAA CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACAAAAC CCCCACACAAAAC CCCCACACACAAAAC CCCCACACACAAAAC CCCCACACAAAAC CCCCACACACACACACACACACACACACACACACACACAC	KKHELYVSPR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGGGGCA CGGGGAGCA TGGGACTGCC AGGATGCACT AGGATGCACT AGGACGAG GTGTGGCTC AGGATGCACT AGGCAGCAG AGGATGACAC AGGATGACAC AGGATGACAC AGGATGACAC AGGATGACAC AGGATGAGAC TTGCCAACGG GCATTGACAC AGATTGACAC CTACCAGTTGCCA AGATTGACAC CTACAGTTGCCAC GGATTGACAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCAC CTACAGTTGCCCAC CTACAGTTGCCCAC CTACAGTTGCCCCCCCCCC	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGGGGGC GCAGGGGGTC CCTGAGCTTT GGATGATGTC CCAGGTCACA AGATGGGACC CTGACCTCT TGCTTTTGGC CATCCTCTGCTG GGGCCAGGG CACCCATGCC TGCTAGGCAGG CACCCATGGC CACACCACCA CCACAGCC CACACCACCA CCCAGAGGCAAC CCCAGAGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGAGGGGCAAC CCCAGGCGCAAC CCCAGGGCAAC CCCAGGGCAAC CCCCAGGCGCAAC CCCAGGGCAAC CCCAGGGCAAC CCCCAGGGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGCGCAAC CCCCAGGCGCAAC CCCCAGGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCGCAAC CCCCAGCCAC CCCCACCAC CCCCAGCCAC CCCCACCAC CCCCACCAC CCCCACCAC CCCCACCA	PEGYAAYYCE DSSNVILKKY 51 1 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACA ACCCAGACAG CGGGCGCAGAC ACTGGAGAAG CCTTCGTTGCC CCCCTTTCTG CGGCAGCTGCA TTCTAGCCC AACCGCAGTTGCA TTCTCAGCCC AACCGCAGTTG GGCCACCCA TTTGAGCCAC TTTGAGCCAC TTTGAGCCAC TTTGAGCCAC GTCTTCCCAG GGCCACCCA TTTAAGCCAC TTTAAGCCAC TTTAAGCCAC GTCTACACCT GTGGCACTAC CCCGGGTACT AACCAGATGC ATCAACAGCG GGCCAGCAC CCCCGGCTACT ACCAGATGC TCCCAGCCAC CGGCCACCAC TGTACACAGCA CCCCAGCCAC TGGCCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCACCAC TGCACCAC TGCACCACCAC TGCACCAC TGCACCACCAC TTCACACTTGCA	360 420 120 180 240 360 420 540 660 660 660 720 780 840 900 1020 1020 1140 1260 1380 1440 1560 1680 1740 1860 1860
505560657075	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequil AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCGGTT CCATTGTCTT TTCGCTGGA ACCCGCCGGT AGCCCGCAG AGCCCGCAG AGCCAGAA CCCAGGAGT AGCCACCCCC ACATTGATGA AGCCCACGA TCAGCAGAA CCCAGGAGT AGCCACGGAGT TCATCTGGA AGCCACGGAG TCATCCTGGA AGCCACGGT TCATCTGGA AGCCACGGAGAA ACGCCACCAC AGCCAGGAGT TCATCTCAGA AGCCACGGT TGGAGTTTAC AGCCACGGT TGGAGTTTAC AGCCACGGAGAAGC AGCAGTGCAA AGCCACGGT TCATCTCAGA TGGAGGTGTA AGGCCAAGCATGCAT AGCCCACTAT AGCCCACTAT AGCCCACTAT AGCCCACTAT AGCCCACTAT ACGCCCCCCA	EALRMANVAE MNATNHAIVO H 59 DNA sequida Accession lence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCTTCGCTC CATCAAGCAG GGTTGAGCG TGCACACGCC AGCCTCGGCA AGCCTCGGAG GCTCTGGC TACTAGCGC GGACTCTGGC TACTAGCCG AGCCTCGGAG AGCACACAC TAGTGGGCT GCTAACACG GAGCTGCAG AGCCTCGCAGA AGCACACTT AGCTGCAGC CGTGTGCGGG AGCCACACT TAGTGGGGGG CGACCACGCC GTGTGGCGGG CGACCACGCC GTGTGGGGGG CGACCTGGGCT GCTGAAGAAG CGTGTGCGAG CGCTCAGGCC GGACTCCGCC TAGTGGGAC CGGGTTCCAC GGACTCCGCC CGGACTCCACGCC CGCGCTCCCCCCCC CGCACTCCCCCCCCCC	NSSDQRQAC TLVHPINPET ##: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA ACGTCCTCC CCGGCCGGG ACTTCCACT TCCTTCAACA GCTGAGATCC GTCAGCAGA TATTCCTGCT AGCATTGCTG AGGTATAGG GGCACATGT ACCTACCG GTCAGCGGAGATC TCTTCAGGT TCCTCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATAGGG TGGCTCTTG GCCACAGTGT ATCTACCGGT CACCTAGCAG CCCACAGAG TTGGCGAATA GGTCAGGGGAG TTGGACGGAG TTGGACGGAG TTGGACGGAG ACACCAAAAC TTCGAGGTCT TGGTACCGT CGGGCAGATT GGCCCAGGAG ACGCCAGAGAC CCCAGGAG CCCCAGGAG TGGTCCGAGAG CCCCAGGAG CCCGGGGAGATC CGCCCGGGGGGGGGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGGGGAGCA TGGGAGCTGC TACATGTGTA AGGCAGCAG AGGATGCACT AGGATGCACT AGGACCACAGA AGGACCACAGA AGGACCACAGA AGGACCACAGA AGGACCACAGA ATGATTCAC AGGATGAC AGGATGAGAC TTGCCAACGG GCACTTGGC AGATTGAAGA TGACCTGCT TCCGGCTGCC TTCCTGAAAG GCACTTGGC GCACTTGGC GCACTTGGC GCACTTGGC TCAAGATGAC CTACAGTTT CGGGACCCCT CCGGCTCCC GGGACCACGT TCCAGGATGAC GCACTTGGC TCCAGGATGAC GCACTTGGC GGACCCCT CCGGCTCCCCC GGGACCACCT CCGGCTCCCCCC GGGACCACCT CCGGCTCCCCCC GGGACCACCT CCGGCTCCCCCC GGGACCACCT CCGGCTCCCCCC GGGACCACCT CCGCTCCCCCCC GGGACCACCT CCGCGCCCCCC GGGACCACCT CCCGAGATGAC CCCCCCCCCC	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGGATC GCAGGGGGTC CCTGAGCTT GGATGATGTC TGAGCAGGT TGAGCAGGT TGAGCAGGT TGAGCAGGT TGAGCAGGT TGCTTTTGGG TCCATCACT GGATGAGGT TCCCATCACT GTCTTCTGCT GGGGCAGGG CATCCCATCACT TCCCCCAAGG CACCCCAAGGC CACACCCATCACT CCCCCAAGGC CACACCCACCC TTCAGCCACAC CCCAGGCCACAC CCCAGGCCACC CCCAGGCCACAC CCCAGGCCACC CCCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCACC CCAGGCCACC CCAGGCCACC CCAGGCCACC CCAGGCCACC CCAGGCCACC CCAGGCCACC CCAGGCCCACC CCAGGCCACC CCAGGCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCCAGCCC CCAGGCCCACC CCACCC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGGCCCACC CCAGCCCC CCACCC CCACCCC CCACCC CCACCC CCACCCC CCACCC CCACCC CCACCC CCCCC CCACCC CCCCC CCCC CCCC CCCC CCACCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGCC ACCCAGACAG CGGGCCAGCC GCAGCTGCGC GCAGCTGCGC CTTCTGGTTGCC CCCCTTTCTG CAGCCAGCT CTGACCAGC ATCTACCCAG TTTCAGCCC ACCGCAGTT CTGACCAGG GGCCCACCCA TTTGAGCCAC GGTCTGCCAG GGCCTACCC ACCGGCTACT ACCAGATGC CCCGGCTACT ACCAGATGC CCCGGCTACT ACCAGATGC CCCCAGCCAC TTGAGCCAC GGTCTACCCAG GGCCACCCA TTGAGCCAC GGTCTACCCAG GGCCACCCA CTGCCACC ACCAGATGC CCCCAGCCAC CGCCAGCAC CCCCAGCCAC CCCCACCAC CCCCAGCCAC CCCCACCAC CCCCACCAC CCCCACCAC CCCCACCA	60 120 180 240 360 420 480 540 660 720 780 960 1080 1140 1290 1380 1440 1560 1560 1560 1680 1740 1860 1920
50 55 60 65 70 75 80	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac; Coding sequity AACTCCCGCC GCGCTCCGGT CCTCAGGTC CCCGCCGGTT TCGCTGTGA ACCCGCAGA ACCCGCAGA ACCCGCAGA ACCCGCAGA TGAAGCATCC ACATTGATGG GTCTGAGGA GTCAGGAG GTCAGGAG GTCAGGAG GTCAGGAG TCATCCTGGA AGCCCACAC TCAGCACAC TCAGCACGGC TCATCTCTGAGA GGCGCACACA TCAGCACGGC TCATCTCAGA AGCCCACACA TCAGCACGGC TCATCTCAGA AGCCACGCGC TGCCTCCTG TGGATTGCT TCATCTCAGA AGCGCACACA TTGACGCACTAT AGCCCACTAT AGCCCACTAT AGCCTACT TGCCTCCTG TTGCTTCCAT TTGCCTCCT TTGCCTCCCT TTGCCTCCCT TTGCCTCCCT TTGCCTCCCT TTGCCTCCCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTCCTCC	EALRMANVAE MNATNHAIVO H 59 DNA sequitence: 150. 11 TCGGGACGCC TTTTCCTGAG GCTCCGCT TTTTCCTAG GCTCTCGCA GCATCAGCAG GGATCAGCA GGACTCTGCC AGCACGCC TGCCAACGCC AGCCTCGGA GCACCACACA TAGTGGGCT CATCAGCAG GAGCTGGG CAACCACACAC TAGTGGGCT CAACCACACAC TAGTGGGCT GGACCACACAC TAGTGGGCT CAACCACACAC TAGTGGGCT CAACCACACAC TAGTGGGAG CATCCACGGAG CAACCACACAC TAGTGGGAG CAACCTGGC TGCTGGGAG CGACTTGCAA GCCCCGGCC TGATGGGAC CCAGGTTCCAA GGACTTCACCG TGATGGGAC CCAGGTTCCAC CGGACTCACGG TGATGGGAC CCGGCCCCCAC TAAGTGGGAC CCGGCCCCCAC CCGGCCCCCAC CCGCCCCCCAC CCAAGTTGGAC CCGGCCCCCCAC CCGCCCCCCCCCC	NSSDQRQAC TLVHPINPET ##: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCGGGA AGGGTCCTCCC CCGGGCCGGA AGGGTCTGCCG CTTTGGCC CTTTGGCC ACCTTCACA ACTTCAACA GCTAGATCC CCAACTACC GTCAGCAGGA TATTCCTGCT AGCATTGAGA CCCAACATGT ATTACAGG GAGGAGGGAGA CCCAAGACA ACACCAAAG CCCCAAGACA CCCCAAGACA ACACCAAGG CCCCAAGACA ACACCAAGG CCCCAAGACA ACACCAAGG CCCCAAGACA CCCCAAGACG CCCCAAGACA CCCCAAGACG CCCCAAGACA CCCCAAGACG CCCCAAGACC CCGGCGGTGG CCGGCCGGTGG CCCGGGCGGGGGGGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGCCACAGA TGAATGGAT AGCCACAGAC ATGGATGCAC ATGGATGCAC ATGGATGCAC ATGGATGCAC ATGCACAGAC TTGCCAACGG GCATTGACAG TGCCACAGG TCACAGTTGC TCCGGCTGCC TCCGGCTGCC TCCGACAGTGC TCCACAGTTGC GCAGATGAC TTCACAGTTGC GCAGATGAC CTGCAGATGAC CTGCAGATGAC TCCGGCTGCC TCCAGATGAC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGCCCTGC CTGCAGATGAC CGGGCCCTGC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CGGCCCTGCC CGCGCCTGCC CTGCCCTGCC CTGCAGATGAC CGCCCTGCCC CGCCCTGCCC CGCCCTGCCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCCC CCCCCCCC	ALIGNODWIIA LINAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGGGGT GCAGGGGGCC CCTGAGCTT TGAGCAGGT TTAGGCAGGT TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGCAG TCCATCACT TCCATCACT TCCATCACT GTCTTTGCAG CACTCACT TCCCCCAAG CACCCATGGC CACCCACGC CACCCACGC CACCCACCACCACCACCACCACCACCACCACCACCACC	PEGYAAYYCE DSSNVILKKY 51 TGGGGGGCCCC CGCCGTGCGC CGCGGCAGAC ACCCAGACAG CGGGCGCTGC GCAGCTGTGG GATGGGGCCC CTTCTGTTGCC CTTCTGTTGCC CTTCTGTTGCA CTTCTGAGCCC AACCGCAGTC ATTGAGCCC AACCGCAGTC CTTACCCAG GGCCACCCA TTTGAGCCCA CCCGGTTACC GGCCACCAG TTGAGCCCA CCCGGTACT AACCAGATG CCCGGCTACT AACCAGATG CCCCAGCAC GGCCAGCAC GGCCAGCAC GGCCAGCAC GGCCAGCAC CCCCAGCAC CTTACACTGCA GGCCAGCAC CTCCAGCACAC GGCCAGCAC CTCCAGCACAC GGCCAGCAC CTCCAGCCAC CTCCAGCCCC CTCCAGCCAC CTCCAGCCAC CTCCAGCCCC CTCCAGCCAC CTCCAGCCCC CTCCAGCCAC CTCCAGCCCC CTCCAGCCAC CTCCAGCCCC CTCCAGCCCC CTCCAGCCCC CTCCAGCCCAC CTCCAGCCC CTCCAGCCC CTCCAGCCC CTCCAGCCC CTCCAGCCC CTCCAGCCC CCCCAGCCAC CTCCAGCCC CTCCAGCCC CTCCAGCCC CTCCAGCCC CTCCAGCCC CTCCAGCCC CTCCAGCCAC CTCCAGCCC CTCCAGCCC CTCCAGCCAC CTCCAGCCC CTCCAGCC CTCCCACC CTCCAGCC CTCCAGCCC CTCCAGCC CTCCCCC CTCCACCC CTCCAGCC CTCCAGCC CTCCCC CTCCAGCC CTCCCC CTCC	360 420 120 180 240 360 480 540 660 720 780 840 960 1020 1140 1200 1140 1500 1560 1620 1680 1740 1860 1980
505560657075	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac; Coding sequity AACTCCCGCC GCGCTCCGGT CCTCAGGTC CCCGCCGGTT TCGCTGTGA ACCCGCAGA ACCCGCAGA ACCCGCAGA ACCCGCAGA TGAAGCATCC ACATTGATGG GTCTGAGGA GTCAGGAG GTCAGGAG GTCAGGAG GTCAGGAG TCATCCTGGA AGCCCACAC TCAGCACAC TCAGCACGGC TCATCTCTGAGA GGCGCACACA TCAGCACGGC TCATCTCAGA AGCCCACACA TCAGCACGGC TCATCTCAGA AGCCACGCGC TGCCTCCTG TGGATTGCT TCATCTCAGA AGCGCACACA TTGACGCACTAT AGCCCACTAT AGCCCACTAT AGCCTACT TGCCTCCTG TTGCTTCCAT TTGCCTCCT TTGCCTCCCT TTGCCTCCCT TTGCCTCCCT TTGCCTCCCT TTGCCTCCCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTTTCCCTCT TTTCCTCC	EALRMANVAE MNATNHAIVO H 59 DNA sequitence: 150. 11 TCGGGACGCC TTTTCCTGAG GCTCCGCT TTTTCCTAG GCTCTCGCA GCATCAGCAG GGATCAGCA GGACTCTGCC AGCACGCC TGCCAACGCC AGCCTCGGA GCACCACACA TAGTGGGCT CATCAGCAG GAGCTGGG CAACCACACAC TAGTGGGCT CAACCACACAC TAGTGGGCT GGACCACACAC TAGTGGGCT CAACCACACAC TAGTGGGCT CAACCACACAC TAGTGGGAG CATCCACGGAG CAACCACACAC TAGTGGGAG CAACCTGGC TGCTGGGAG CGACTTGCAA GCCCCGGCC TGATGGGAC CCAGGTTCCAA GGACTTCACCG TGATGGGAC CCAGGTTCCAC CGGACTCACGG TGATGGGAC CCGGCCCCCAC TAAGTGGGAC CCGGCCCCCAC CCGGCCCCCAC CCGCCCCCCAC CCAAGTTGGAC CCGGCCCCCCAC CCGCCCCCCCCCC	NSSDQRQAC TLVHPINPET ##: NM_002: .3362 21 TCGGGGTCGG CCTGTGCCG CCGCGGGA AGGGTCCTCCC CCGGGCCGGA AGGGTCTGCCG CTTTGGCC CTTTGGCC ACCTTCACA ACTTCAACA GCTAGATCC CCAACTACC GTCAGCAGGA TATTCCTGCT AGCATTGAGA CCCAACATGT ATTACAGG GAGGAGGGAGA CCCAAGACA ACACCAAAG CCCCAAGACA CCCCAAGACA ACACCAAGG CCCCAAGACA ACACCAAGG CCCCAAGACA ACACCAAGG CCCCAAGACA CCCCAAGACG CCCCAAGACA CCCCAAGACG CCCCAAGACA CCCCAAGACG CCCCAAGACC CCGGCGGTGG CCGGCCGGTGG CCCGGGCGGGGGGGG	KKHELYVSPR VPKPCCAPTQ 321 31 GCTCCGGCTG CCGCGAGCA TGGGAGCTGC TGCTGCCGCT TACATGTGTA AGGCCACAGA TGAATGGAT AGCCACAGAC ATGGATGCAC ATGGATGCAC ATGGATGCAC ATGGATGCAC ATGCACAGAC TTGCCAACGG GCATTGACAG TGCCACAGG TCACAGTTGC TCCGGCTGCC TCCGGCTGCC TCCGACAGTGC TCCACAGTTGC GCAGATGAC TTCACAGTTGC GCAGATGAC CTGCAGATGAC CTGCAGATGAC TCCGGCTGCC TCCAGATGAC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGGCCCTGC CTGCAGATGAC CGGGCCCTGC CTGCAGATGAC CGGGCCCTGC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CTGCAGATGAC CGGCCCTGCC CGGCCCTGCC CGCGCCTGCC CTGCCCTGCC CTGCAGATGAC CGCCCTGCCC CGCCCTGCCC CGCCCTGCCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCTCC CGCCCCCC CCCCCCCC	ALIGNODWIIA LINAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGGGGT GCAGGGGGCC CCTGAGCTT TGAGCAGGT TTAGGCAGGT TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGCAG TCCATCACT TCCATCACT TCCATCACT GTCTTTGCAG CACTCACT TCCCCCAAG CACCCATGGC CACCCACGC CACCCACGC CACCCACCACCACCACCACCACCACCACCACCACCACC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCCGTGCGC CCGGCCAGCC ACCCAGACAG CGGGCCAGCC GCAGCTGCGC GCAGCTGCGC CTTCTGGTTGCC CCCCTTTCTG CAGCCAGCT CTGACCAGC ATCTACCCAG TTTCAGCCC ACCGCAGTT CTGACCAGG GGCCCACCCA TTTGAGCCAC GGTCTGCCAG GGCCTACCC ACCGGCTACT ACCAGATGC CCCGGCTACT ACCAGATGC CCCGGCTACT ACCAGATGC CCCCAGCCAC TTGAGCCAC GGTCTACCCAG GGCCACCCA TTGAGCCAC GGTCTACCCAG GGCCACCCA CTGCCACC ACCAGATGC CCCCAGCCAC CGCCAGCAC CCCCAGCCAC CCCCACCAC CCCCAGCCAC CCCCACCAC CCCCACCAC CCCCACCAC CCCCACCA	360 420 120 180 240 360 480 540 660 720 780 840 960 1020 1140 1200 1140 1500 1560 1620 1680 1740 1860 1980

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				GAAGCTCCCA			1980
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				GKGRYGEVWM			240
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50				RDLKSKNILV HFQSYIMADM			360 420
	EEYQLPYHDL	VPSDPSYEDM	REIVCIKKLR	PSFPNRWSSD			480
	RLTALRVKKT	LAKMSESQDI	KL				
66	Seq ID NO:	65 DNA sequ	ence				
55		d Accession lence: 28	#: NM_006	475.1			
	1	11	21	31	41	51	
	l	1	1	1		1	
60				ATTCCCTTTT			60 120
00				AATGTCTGTG			180
				AACTGGTATA			240
				GGTTATATGA TATGGCACTC			300 360
65	ACAACGCAGC	GCTATTCTGA	CGCCTCAAAA	CTGAGGGAGG	AGATCGAGGG	AAAGGGATCC	420
				TGGGACAACT			480
				CTGAATGCTT GGCATGATTA			540 600
70	TTGGGGCTTT	TCATTAACCA	TTATCCTAAT	GGGGTTGTCA	CIGITAATIG	TGCTCGAATC	660
70				GTTGTCCATG GAAGCAGAAG		TGTGCTTACA	720
				GCCCTTGGAA			780 840
	TTTGCTCCCA	CCAATGAGGC	TTTTGAGAAA	CTTCCACGAG	GTGTCCTAGA	AAGGTTCATG	900
75				AAGTACCACA		TCTCCAGTGT AATTGAGATA	960 1020
				GGAATCAAAA			1080
						TTCTGCCAAA	1140
				ACCACCTTCA GAATACACTT		TGTGAATAAT	1200 1260
80	GCATTTTCTG	ATGATACTCT	CAGCATGGTT	CAGCGCCTCC	TAAATTAAT	TCTGCAGAAT	1320
				GAGCTTTACA			1380
						TGAAAATTCA COGOGAGATC	1440 1500
95	ATCAAGCCAG	CAGAGAAATC	CCTCCATGAA	AAGTTAAAAC	AAGATAAGCG	CTTTAGCACC	1560
85	TTCCTCAGCC	TACTTGAAGC	TGCAGACTTG	AAAGAGCTCC	TGACACAACC	TGGAGACTGG	1620

			TGATGCTTTT				1680
	CTGATACGGG	ACAAAAATGC	TCTTCAAAAC	ATCATTCTTT	ATCACCTGAC	ACCAGGAGTT	1740
			ACCTGGTGTT				1800
			AAATGATACA				1860
5			TGGTGTAATT				1920
9							
			TCAACTGCTG				1980
	CAAATTAAGT	TTGTTCGTGG	TAGCACCTTC	AAAGAAATCC	CCGTGACTGT	CTATACAACT	2040
	AAAATTATAA	CCAAAGTTGT	GGAACCAAAA	ATTAAAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100
	ATTATCAAAA	CTGAAGGACC	CACACTAACA	AAAGTCAAAA	TTGAAGGTGA	ACCTGAATTC	2160
10			AACAATAACT				2220
10							
			TGGAGTGCCT				2280
			TGAAATAAAA				2340
	ACAGAAGAAA	CTCTGAAGAA	ATTGTTACAA	GAAGAGGTCA	CCAAGGTCAC	CAAATTCATT	2400
			ATTTGAAGAT				2460
15			AGCCAACAAA				2520
13							
			ATCCAAAAAC				2580
			TTGTGAGAGC				2640
	ACAAAGAAGC	AATCATCAAA	TAATTCTGAA	CACAAATTTA	ATATTTTTTT	TTCTGAATGA	2700
			GAGTTAGCCT				2760
20			CTTGACATTA				2820
20							
			ATTCATTACA				2880
			TGTATGTATG				2940
	TATCTCTCCA	TGGGAAGCTA	AGTTATAAAA	ATAGGTGCTT	GGTGTACAAA	ACTITITATA	3000
			CTATATGAGT				3060
25							3120
23			GAATGTTTGT				
			CCATTTTTCA			AAATTGAGTA	3180
	ATTCAGAAAA	ACTCAAGATT	TAAGTTAAAA	AGTGGTTTGG	ACTTGGGAA		
						•	مد
	Sea ID NO.	66 protein	Samience				
30					•		
5 0	Protein Acc	ession #: N					
	1	11	21	31	41	51	
	.1	1	1		!	1	
	•	T.T.T.TUMBTM	ANNHYDKILA	HEDTREPHAG	PNUCATOOTT.	CTKKKVESTC	60
							120
25			PGYMRMEGMK				
35			AWDNLDSDIR				180
	NGMIIPSMYN	NLGLFINHYP	NGVVTVNCAR	IIHGNQIATN	GVVHVIDRVL	TQIGTSIQDF	240
	TEAEDDLSSP	RAAATTSDIL.	EALGRDGHFT	LPAPTNEAFE	KLPRGVLERF	MGDKVASEAL	300
			FETLEGNTIE				360
40			QTTFTDLVAQ				420
40	VQRLLKLILQ	NHILKVKVGL	NELYNGQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKGSKQG	480
	RNGAIHIFRE	IIKPAEKSLH	EKLKQDKRFS	TFLSLLEAAD	LKELLTOPGD	WTLPVPTNDA	540
			NIILYHLTPG				600
	my v thirt was						660
		ESDIMTTNGV	IHVVDKLLYP	ADTPVGNDQL	PRIFNKFIKA	IQIKFVRGST	660
15	FKEIPVTVYT	ESDIMTTNGV TKIITKVVEP	IHVVDKLLYP KIKVIEGSLQ	ADTPVGNDQL PIIKTEGPTL	LEILNKLIKY TKVKIEGEPE	IQIKFVRGST FRLIKEGETI	720
45	FKEIPVTVYT	ESDIMTTNGV TKIITKVVEP	IHVVDKLLYP	ADTPVGNDQL PIIKTEGPTL	LEILNKLIKY TKVKIEGEPE	IQIKFVRGST FRLIKEGETI	
45	FKEIPVTVYT TEVIKGEPII	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR	ADTPVGNDQL PIIKTEGPTL EERIITGPEI	LEILNKLIKY TKVKIEGEPE KYTRISTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL	720
45	FKEIPVTVYT TEVIKGEPII	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV	IHVVDKLLYP KIKVIEGSLQ	ADTPVGNDQL PIIKTEGPTL EERIITGPEI	LEILNKLIKY TKVKIEGEPE KYTRISTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL	720
45	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG	ADTPVGNDQL PIIKTEGPTL EERIITGPEI	LEILNKLIKY TKVKIEGEPE KYTRISTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL	720
45	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO:	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN	LEILNKLIKY TKVKIEGEPE KYTRISTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL	720
	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO:	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN	LEILNKLIKY TKVKIEGEPE KYTRISTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL	720
45 50	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA seq	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS se	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN	LEILNKLIKY TKVKIEGEPE KYTRISTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL	720
	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac Coding seq	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession uence: 1-92°	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS se	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ	720
	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS se	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN	LEILNKLIKY TKVKIEGEPE KYTRISTGGG	IQIKFVRGST FRLIKEGETI ETEETLKKLL	720
	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac Coding seq 1	ESDIMTTNGV TRIITKVVEP KRYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession tence: 1-92*	IHVVDKLLYP KIKVIEGSLQ PVEITEKBTR DEEIKRLLQG uence n #: EOS se 7 21	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence	LBILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51	720 780
	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac Coding seq 1 ATGCCTGGGG	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS se 7 21 GGGCCCCGCC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG	LBILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG	IQIKPVRGST FRLIKEGETI ETESTLKKLL REGRSQ 51] GCTGGCGCGA	720 780
50	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCTGGGG CTAGCGCTGG	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG	IHVVDKLLYP KIKVIEGSLQ PVEITEKBTR DEEIKRLLQG uence n #: EOS se 7 21 GGGCCCGCC CTGGGTCTCC	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC	LBILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC	720 780
	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCTGGGG CTAGCGCTGG	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG	IHVVDKLLYP KIKVIEGSLQ PVEITEKBTR DEEIKRLLQG uence n #: EOS se 7 21 GGGCCCGCC CTGGGTCTCC	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC	LBILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC	720 780
50	FKEIPVTVYT TEVINGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCTGGG CTAGGGCTGG TTCTCCTCT	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession tence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCCGTT	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS se 7 21 GGGCCCCGCC CTGGGTCTCC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG	LBILNKLIKY TKVKKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGGG CCACCTCCTC CCCAGCCCCC	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCCGGAC	720 780 60 120 180
50	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequin I ATGCCTGGGG CTAGCGCTGG TTCTCCTCCT CAGTGCCCCG	ESDIMTTNGV TKIITKVUEF KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA	IHVVDKLLYP KIKVIEGSLØ PVEITEKBTR DEEIKRLLQG Ueence n #: EOS se 7 21 GGGCCCCGCC CTGGGTTCTCC CTGGTTCTCC GTGCTCCGAG	ADTPVGNDQL PIIKTEGPTI ERRIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA	LBILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCCAGCCCCC CAGTCAAGTG	IQIKPVRGST FRLIKEGETI FREITLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CGTTAACCGC	720 780 60 120 180 240
50	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac Coding sequ I ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AATCTGACCGG	ESDIMTTNGV TKIITKVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTTTCGGA AGGTGCCCAC	IHVVDKLLYP KIKVIEGSLQ PVEITEKBTR DEEIKRLLQG Uence n #: EOS se 7 21 GGGCCCCGCC CTGGCTTCCC GTGCTCCCAGGGGGGGGGG	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGA GCCTACGTGC	LBILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCCC CAGTCAAGTG GCAACCTCTT	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51] GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CGTTAACCGC	720 780 60 120 180 240 300
50	FKEIPVTVYT TEVINGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGG CTAGGGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG	ESDIMTTNGV TKIITKVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession uence: 1-92' 11 GGTGCTCCGG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG in #: EOS se 7 21 GGGCCCCGCC CCTGGCTTCC CCTGGCTTCC GTGCTCCGG GGACCTGCCC CCTCCTTTAC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG	LBILNKLIKY TKVKLIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTC ATGTGCTGGG	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTTACCGGC CCAACTGCCC	720 780 60 120 180 240 300 360
50 55	FKEIPVTVYT TEVINGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGG CTAGGGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG	ESDIMTTNGV TKIITKVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession uence: 1-92' 11 GGTGCTCCGG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA	IHVVDKLLYP KIKVIEGSLQ PVEITEKBTR DEEIKRLLQG Uence n #: EOS se 7 21 GGGCCCCGCC CTGGCTTCCC GTGCTCCCAGGGGGGGGGG	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG	LBILNKLIKY TKVKLIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTC ATGTGCTGGG	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTTACCGGC CCAACTGCCC	720 780 60 120 180 240 300 360 420
50	FKEIPVTVYT TEVIRGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGGCGGTT CGCTGTGCGA AGGTGCCCAC ACCTGGACTT	INVUNKLLYP RIKVIEGSLQ PVEITEKBTR DEEIKRLLQG uence n #: EOS ser 7 21 GGGCCCGGCC CTGGGTTCTCC CTGGGTTCTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAATA	ADTPVGNDQL PIIKTEGPTIL EERIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTTTCTCT GCCGTGTCCG GCCTGCCG GCCTACTGCG GCCTACTGCG TCGCTGGGG TCGCTGGGG TCGCTGGGGG TCGCTGGGGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA	IQIKPVRGST FRLIKEGETI FREIRKLL REGRSQ 51 GCTGGCGCGA GCATCCTC GCTGCCGGAC CCTTACCGC CCTACCGCC CCACTGCCC CGTGTCCTTC	720 780 60 120 180 240 300 360
50 55	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGGGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA	ESDIMTTNGV TKIITKVEE KKYTKIIDGV REGDGHLFE 67 DNA sequid Accession Lence: 1-92* 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC ACCAGCAACCA ACCTGGACTT CACATCTAGA	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG H#: EOS se 7 21 GGGCCCCGCC CTGGSTCTCC CTGGCTTCC CTGGTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCCC GCAGCGCGCG GCCTACGTGC CTGCCGCGGG TCGCCGCGGG TCGCTGGGACACA	LBILNKLIXY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCTGACCTAA	IQIKPVRGST FRLIKEGETI FREITLKKLL REGRSQ 51] GCTGGCGCGA GGCATCCTCC GCTGCCGGA CGTTAACCGC CCAACTGCCC CGTGCCTTCAC	720 780 60 120 180 240 300 360 420
50 55	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGG TTCTCCTCT CAGTGCCCCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC	ESDIMTTNGV TKIITKVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTTCTGGA AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT TCACATCTAGA TGGCTGAGTT	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG Lence n #: EOS se 7 21 GGGCCCCGCC CTGGCTTCC CTGGCTTCC GTGCTCCGG GGACCTGCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGCTCTA	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGGCGCA GCTTACGTGC CTGCCGCGGG TCGCTGGTGA CTGCAGGACA CCCCACATTA	LBILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCTCAA GGGTTTTCCT	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTC GCTGCCGGAC CCTTACCGGC CCTACCGC CCACTGCC CGTGTCCTTC GGTCCTTCAC GGACAACAAT	720 780 60 120 180 240 300 360 420 540
50 55	FKEIPVTVYT TEVIRGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGG TTCTCCTCT CAGTGCCCG AATCTGACCG AACTGACCG AACCAGCTGG ACCACCTGA AATGGCACCC CCCTGGGTCT	ESDIMTTNGV TKIITKVVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGCGCCGTT CGCTGTGCGA ACGTGCCCAC ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCCCA TGGCTGAGTT GCGACTGCCCA TGGCTGACTT GCGACTGCCCA	IHVVDKLLYP KIKVIEGSLQ PVEITEKETR DEEIKRLLQG uence n #: EOS se 7 21 GGGCCCGCC CTGGTTCC CTGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC	ADTPVGNDQL PIIKTEGPTL EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT	LBILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAACTT ATGCCGCAA ATGCCCTCAA AGGGTTTTCCT GGCTCAAGGA	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGGAC GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTAACCGC CCTACCGC CCACTGCCC GGTCCTTC GGTCCTTCC GGTCCTTCC GGACAACAAT AACAGAGGTA	720 780 60 120 180 240 360 420 480 540 600
50 55	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I I ATGCCTGGGG CTAGGCTGG TTCTCCTC CAGTGCCCG AATCTGACCG AACCAGCTGG ACCAGCTGG ACCAGCTGG ACCAGCTGG ACCTGGGCCCC CCCTGGGGCCCC CCTGGGGCA	ESDIMTTNGV TKIITKVEE KKYTKIIDGV KKYTKIIDGV 1EGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCCA AAGACCGGCT	IHVVDKLLYP KIKVIEGSLQ FVEITEKBTR DEEIKRLLQG Hence h #: EOS se 7 21 GGGCCCCGCC CTGGGTTCC GTGCTTCC GTGCTTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN QUENCE 31 GCCGGGGACG TCGTTTCTC GCCGCGGCA GCCTACGTGC GCAGCGCGCA GCTACGTGC CTGCCGCGGCA CCCCACGTTA ATGGTGACCT TATCCGGAAA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAGGA AAATGAGGA	IQIKPVRGST FRLIKEGETI FREITLKKLL REGRSQ 51 GCTGGCGGACGCGACGCCGCGCGACCGCCCGACCGCCCGACCGCCCCGACCGCCCCGTTAACCGCCCAACTGCCCCGTGTCCTTCCGGTCCTTCACGGACAACAATACAACAACAACTACCCCTTCCCGTCCTTCACGGACAACAATACAACAAGAGGTACAGAGGTACCGGTCCTCC	60 120 180 240 300 420 480 540 660
50 55 60	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AACCTGACCCG AACCTGACCCGCACCTGGACCCCCCCCTGGGTCTC TGGCAGGGCTGGTCTGTGCAGGGCCCCCTGGGACCTCA	ESDIMTTNGV TKIITKVEE KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG TACTCCTGGG AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT TGACATCTAGA AGGACTGCCA AAGACCGGCT AAGACCGGCT AAGACCGGCT ACAGTGCTGA	IHVVDKLLYP KIKVIEGSLQ FVEITEKBTR DEEIKRLLQG Hence Hence GGGCCCCGCC CTGGTTCCC CTGGTTCCC CTGGTTCCCAAGTATAAT AAGCCTCCAC GCAAGGTCTAC CATGGCAGAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CCTGGACTGT	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTCTC GCCGTGTCCC GCCGTGTCCC GCCGTGGCG GCAGCGCGACGCA GCCTACGTGC CTGCCGCGGG TCGCTGGGGA CCCCACATTA ATGGTGACCA TATCCGGACA TATCCGGATTC	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAGTG GCAACCTCTT ATTGCTGGG GCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAAGGA TTCCCCCATC	IQIKPVRGST FRLIKEGETI FRLIKEGETI REGRSQ 51 GCTGGCGGGA GGCATCCTCC GCTGCCGGAC CCTTACCGC CCTTACCGC CCTACCGC CCTTACCGC CCTACCGC CCTTACCGC CCTACCGC CCTACCACC CCTGCAACC CCTGCAACC CCTGCAACC	720 780 60 120 180 240 300 360 420 540 600 720
50 55	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AACCTGACCCG AACCTGACCCGCACCTGGACCCCCCCCTGGGTCTC TGGCAGGGCTGGTCTGTGCAGGGCCCCCTGGGACCTCA	ESDIMTTNGV TKIITKVEE KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG TACTCCTGGG AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT TGACATCTAGA AGGACTGCCA AAGACCGGCT AAGACCGGCT AAGACCGGCT ACAGTGCTGA	IHVVDKLLYP KIKVIEGSLQ FVEITEKBTR DEEIKRLLQG Hence Hence GGGCCCCGCC CTGGTTCCC CTGGTTCCC CTGGTTCCCAAGTATAAT AAGCCTCCAC GCAAGGTCTAC CATGGCAGAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CACCTGTCAC CCTGGACTGT	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTCTC GCCGTGTCCC GCCGTGTCCC GCCGTGGCG GCAGCGCGACGCA GCCTACGTGC CTGCCGCGGG TCGCTGGGGA CCCCACATTA ATGGTGACCA TATCCGGACA TATCCGGATTC	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAGTG GCAACCTCTT ATTGCTGGG GCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAAGGA TTCCCCCATC	IQIKPVRGST FRLIKEGETI FRLIKEGETI REGRSQ 51 GCTGGCGGGA GGCATCCTCC GCTGCCGGAC CCTTACCGC CCTTACCGC CCTACCGC CCTTACCGC CCTACCGC CCTTACCGC CCTACCGC CCTACCACC CCTGCAACC CCTGCAACC CCTGCAACC	60 120 180 240 300 420 480 540 660
50 55 60	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGG TTCTCCTCCT CAGTGCCCGG AACCAGCTGG ACCTGAGGC CGCAACCTGA AATGGCACCC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA TTGGAACTCA TCTTATGTCT	ESDIMTTNGV TKIITKVEE KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG TACTCCTGGG CGGCGCGTTTCGCA AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCCAA AGGTGCCCAA TGGCTGAGTT ACAGTGCTGA TCCTGGGTAT TCCTGGGTAT	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG Lence n #: EOS se 7 21 GGGCCCCGCC CTGGCTTCC CTGGCTTCC CTGGTTCCAA GGACCTGCCA AAGTAATAAT AAGCCTCCAA CCAAGGCTCTA CATGGCAGAC CACCTGTGCA CACCTGTGCA CACCTGTGCA TGTTTTAGCC	ADTPVGNDQL PILKTEGPTL EERIITGPEI DTPVRKLQAN 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCCTGCGGGG TCGCTGGGGC TCGCTGGGGACA CCCCACATTA ATGGTGACCT TATCCGGAATA ATGGTGACCT TATCCGGATGC CTGATGACCT TATCCGGATGC CTGATGACCT TATCCGGATG	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAAGGA AAATGAAGGA AAATGAAGGA CTATTTTCCT CTATTTTCCT	IQIKPVRGST FRLIKEGETI ETEETLKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CGTGTCCTTCAC GGACAACAAT AACAGAGGTA ACGAGGTACTCCC CCTGGTTCTTC	720 780 120 180 240 420 420 480 600 600 720 780
50 55 60	FKEIPVTVYT TEVIRGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGG TTCTCCTCT CAGTGCCCGG AATCTGACCG AACTGACCG AACTGACCG AATGGCACCTGA AATGGCACCTGG TTGGAACCTGG TTGGAACTCA TTGGAACTCA TTGGAACTCA TTGGAACTCA TTGTATGTCT TATTTGAACCC	ESDIMTTNGV TKIITKVUEP KKYTKIIDGV KKYTKIIDGV 1EGGDGHLFE 67 DNA sequid Accession Lence: 1-92* 11 GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT TGCGACTGCCA AGGACCGCT ACAGTGCCA ACGTGCCA ACGTGCTA ACCTGGGTAT GCCAAGTGCTGA TCCTGGGTAT GCCAAGTGCTGA TCCTGGGTAT GCCAAGGGGAT	INVUDKLLYP KIKVIEGSLO PVEITEKBTR DEEIKRLLQG IN #: EOS se 7 21 GGGCCCCGCC CTGGCTTCC GTGCTTCCCTTTAC AAGTAATAAT AAGCCTCAC GCAAGGTCTAC CACCTGTGCA CACCTGTGCA CTTCGTTAC CACCTGTAC CACCTGTAC CACCTGTAC CACCTGTAC CACCTGTAC CAAAAAAGTGG	ADTPVGNDQL PIIKTEGPTIL ERRIITGEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTCTC GCCGTGGC GCCTACGTGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACC TATCCGGAAA GACCGATTC TATCCGGAAA GACCGATTACA ATGGTAACGA ATGGTAACA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTACGT GGCTCAAGGA AAATGAGGAA TTCCCCCATC TCAGGAGTGC TCAGGAGTGC	IQIKPVRGST FRLIKEGETI FREIRKILL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCAGGCC CCAACTGCC CCTGTCCTTC GGTCCTTCAC GGACAACAT ACCAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT	720 780 60 120 180 240 300 420 480 540 660 720 780 840
50 55 60	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGOGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCTGGGTCT GTGCAGGC CCCTGGGTCT TTTTATTCT TATTTGAACC CACATGGAAG CCACATGGAAG	ESDIMTTNGV TKIITKVEE KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCAC CCAGCACCA ACCTGGACTT CACATCTAGA TGCGTGAGTT GCGACTGCCA AAGACCGGCT ACAGTGCTGA TCCTGGGTTA TCACATCTATA	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG IHENCE I	ADTPVGNDQL PIIKTEGPTIL ERRIITGEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTCTC GCCGTGGC GCCTACGTGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACC TATCCGGAAA GACCGATTC TATCCGGAAA GACCGATTACA ATGGTAACGA ATGGTAACA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTACGT GGCTCAAGGA AAATGAGGAA TTCCCCCATC TCAGGAGTGC TCAGGAGTGC	IQIKPVRGST FRLIKEGETI FREIRKILL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCAGGCC CCAACTGCC CCTGTCCTTC GGTCCTTCAC GGACAACAT ACCAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT	720 780 120 180 240 420 420 480 600 600 720 780
50 55 60	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGOGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCTGGGTCT GTGCAGGC CCCTGGGTCT TTTTATTCT TATTTGAACC CACATGGAAG CCACATGGAAG	ESDIMTTNGV TKIITKVUEP KKYTKIIDGV KKYTKIIDGV 1EGGDGHLFE 67 DNA sequid Accession Lence: 1-92* 11 GGTGCTCCCG TACTCCTGGG AGGTGCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT TGCGACTGCCA AGGACCGCT ACAGTGCCA ACGTGCCA ACGTGCTA ACCTGGGTAT GCCAAGTGCTGA TCCTGGGTAT GCCAAGTGCTGA TCCTGGGTAT GCCAAGGGGAT	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG IHENCE I	ADTPVGNDQL PIIKTEGPTIL ERRIITGEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTCTC GCCGTGGC GCCTACGTGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACC TATCCGGAAA GACCGATTC TATCCGGAAA GACCGATTACA ATGGTAACGA ATGGTAACA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTACGT GGCTCAAGGA AAATGAGGAA TTCCCCCATC TCAGGAGTGC TCAGGAGTGC	IQIKPVRGST FRLIKEGETI FREIRKILL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCAGGCC CCAACTGCC CCTGTCCTTC GGTCCTTCAC GGACAACAT ACCAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT	720 780 60 120 180 240 300 420 480 540 660 720 780 840
50556065	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGOGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCTGGGTCT GTGCAGGC CCCTGGGTCT TTTTATTCT TATTTGAACC CACATGGAAG CCACATGGAAG	ESDIMTTNGV TKIITKVEE KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCAC CCAGCACCA ACCTGGACTT CACATCTAGA TGCGTGAGTT GCGACTGCCA AAGACCGGCT ACAGTGCTGA TCCTGGGTTA TCACTGCTTA TCCTGGGTTA TCACTGCTTA TCACTGCTTA TCCTGGGTTA TCACTGGTTA TCACTGCTTA	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG IHENCE I	ADTPVGNDQL PIIKTEGPTIL ERRIITGEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTCTC GCCGTGGC GCCTACGTGC CTGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACC TATCCGGAAA GACCGATTC TATCCGGAAA GACCGATTACA ATGGTAACGA ATGGTAACA	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTACGT GGCTCAAGGA AAATGAGGAA TTCCCCCATC TCAGGAGTGC TCAGGAGTGC	IQIKPVRGST FRLIKEGETI FREIRKILL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCAGGCC CCAACTGCC CCTGTCCTTC GGTCCTTCAC GGACAACAT ACCAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT	720 780 60 120 180 240 300 420 480 540 660 720 780 840
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50556065	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT TCAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCGGACCTGA AATGGCACCC CCCTGGGTCT TGTGCAGGGCA TTGGAACTCA TCTTATGTCT TATTTGAACC CACATGGAAC AGTTCTAACT Seq ID NO: Protein AC	ESDIMTTNGV TKIITKVEE KKYTKIIDGV RKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCCGCTT CGCTGTGCGA AGGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGCGTGAGTT GCGACTGCCA ACAGCGGT TCCTGGGTA TCCTGGTA TCCTGGTA TCCTGGTA TCCTGGTA TCCTGGTA TCCTGGTA TCCTGGTA TCCTGGTA	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG IH: EOS SE 21 GGGCCCCGCC CTGGSTTCC CTGGTTCCC CTGGTTCCGAG GGACCTGCCC CTTCCTTTAC CAAGTAATAAT AAGCCTCAC CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACAGTCTA CACCTGTGCA CACAGTTTTAGCC CACCTGTGCA CACAGTGTA AAAAAGTGG CAGATATGAA CGAGTGA SEQUENCE EOS SEQUENCE	ADTPVGNDQL PIIKTEGPTI ERRIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCAGCGCGCGC GCCTACGTGC TCGCCGCGGG TCGCTGGGG TCGCTGGGGAC TCGCGCGGGAC TCGCGCGGGAC TCGCGCGGGAC TCGCGCGGGAC TCGCGCGGAC TCGCGGGGAC ATGCGGATAC ATGGTGACC ATGCATAACA ATCATAACGG ATCATAACA ATCATAACGG	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGG GCTCAACGA ATGCCTCAA GGGTTTTCCT GGCTCAAGGA TTCCCCCATC CTATTTTCCT TCAGAGATG ACCCCAGATT	IQIKPVRGST FRLIKEGETI FRLIKEGLI REGRSQ SI SI GCTGGCGCGA GGCATCCTCC GCTTACCGC CCTTACCGC CCTTACCGC CCTTACCGC CCTTACCGC CCTTACCGC CCTTCTCAC GGCAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCAAACC CCTGCAGGGA AACAAACCTC	720 780 60 120 180 240 300 420 480 540 660 720 780 840
50556065	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac Coding seq I ATGCCTGGGG CTAGGGCTGG TCTCCTCCT CAGTGCCCGG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACGCC CTGGGTCT GTGCAGGGC TTGGAGGGCT ATTTGAACC CACATGGAA TGTTATGTCT TATTTGAACC CACATGGAAC AGTTCTAACT Seq ID NO: Protein Ac 1	ESDIMTTNGV TKIITKVUE KKYTKIIDGV KKYTKIIDGV 1EGGDGHLFE 67 DNA sequid Accession Lence: 1-92* 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCA ACGTGCCAC ACATCTAGA TGCGTGACTT GCGACTGCCA AGACCGGCT ACAGTGCTGA TCCTGGGTAT GCAAGTGCTGA TCCTGGGTAT GCAAGTGCTGA TCCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT GCAAGGGGAT GCGATGTCCT 68 Protein	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG H: EOS se T 21 GGGCCCCGCC CTGGGTCTCC CTGGGTCTCC CTGGCTCCAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA CCACGTGCA CCACGTCA CC	ADTPVGNDQL PIIKTEGPTI ERRIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTTCTTC GCCGTGTCCG GCAGTGCGGC GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATAC ATGCTGATACCA ATCATACCG ATGCATACCA ATCATACCG ATCAATGCGG	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCCCCC CCAGCCCCC CAGCCCCCT ATTTGCTGG GCTAAGTA ATGCCTCAA GGCTTACCT GGCTCAAGGA AATGAGGAA TTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGCT ACCCCAGCT ACCCCAGCT ACCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT	IQIKPVRGST FRLIKEGETI FRLIKEGETI FREGREQ 51 GCTGGCGGCGGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCTTACCGGC CCTACCGGC CCTTACCGC CCTGCTCTTC GGTCCTTCAC GGACAACAAT AACAACGAGGTA AACAACACCTC CCTGGTTTTG CTGCAGAGAC CCTGGTTTTG CTGCAGAGCT 51	720 780 60 120 180 240 300 420 480 540 660 720 780 840
50556065	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGG TTCTCCTCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AACTGACCG AACTGACCTGA ACTGGCACCTGA CTGCAGCGCACCTGG ATTGGAACCTG TTGGAACTGA TTGTATGTCT TATTTGAACCC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac I	ESDIMTTINGV TKIITKVUE KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCA ACGTGCCAC ACATCTAGA TGCGAGATT CACATCTAGA TCCTGGGTA TGCGAGTGCCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA TCCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGTAT GCAAGGGGAT CCTGGTAT GCAAGGGGAT CCTGGTAT CGGATGTCCT 68 Protein cession #: 11	IHVUDKLLYP KIKVIEGSLO FVEITEKETR DEEIKRLLQG IHENCE IN #: EOS SE 7 21 GGGCCCCGCC CTGGCTTCC CTGGCTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCAC GCAAGGTCTA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTAC CAAAAAAGTGG CAGATATGAA CGAGTGA SEQUENCE EOS SEQUENC 21	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTCTCT GCCGTGTCCG GCAGCGCGCA GCCTACGTGA CTCGCGCGG TTGGAGGACA CTCGAGGACA CTCCACATATA ATGGTGACT TATCCGGAAA GACCCGATTC CTGATAGGG ATGCATAACA ATCAATGCGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCCTAAGTG ATGCCTGACTA ATGCCCTCAA GGGTTTTCCT ATGTTTCCT CTATTTTCCT CTATTTTCCT TCAGAGATGG ACCCCAGATT 41 41	IQIKPVRGST FRLIKEGETI FRLIKEGETI FREGRSQ 51 GCTGGCGCGA GGCATCCTCC CCTGCACGGC CCAACTGCC CCTTCAC GGACAACAAT TCGGGTCCTTC CGTCCTTCAC GGACAACAAT TCGGGTCCTC CCTGGAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC	720 780 120 180 240 360 420 480 540 660 720 840 900
50 55 60 65 70	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGG TTCTCCTCT CAGTGCCCGG AATCTGACCG AACCAGCTGG AACTGACCG AACTGACCTGA ACTGGCACCTGA CTGCAGCGCACCTGG ATTGGAACCTG TTGGAACTGA TTGTATGTCT TATTTGAACCC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac I	ESDIMTTINGV TKIITKVUE KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCA ACGTGCCAC ACATCTAGA TGCGAGATT CACATCTAGA TCCTGGGTA TGCGAGTGCCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA ACAGTGCTGCA TCCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGGTAT GCAAGGGGAT CCTGGTAT GCAAGGGGAT CCTGGTAT GCAAGGGGAT CCTGGTAT CGGATGTCCT 68 Protein cession #: 11	IHVUDKLLYP KIKVIEGSLO FVEITEKETR DEEIKRLLQG IHENCE IN #: EOS SE 7 21 GGGCCCCGCC CTGGCTTCC CTGGCTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCAC GCAAGGTCTA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTAC CAAAAAAGTGG CAGATATGAA CGAGTGA SEQUENCE EOS SEQUENC 21	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTCTCT GCCGTGTCCG GCAGCGCGCA GCCTACGTGA CTCGCGCGG TTGGAGGACA CTCGAGGACA CTCCACATATA ATGGTGACT TATCCGGAAA GACCCGATTC CTGATAGGG ATGCATAACA ATCAATGCGG	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCCTAAGTG ATGCCTGACTA ATGCCCTCAA GGGTTTTCCT ATGTTTCCT CTATTTTCCT CTATTTTCCT TCAGAGATGG ACCCCAGATT 41 41	IQIKPVRGST FRLIKEGETI FRLIKEGETI FREGRSQ 51 GCTGGCGCGA GGCATCCTCC CCTGCACGGC CCAACTGCC CCTTCAC GGACAACAAT TCGGGTCCTTC CGTCCTTCAC GGACAACAAT TCGGGTCCTC CCTGGAAACC CCTGGAAACC CCTGGAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC	720 780 60 120 180 240 300 420 480 540 660 720 780 840
50 55 60 65 70	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGOGCTGG TTCTCCTCT TCAGTGCCCOG AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCCTGGGTCT GTGCAGGGCA TTGGAACTCA TCTTATGTCT TATTTTGAACC CACATGGAAC AGTTTAGACT CACATGGAAC AGTTTAGACT Seq ID NO: Protein Ac I MPGGCSRGPA	ESDIMTTNGV TKIITKVEE KKYTKIIDGV RKYTKIIDGV 1EGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCAC CCAGCACCAC ACATCTAGA TGGCTGAGTT GCAATCTAGA TGCTGGTGTG CACATCTAGA TGCTGGTGT CACATCTAGA TGCTGGTGT CACATCTAGA TGCTGGAGTT CACATCTAGA TGCTGGATT CGCATGCTGA TCCTGGGTAT TCCTGGTAT TCCT	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG IHENCE IN #: EOS SE 7 21 GGGCCCCGCC CTGGGTTCC GTGCTTCCC GTGCTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC CAGGAGAC CACCTGTGCA CACCTGTGCA CACCTGTGCA CACGAGAC CACCTGTGCA CACGAGAC CACCTGTGCA CAGATATGAA LALVLLGWVS	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTTCTC GCCGTGTCCG GCAGCGCGCA GCTACGTGCA GCCTACGTGA TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGGCG ATGCATAACA ATCAATGCGG	LEILNKLIXY TKVKLEGEPY KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CCAGTCAAGTG GCAACCTCTT ATGCCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AATGAGGAA ATTCCCCCATC CTATTTTCC TATTTTCCT ACCCCAGATT 41 FSSSAPFLAS	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRETEKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTAACCGC CCTAACCGCC CCTGCTCTC GGTCCTTC CGTCCTTC CGTCCTTC CGTCCTTC CCTGCAAACC CCTGGTCTTC CCTGCAAACC CCTGGTCCTC CCTGCAAACC CCTGGTCCTC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC CTGCAAACC TGCAGGGTA AACAAACCTC	720 780 120 180 240 360 420 480 540 660 720 840 900
50556065	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seqt ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AACCAGCTGG ACCAGCTGG ACCAGCTGG ACCAGGCC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA TCTTATGTCT TATTTGAACC CACATGGAAC Seq ID NO: Protein Ac	ESDIMTTINGV TKIITKVEEP KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG TACTCCTGGG AGCTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TCGCTGAGTT TCACATCTAGA TCGCTGAGTT ACAGTGCTG ACAGTGCTA TCCTGGGTAT CCTGGGTAT CGGATGCCTA ACAGTGCTGA TCCTGGGTAT CGGATGTCCT 68 Protein Cession #: 11 AGDGRLRLAR ARTVKCVNR	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG IHENCE IHE EOS SE 7 21 GGGCCCCGCC CTGGGTTCC CTGGGTCTCC CTGGCTTCC CTGGTTCCAA GGACCTGCAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CCTCGACTGT TGTTTTAGCC AAAAAAGTGA CCTCGACTGT TGTTTTAGCC AAAAAAGTGA SEQUENCE EOS SEQUENC 21 LALVLLGWVS NLTEVPTDLF	ADTPVGNDQL PIIKTEGPTI EERIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCC GCCGTGTCCC GCCGTGTGCC TCGCCGCGGGACG TCGCCGCGGGACG TCGCTGCGCGGACA CCCCACATTA ATGGTGACCA TATCCGGAAA GACCCGATTC CTGATAGGCG ATGCATAACA ATCAATGCGG e 31 SSSSPTSSASS AYVRNLFLTG	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCCCC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATTGCTGGG GCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGAA TTCCCCCATC CTATTTTCCT TCAGAGATG ACCCCAGATT 41 FSSSAPFLAS NQLASNEFLY	IQIKPVRGST FRLIKEGETI FRLIKEGETI FREITEKKLL REGRSQ 51 GCTGGCGCGA GGCATCCTCC GCTGCCGGAC CCTTACCGC CCTTACCGC CCTTACCGC CCTGCTCTC CGTCCTTCAC GGACAACAAT AACAAGAGTA TCCGGTCCTTC CCTGCAAACC CCTGGTTTTG CCTGCAAACC CCTGGTTTTG CTGCAGGAT AACAAACCTC	720 780 60 120 180 240 360 420 540 660 720 780 840 900
50 55 60 65 70	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq I ATGCCTGGGG CTAGGGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACTGAACCTG AATGGCACCC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA TTGAACTCA TTATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac I MPGGCSRGPA QCPALCECSE SLRHLDLSNN	ESDIMTINGV TKIITKVEP KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92* 11 GGTGCTCCCG TACTCCTGGG AGGTGCCCAC ACCTGTGCGA ACGTGCCAC ACCTGGACTT CACATCTAGA TCGCTGAGTT CACATCTAGA TCGCTGAGTT CACATCTAGA AGACCGGCT ACAGTGCCA ACGTGCTGA AGACCGGCT ACAGTGCTGA TCCTGAGTT CCGATTCATA CGATTCCTGA TCCTGAGTT CCAATCTAGA AGACCGGCT ACAGTGCTGA TCCTGAGTT CCAATCTAGA ACTGCTGA TCCTGAGTT TCAGTAT CGATGTCCT 68 Protein Cession #: 11 AGDGRLRLAR AARTVKCVNR SLVSLTYVSF	INVUDKLLYP KIKVIEGSLYP KIKVIEGSLYP KIKVIEGSLYP KIKVIEGSLYP PVEITEKBTR DEEIKRLLQG INTERPORT IN #: EOS se 7 21 GGGCCCCGCC CTGGGTTCTCC CTGGGTTCTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAA AAGCCTCCAC GCAAGGTCTA CACTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTACTGA CAGATATGAA CAGGTGA sequence EOS sequence 21 LALVLLGWVS KILTEVPTDLE RNLTHLESLE	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTTCTTCTC GCCGTGGC GCCTACGTGC CTGCCGCGGC TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTCC ATGAATGCG ATCAATGCGG ### Common com	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA ATGCCTCAA GGCTTTTCCT CGGTCAAGGA AAATGAGGAA ATTTCCT CTATTTTCT TCAGAGATGC ACCCCAGATT 41 FSSSAPFLAS NQLASNHPLY NGTLABLQGL	IQIKPVRGST FRLIKEGETI FRLIKEGETI FREITERLIKLL REGRSQ 51 GCTGGCGCCA GGCATCCTCC GCTGCCCCCCGGAC CGTTACCGC CCTACCGGC CCTACCGCC CCTGCTCCTC GGTCCTTC GGTCCTTC CCTGCAACC CTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CTGCACACC CT	720 780 120 180 240 420 480 540 600 660 720 840 900
50 55 60 65 70	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGGGCTGG TTCTCCTCT TCAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCTGGGTCT GTGCAGGCC CCCTGGGTCT TTTTTGAACC CACATGGAAC TCTTATGTCT TATTTGAACT CACATGGAAC AGTTCTAACT Seq ID NO: Protein Ac I MPGGCSRGPA QCPALCECSE SLRHLDLSNE PWVDCEMAD	ESDIMTTNGV TKIITKVEE KKYTKIIDGV RKYTKIIDGV REGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCAC CCAGCACCAC ACATCTAGA TGGCTGAGTT GCAATCTAGA TGCTGGGTA TCCTGGGTAT GCAATCTAGA TGCTGGTAGTA CGCTGGTAT CACATCTAGA TGCTGGACTT CACATCTAGA TGCTGGACTT CACATCTAGA TGCTGGACTT ACAGTGCTGA TCCTGGGTAT TCCTGGGAT TCCTGGAT TCCTGGGAT TCCTGGG	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLLQG IHENCE IN #: EOS SE 7 21 GGGCCCCGCC CTGGGTTCC GTGCTTCCCTTACC GTGCTTCCCGAG GGACCTGCCC CTTCCTTTAC CAGGAGAC CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTGCA CACTGTGCA CACTGTCA CACTGT	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTTCTC GCCGTGTCCG GCAGCGCGCA GCTACGTGCA GCCTACGTGC TCGCGCGGGA CCCCACATTA ATGGTGACCT TATCCGGAAA ATGGTGACCT ATCATAGCG ATGATAACA ATCAATGCGG e 31 SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEWMENVL	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CCAGCCCCC ATTCAAGTG GCAACCTCTT ATGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT ATGCCTGAC TCAAGTG AAATGAGGAA ATTCCCCATC CTATTTTCCT TCAGAGTG ACCCCAGATT 41 FSESAPFLAS NQLASMFFLY NGTLAELGGL LEILNSADLDC	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRLIKEGETI FREGRSQ 51 GCTGGCGGCGA GGCATCCTCC GCTGCCGGAC CCTTAACCGC CCTTAACCGC CCTTACCGGC CCTGCTTCC GGTCCTTC CGTCCTTC CGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCCTC CTGCAAACC CTGCAAACC CTGCAAACC TGCAGGGT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVPLINN DPILPPSLQT	720 780 120 180 240 300 420 480 540 660 720 840 900
50 55 60 65 70	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding sequil ATGCCTGGGG CTAGGGCTGG TTCTCCTCT TCAGTGCCCGG AATCTGACCG AACCAGCTGG AGCCTCAGGC CCCTGGGTCT GTGCAGGCC CCCTGGGTCT TTTTTGAACC CACATGGAAC TCTTATGTCT TATTTGAACT CACATGGAAC AGTTCTAACT Seq ID NO: Protein Ac I MPGGCSRGPA QCPALCECSE SLRHLDLSNE PWVDCEMAD	ESDIMTTNGV TKIITKVEE KKYTKIIDGV RKYTKIIDGV REGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCAC CCAGCACCAC ACATCTAGA TGGCTGAGTT GCAATCTAGA TGCTGGGTA TCCTGGGTAT GCAATCTAGA TGCTGGTAGTA CGCTGGTAT CACATCTAGA TGCTGGACTT CACATCTAGA TGCTGGACTT CACATCTAGA TGCTGGACTT ACAGTGCTGA TCCTGGGTAT TCCTGGGAT TCCTGGAT TCCTGGGAT TCCTGGG	INVUDKLLYP KIKVIEGSLYP KIKVIEGSLYP KIKVIEGSLYP KIKVIEGSLYP PVEITEKBTR DEEIKRLLQG INTERPORT IN #: EOS se 7 21 GGGCCCCGCC CTGGGTTCTCC CTGGGTTCTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAA AAGCCTCCAC GCAAGGTCTA CACTGTGCA CACCTGTGCA CACCTGTGCA CACCTGTACTGA CAGATATGAA CAGGTGA sequence EOS sequence 21 LALVLLGWVS KILTEVPTDLE RNLTHLESLE	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTTCTC GCCGTGTCCG GCAGCGCGCA GCTACGTGCA GCCTACGTGC TCGCGCGGGA CCCCACATTA ATGGTGACCT TATCCGGAAA ATGGTGACCT ATCATAGCG ATGATAACA ATCAATGCGG e 31 SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEWMENVL	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CCAGCCCCC ATTCAAGTG GCAACCTCTT ATGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT ATGCCTGAC TCAAGTG AAATGAGGAA ATTCCCCATC CTATTTTCCT TCAGAGTG ACCCCAGATT 41 FSESAPFLAS NQLASMFFLY NGTLAELGGL LEILNSADLDC	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRLIKEGETI FREGRSQ 51 GCTGGCGGCGA GGCATCCTCC GCTGCCGGAC CCTTAACCGC CCTTAACCGC CCTTACCGGC CCTGCTTCC GGTCCTTC CGTCCTTC CGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCCTC CTGCAAACC CTGCAAACC CTGCAAACC TGCAGGGT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVPLINN DPILPPSLQT	720 780 120 180 240 420 480 540 600 660 720 840 900
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50 55 60 65 70 75	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq ATGCCTGGGG CTAGGCCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACTGAACTCA TGGAAGGCT CAGGCCCCGGAACCTGA AATGGCACGCC CCCTGGGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac Coding seq	ESDIMTTINGV TKIITKVLEE KKYTKIIDGV KKYTKIIDGV LEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCTT CGCTGTGCGA ACGTGCCCAC ACCTGGACTT CACATCTAGA TCGCTGAGTT TCACATCTAGA TCGCTGAGTT GCAACCGGT ACAGTGCTA ACGTGATT GCAACGGGT TCCTGGGTAT GCAACGGGT TCCTGGGTAT CGGATTCCTG ACAGTGCTGA TCCTGGGTAT CGGATTCCTG ACAGTGCTGA TCCTGGGTAT CGGATCTCTG ACAGTGCTGA TCCTGGGTAT CGGATCTCTTA CGGATCTCT 68 Protein Cession #: 11 AGDGRLRLAR AARTVKCVNR SLUSLTTVSF MVTWLKETEV LIGAIFLLVL 69 DNA sequid Accession LIGAIFLLVL 69 DNA sequid Accession LIGAIFLLVL 69 DNA sequid Accession LIGAICACCO LIG	IHVVDKLLYP KIKVIEGSLQ FVEITEKETR DEEIKRLIQG I #: EOS se T 21 GGGCCCCGCC CTGGGTCTCC CTGGCTTCC CTGGCTCCC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGCT CACTGGACTGT TGTTTTAGCC AAAAAAGTGA CAGGTGAA CGAGTGAA CGAGTGAA Sequence EOS sequenc 21 LALVLIGWVS NLTEVPTDLF RNLTHLESLE VQGKDRLTCA YLNRKGIKKA	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTTCTTC GCCGTGGC GCCTTACTGC CTGCCGCGGC TCGCTGGTGA CTGCGCGGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCG ATGCATAACA ATCATGCGG ** 1 SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMERRVL MENIRDACRD	LEILNKLIXY TKVKLEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CCAGCCCCC ATTCAAGTG GCAACCTCTT ATGCTGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT ATGCCTGAC TCAAGTG AAATGAGGAA ATTCCCCATC CTATTTTCCT TCAGAGTG ACCCCAGATT 41 FSESAPFLAS NQLASMFFLY NGTLAELGGL LEILNSADLDC	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRLIKEGETI FREGRSQ 51 GCTGGCGGCGA GGCATCCTCC GCTGCCGGAC CCTTAACCGC CCTTAACCGC CCTTACCGGC CCTGCTTCC GGTCCTTC CGTCCTTC CGTCCTTC CCTGCAAACC CCTGGTCTTC CTGCAAACC CCTGGTCCTC CTGCAAACC CTGCAAACC CTGCAAACC TGCAGGGT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVPLINN DPILPPSLQT	720 780 120 180 240 300 420 480 540 660 720 840 900
50 55 60 65 70 75	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCTGGGG CTAGOGCTGG TTCTCCTCT TCAGTGCCCGGAACCTGA AATCTGACCG AACCAGCTGG AGCCTCGAGCTCGG TCTCTTATTCT TTATTTAACC CACATGGAAC TCTTAATCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCEMAD SYVFLGIVLA SNSDVLE Seq ID NO: Nucleic Ac Coding seq 1	ESDIMTTNGV TKIITKVVEE KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGGCGTCCCAG ACGTGCCAA ACGTGCCAA ACCTGGACTT CACATCTAGA TCCAGGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTAT CACATCTAGA TCCAGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGTCCT 68 Protein Cession #: 11 AGDGRLRLAR AARTVKCVNR SLVSLTYVSF MVTWLKETEV LIGAIPLLVL 69 DNA sequid Accession Lence: 26	INVUNKLLYP KIKVIEGSLE KIKVIEGSLE DEEIKRLLQG IN #: EOS se 7 21 GGGCCCCGCC CTGGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAA AAGCCTCCAC GCAAGGTCTA CACTGGACGAC CACCTGTGCA CACCTGTGCA CACCTGTGCA CACTGTAC AAAAAAGTGA Sequence EOS sequenc 21 LALVLLGWVS NLTEVPTDLE RNLTHLESLE VQGKDRLTCA YLNRKGIKKG QUENCE	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN Quence 31 GCCGGGGACG TCGTTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC TCGCTGGGGAC TCGCTGGGGAC ATGAGACA TCAATGAGCG ATGAACA ATGATAACA ATCAATGCGG ATGATAACA ATCAATGCGG ATGATAACA ATCAATGCGG LEDNALKVLH TYPEGMENRVL TYPEGMENRVL MENIRDACRD	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL GCGTCTGCG CCACCTCCTC CCAGCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA ATGCCCTAA ATGCCTCAA GGGTTTTCCT TCAGGAAC AAATGAGGA AAATGAGGA ACCCCAGATT 1 FSSSAPFLAS NQLASNHFLY NGTLABLQGL LEINSADLDC HMEGYHYRYE	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRLIKEGETI ETEETLEKLL REGRSQ 51 GCTGGCGCCA GGCATCCTCC CCTGCTCCCC CCTGCTCCCC CCTGCAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAGGAT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVPLININ DPILPPSLQT INADPRLTNL	720 780 120 180 240 300 420 480 540 660 720 840 900
50 55 60 65 70	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq ATGCCTGGGG CTAGGCCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACCAGCTGG AACTGAACTCA TGGAAGGCT CAGGCCCCGGAACCTGA AATGGCACGCC CCCTGGGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac Coding seq	ESDIMTTNGV TKIITKVVEE KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGGCGTCCCAG ACGTGCCAA ACGTGCCAA ACCTGGACTT CACATCTAGA TCCAGGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTAT CACATCTAGA TCCAGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGTCCT 68 Protein Cession #: 11 AGDGRLRLAR AARTVKCVNR SLVSLTYVSF MVTWLKETEV LIGAIPLLVL 69 DNA sequid Accession Lence: 26	INVUNKLLYP KIKVIEGSLE KIKVIEGSLE DEEIKRLLQG IN #: EOS se 7 21 GGGCCCCGCC CTGGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAA AAGCCTCCAC GCAAGGTCTA CACTGGACGAC CACCTGTGCA CACCTGTGCA CACCTGTGCA CACTGTAC AAAAAAGTGA Sequence EOS sequenc 21 LALVLLGWVS NLTEVPTDLE RNLTHLESLE VQGKDRLTCA YLNRKGIKKG QUENCE	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTTCTTC GCCGTGGC GCCTTACTGC CTGCCGCGGC TCGCTGGTGA CTGCGCGGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCG ATGCATAACA ATCATGCGG ** 1 SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMERRVL MENIRDACRD	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL GCGTCTGCG CCACCTCCTC CCAGCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA ATGCCCTAA ATGCCTCAA GGGTTTTCCT TCAGGAAC AAATGAGGA AAATGAGGA ACCCCAGATT 1 FSSSAPFLAS NQLASNHFLY NGTLABLQGL LEINSADLDC HMEGYHYRYE	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRLIKEGETI ETEETLEKLL REGRSQ 51 GCTGGCGCCA GGCATCCTCC CCTGCTCCCC CCTGCTCCCC CCTGCAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CCTGCAAACC CTGCAGGAT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVPLININ DPILPPSLQT INADPRLTNL	720 780 120 180 240 300 420 480 540 660 720 840 900
50 55 60 65 70 75	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCTGGGG CTAGOGCTGG TTCTCCTCT TCAGTGCCCGGAACCTGA AATCTGACCG AACCAGCTGG AGCCTCGAGCTCGG TCTCTTATTCT TTATTTAACC CACATGGAAC TCTTAATCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCEMAD SYVFLGIVLA SNSDVLE Seq ID NO: Nucleic Ac Coding seq 1	ESDIMTTNGV TKIITKVVEE KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGGCGTCCCAG ACGTGCCAA ACGTGCCAA ACCTGGACTT CACATCTAGA TCCAGGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTAT CACATCTAGA TCCAGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGTCCT 68 Protein Cession #: 11 AGDGRLRLAR AARTVKCVNR SLVSLTYVSF MVTWLKETEV LIGAIPLLVL 69 DNA sequid Accession Lence: 26	INVUNKLLYP KIKVIEGSLE KIKVIEGSLE DEEIKRLLQG IN #: EOS se 7 21 GGGCCCCGCC CTGGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAA AAGCCTCCAC GCAAGGTCTA CACTGGACGAC CACCTGTGCA CACCTGTGCA CACCTGTGCA CACTGTAC AAAAAAGTGA Sequence EOS sequenc 21 LALVLLGWVS NLTEVPTDLE RNLTHLESLE VQGKDRLTCA YLNRKGIKKG QUENCE	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTTCTTC GCCGTGGC GCCTTACTGC CTGCCGCGGC TCGCTGGTGA CTGCGCGGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCG ATGCATAACA ATCATGCGG ** 1 SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMERRVL MENIRDACRD	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL 41 GGCGTCTGCG CCACTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGGGG GCCTGACCTA ATGCCCTCAA GGGTTTTCCT TATGTTGGG AAATGAGGAA TTCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT 41 FSSSAPFLAS NOLASMHFLY NGTLABLQGL LELNSADLDC HMEGYHYRYE 41	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRLIKEGETI FREGRSQ 51 GCTGGCGCGGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CCTGCAACAC CCTTCAC GGACAACAAT TCGGGTCCTT CCTGCAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVPLDINN DPILPPSLQT INADPRLTNL	720 780 120 180 240 300 420 480 540 660 720 840 900
50 55 60 65 70 75	FKEIPVTVYT TEVIHGEPII QEEVTKVTKF Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCTGGGG CTAGOGCTGG TTCTCCTCT TCAGTGCCCGGAACCTGA AATCTGACCG AACCAGCTGG AGCCTCGAGCTCGG TCTCTTATTCT TTATTTAACC CACATGGAAC TCTTAATCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCEMAD SYVFLGIVLA SNSDVLE Seq ID NO: Nucleic Ac Coding seq 1	ESDIMTTNGV TKIITKVVEE KKYTKIIDGV IEGGDGHLFE 67 DNA sequid Accession Lence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGGCGTCCCAG ACGTGCCAA ACGTGCCAA ACCTGGACTT CACATCTAGA TCCAGGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTT CACATCTAGA TCCAGGTAT CACATCTAGA TCCAGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGCTGA TCCAGGGTAT CAGATGTCCT 68 Protein Cession #: 11 AGDGRLRLAR AARTVKCVNR SLVSLTYVSF MVTWLKETEV LIGAIPLLVL 69 DNA sequid Accession Lence: 26	INVUNKLLYP KIKVIEGSLE KIKVIEGSLE DEEIKRLLQG IN #: EOS se 7 21 GGGCCCCGCC CTGGGTTCCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAA AAGCCTCCAC GCAAGGTCTA CACTGGACGAC CACCTGTGCA CACCTGTGCA CACCTGTGCA CACTGTAC AAAAAAGTGA Sequence EOS sequenc 21 LALVLLGWVS NLTEVPTDLE RNLTHLESLE VQGKDRLTCA YLNRKGIKKG QUENCE	ADTPVGNDQL PIIKTEGPTIL ERRIITGPEI DTPVRKLQAN quence 31 GCCGGGGACG TCGTTCTTC GCCGTGGC GCCTTACTGC CTGCCGCGGC TCGCTGGTGA CTGCGCGGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCG ATGCATAACA ATCATGCGG ** 1 SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMERRVL MENIRDACRD	LEILNKLIKY TKVKIEGEPE KYTRISTGGG KKVQGSRRRL GCGTCTGCG CCACCTCCTC CCAGCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA ATGCCCTAA ATGCCTCAA GGGTTTTCCT TCAGGAAC AAATGAGGA AAATGAGGA ACCCCAGATT 1 FSSSAPFLAS NQLASNHFLY NGTLABLQGL LEINSADLDC HMEGYHYRYE	IQIKPVRGST FRLIKEGETI FRLIKEGETI FRLIKEGETI FREGRSQ 51 GCTGGCGCGGA GGCATCCTCC GCTGCCGGAC CCTTACCGGC CCAACTGCCC CCTGCAACAC CCTTCAC GGACAACAAT TCGGGTCCTT CCTGCAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVPLDINN DPILPPSLQT INADPRLTNL	720 780 120 180 240 300 420 480 540 660 720 840 900

			CCGCCATGGT				60
			CCGGACAGGG				120
			AGGAAACCAA				180
-			TCACGTTCCT				240
5			GCACCGGCCT				300
			GCGTGGCCTG				360
			CGGGCAACGG				420
			GAGTCCGCTG				480
10			GCGGCCCCAC				540
10			CGGACATCAA				600
			ACACCCGGGG				660 720
			COGGCTGCCA				780
			AGCATGCAGA GGGCCGGCAA				840
15			AGCTGCGCTG				900
13			GGCAGGAGGA				960
			ACGGGGTCCC				1020
			CGGACGAGGA				1080
			AAAAGGACAC				1140
20			GGATCCGCAA				1200
20			ATGGCGATGG				1260
			CGGATGTGGA				1320
			ACGGACATCA				1380
			CAGACCACGA				1440
25			ACAGTCGGGA				1500
			GCGTGGGCGA				1560
			TGTGTCCGGA				1620
			TGGACCCGGA				1680
			AGATCGTGCA				1740
30			GCGTGGACTT				1800
	GGATGACGAC	TATGCGGGCT	TCATCTTTGG	CTACCAGGAC	AGCTCCAGCT	TCTACGTGGT	1860
	CATGTGGAAG	CAGATGGAGC	AAACGTATTG	GCAGGCGAAC	CCCTTCCGTG	CTGTGGCCGA	1920
	GCCTGGCATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
2.5	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
35			AGAAGTCCTA				2100
			TCTATGAGGG				2160
			GTGGCCGCCT				2220
			ACCGCTGCAA				2280
40			GACCAGGGTG				2340
40			CACCCAGCCC		CGTCCTGAGG	GGGAAGTGAG	2400
	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGCAGGG			
		70 Protein					
15	Protein Acc	cession #: 1	NP_000086.1				
45				31	41	51	
45	Protein Acc	cession #: 1 11 	NP_000086.1	1	1	1	50
45	Protein Acc	cession #: 1 11 LTLAALGASG	QGQSPLGSDL	 GPQMLRELQE	 TNAALQDVRD	 WLRQQVREIT	60
45	Protein Acci 1 MVPDTACVLL FLKNTVMECD	cession #: 1 11 LTLAALGASG ACGMQQSVRT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH	 GPQMLRELQE CAPGFCFPGV	 TNAALQDVRD ACIQTESGGR	 WLRQQVREIT CGPCPAGFTG	120
	Protein Acci 1 MVPDTACVLL FLKNTVMECD NGSHCTDVNE	11 11 LTLAALGASG ACGMQQSVRT CNAHPCFPRV	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR	 GPQMLRELQE CAPGFCFPGV CEACPPGYSG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD	120 180
45 50	Protein Acc 1 MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN	CEBBION #: 1 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ	 GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH	120 180 240
	Protein Acc 1 MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS	CEBBION #: 1 11 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT	GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL	TNAALQDVRD ACIQTESGGR PTHQGVGLAP CQRGAQRFCP RCPEPQCRKD	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ	120 180 240 300
	Protein Acci 1 MVPDTACVLL PLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD	cession #: 1 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL	GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK	120 180 240 300 360
50	Protein Acc 1 MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA	cession #: 1 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD	120 180 240 300 360 420
50	Protein Acci 1 MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC	cession #: 1	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT	 GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD	 TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS	120 180 240 300 360 420 480
	Protein Acc 1 MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP	cession #: P 11 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVQDDFDA	GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTDD PNSDQKDSDD VVNSAQEDSD DKVVDKIDVC	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDNC HDGQGDACDNC HDGQGDACDDD PENAEVILID	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD	120 180 240 300 360 420 480 540
50	Protein Acc 1 MVPDTACVLL PLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGBAC RDNCRLVPNP PEGDAQIDPN	cession #: P 11 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVLNQGREI	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILGGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPP GDVCQDDFDA VQTMNSDPGL	GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKNGDACDN DGIGDACDN DGIGDACDN PENAEVTLTD DPEGTFHVNT	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI	120 180 240 300 360 420 480 540
50	Protein Acc 1 MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY	CESSION #: 1 ILTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL FNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV	GPQMLRELQE GPQMLRELQE CAPGFCPFGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEGGIQLKAV	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDN HDGQGDACDD PENAEVTLTD DFEGTPHVNT KSSTGPGEQL	I WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50 55	Protein Acc 1 MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD	CESSION #: P 11 LILLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILGGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPP GDVCQDDFDA VQTMNSDPGL	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV APEGIQLKAV QVGYIRVRFY	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDN HDGQGDACDD PENAEVTLTD DFEGTPHVNT KSSTGPGEQL	I WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540
50	Protein Acc 1 MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD	CESSION #: P 11 LILLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV APEGIQLKAV QVGYIRVRFY	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDN HDGQGDACDD PENAEVTLTD DFEGTPHVNT KSSTGPGEQL	I WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50 55	Protein Acci	CESSION #: P 11 LILLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV APEGIQLKAV QVGYIRVRFY	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDN HDGQGDACDD PENAEVTLTD DFEGTPHVNT KSSTGPGEQL	I WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50 55	Protein Acc I MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDODGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO:	CESSION #: P	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEGGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDN HDGQGDACDD PENAEVTLTD DFEGTPHVNT KSSTGPGEQL	I WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50 55	Protein Acci	CESSION #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGF RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE uence n #: NM_024	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEGGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDN HDGQGDACDD PENAEVTLTD DFEGTPHVNT KSSTGPGEQL	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 480 540 600 660
50 55 60	Protein Acci	cession #: P 11 LTLAALGASG ACGMQQSVRT CNAHPCFPRI CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA sequid Accession	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGF RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE uence n #: NM_024	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNFPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEGGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDN HDGQGDACDD PENAEVTLTD DFEGTPHVNT KSSTGPGEQL	I WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600 660
50 55	Protein Acc MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequil	CESSION #: P 11 LILLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accession uence: 71	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE uence n #: NM_024 919 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AVGYTAFNGV AEGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDKWGDACDN HDGQGDACDD PENAEVILID DPEGTPHVNT KSSTGPGEQL EGPELVADSN	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 480 540 600 660 720
50 55 60	Protein Acci	cession #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GMGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAL SYRWFLQHRP CNDTIPEDYE uence n #: NM_024 919 21 GGCAGCTCCA	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP CREPPQCRKD EDKWGDACDN DGIGDACDN DGIGDACDN DFENABYTLTD DPESTFHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC	120 180 240 300 360 420 480 540 660 720
50 55 60	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Accoding sequence GAGTCACCAA TTCCCCAGCC ACCODING GAGTCACCAA TTCCCCAGCC ACCODING AC	CESSION #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYB uence n #: NM_024 921 GGCAGCTCCA TGGGGCAGAT	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PMSAQEDSD DKVVDKIDVC AVGYTAFMGV AEPGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCAGCCAGT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGGGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT	120 180 240 300 360 420 540 600 660 720
50 55 60	Protein Acc MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDDDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Acc Coding sequents of the control of t	CESSION #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE Uence n #: NM_024 919 21 GGCAGCTCCA TCGGGCAGAT CACTCATCAT	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AVGYTAFNGV AVGYTAFNGV THQLRQA 626 31 CTCAGCCAGT CCTCAGCCAGT TCGCTTTGGT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCKD BGIGDACDN BGIGDACDN HDGQGDACDN PENAEVILIT DPEGTPHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT	120 180 240 300 360 420 540 600 720
50556065	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ GAGTCACCAA TTCCCCAGCC CATTCTGGCT CACAGTCACT	CESSION #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE uence n #: NM_024 919 21 GGCAGCTCCA TGGGGCAGAT CACTCATCAT CACCTACAT	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGCGAG	TNAALQDVRD TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVTLTD DFESTFHVNT KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA AGTTCAGGGA GATGGAATCC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGACATCCAT TGACATCCAT	120 180 240 300 360 420 540 600 660 720
50 55 60	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Accoding sequ GAGTCACCAA TTCCCCAGCC TATTCTGGCT CCCAGTCACT TTTTGAACCT	CESSION #: P	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PMSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT TGATTGCGGAG CCTGATACAA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDDC DGIGDACDDC PENAEVILTD DPEGTFHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA AGATGGAATCC TGGCTGAAGGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCTAC AAGGTGTTTT	120 180 240 300 360 420 540 600 660 720 60 120 180 240 300
50556065	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Acc Coding sequ 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTGAACCT TTTGAACCT AGGCTTGGTC	CESSION #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPT HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE Uence n #: NM_024 919 GGCAGCTCCA TGGGGCAGAT TGCGGGCAGAT TAGGAGGCAA TTTCTGATAT AAGAAGGCAA	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AVGYTAFNGV AUGYTAFNGV THQLRQA 31 CTCAGCCAGT CCTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAG AGATGAGCTG	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVTLTD DFEGTFHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATCC TGGCTGAAGG TCGGAGAGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEN NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT	120 180 300 360 420 480 540 600 720
50556065	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT AGGCTTGGTC CAGAGGCCGG	CESSION #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSPQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE uence n #: NM_024 919 21 GGCAGCTCCA TCGGGCAGAT TCACTCATCAT CAGCTGGGAA TTTCTGATAT AAGAAGGCAA ATTGCTGATCA	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGCGGAG AGGTGATACAA AGATGAGCTG	TNAALQDVRD TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECHORY EDKWGDACDN DGIGDACDNC HDGQGDACDN PENAEVTLTD DFEGTFHVNT KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGAATCC TGGCTGAAGG TCGGAGCAGG GGCAATGCCT	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGGGGCT	120 180 240 300 360 420 540 600 720 60 120 180 240 300 420
50556065	Protein Acci	CESSION #: 11 LILLAALGASG ACGMQQSVRT CNAHPCFPRI CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI BSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMKQMEQT PRNVGWKQKE NIIWANLRYR 71 DNA sequid Accession uence: 71 11 GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGTTCGCCT GACATCAAAC ACAGCAGTGT CAACTCACAG	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPEFE RGSFQCGPCQ GMGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTNNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE uence n #: NM_024 919 21 GGCAGCTCCA TGGGGCAGAT TGGGGCAGAT TTCTGATAT AAGAAGGCAA ATTGCTGATCA ATGCTGGCACA	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT TGGCTTTGGT TGATTAGAAATGTT CTACAAAATGTT CTACAAAATGTT CTACAAAATGTT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CORGAQRFCP CORGAQRFCD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILTD DFESTFHVNT KSSTGPGGL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATGC TGGGTGAAGG GGCAATGCC TGATATCATCA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG GCTGGGAACC GCATCATCAT GAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGGGCT CTTCTAAAGG	120 180 240 300 360 420 600 660 720 60 120 180 240 300 360 420 480
5055606570	Protein Acc 1 MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGAGGCCGG GAAAACGTG CAAGGGGAAT	CESSION #: 11 LITLAALGASG ACGMQGSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GCEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKQKK NIWANLRYR 71 DNA sequid Accession Lence: 71 11 GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGTCAAC CATGAGTTCA ACAGCAGTGT CAACTCACAG GCTAACCTTG GCATTCAGAG GCTAACCTTG	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPT ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE Uence n #: NM_024 919 21 GGCAGCTCCA TCGGGCAGAT CACTCATCAT CAGCTGGAA ATGCTGGATAA ATGCTGGATCA	GPOMLRELQE CAPGPCPPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PMSAQEDSD DKVVDKIDVC AVGYTAFMGV AEPGIQLKAV QVGYIRVRFY THQLRQA 31 CTCAGCCAGT CCTCAGCCAGT CCTCTTCTGG TGGCTTTGGGT CATTGCGGAG AGATGAAGCTG AGTGATACAA AGATGACTT TGGAGCCTTCT TGGAGCCTTCT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILTD DFESTFHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATCC TGGGTGAAGG TCGGAGCAGG GGCAATGCCT TATATCATCA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGAGGG AAGTGATGTT	120 180 240 300 360 420 600 660 720 60 120 180 240 300 360 420 480 540
50556065	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDDDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGAGGCCGG GAAAAACGTG CAAGGGGAAT GGACTATAAT	CESSION #: 1 ILTLAALGASG ACGMQGVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accession uence: 71 11 GGAGGCTACC GGAGCTACC GGAGCTACC CATGAGTTCA ACAGCAGTGT CAACCTTACAGG GCCAGCTCAG GCCAGCTCAG GCCAGCTCAG GCCAGCTCAG GCCAGCTCAG	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE Uence n #: NM_024 919 21 GGCAGCTCCA TCACCATCAT CAGCTGGGAA TTTCTGATAA TTGCTGATCA ATGCTGGCAAC AGACCTTGCG	GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGTTAFNGV AVETTAFNGV AVETTAFNGV THQLRQA 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTCGT TGGCTTAGTAATGTT CTACAAATGTT TGGAGCCTTC GTGTGAGCCTTC GTGTGAGCCTTC GTGTGAGCCTT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CORGAQRFCP RCPEPQCRKD EDKMGDACDN DGIGDACDNC HDGQGDACDD PENAEVILID DFEGTHVNT KSSTGPGQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATCC TGGCTGAGGGGGGCAGGGCA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGOGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC	120 180 240 360 420 540 660 720 60 120 180 240 300 420 480 540 600
5055606570	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ GAGTCACCAA TTCCCCAGCC TTTTGAACCT CACAGTCACT CAGAGGCCGG GAAAACGTG CAAGTGATAT GCACAGTGATC CACAGTGATAT CACAGTGGTC CACAGTGTC CACAGTGGTC CACAGTGTC CACAGTGGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGTGTC CACAGT	CESSION #: P	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANFFRAV SYRWFLQHRP CNDTIPEDYE LUENCE In #: NM_024 919 21 GGCAGCTCCA TGGGCCAGAT TGCTGGGAA TTTCTGATAT AAGAAGGCA ATTCTGATCA ATGCTGGCAC AGTATAAAAC AGACCTTGGAA AGACCTTGGAA AGACCTTGCAA AGACCTTGCAA AGACCTACA AGACCTACAA AGACCTACAAA AGACCTACAAA AGACCTACAAAAAAAAAA	GPOMLRELQE GPOMLRELQE GPOMLRELQE CAPGPCPPGYSG PGFYGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAG CGTGATACAA AGATGATGT TGGAGCCTAC GGGAGCCAAC	TMAALQDVRD TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP CREPPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN DFENABVTLTD DPESTPHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GGCATACTCGGGAGCAGG TCGGGCGATGCT TATATCATCA AGCATGCGG GGCATGCT TATATCATCA AGCATGCGG TCCGGATGGT TTCTCGGAAGG TTCTCGGAAGG TTCTCGGAAGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGACCACTCCAT TAGACTGCAC AAGGTGTTTT ATGAAATGTT CTTTGGGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCCCCAATAC	120 180 240 300 360 420 600 660 720
5055606570	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGGGGCCGG GAAAAACOTG CAAGGGGAAT GGACTATAAT CACAGTGTCT CAGGTTTGAGCT CAGGTGTCT CAGGTGTCT CAGGTGTCT CAGGTGTTC CAGGTGTTC CAGCTTTGAGCT CAGCTTTGAGCT CAGCTTTGAGCT CAGCTTTTGAGCT CAGCTTTGAGCT CAGCTTTTGAGCT CAG	LEASION #: 11 LITLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio. 11 GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGCGCT GACATCAACA CATGAGTTCA CAGCAGTGTT CAACTCACAG GCTAACCTTG GCCAGCTCAG TGGGCATCCC CTGGAACTCTG	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYB 1 GGCAGCTCCA TGGGGCAGAT CAGCTGGGA TTTCTGATAT AAGAAGGCAA ATGCTGGCA AGGATTGACG AAGATTGACG AGATTGACG AGATTGACG AGATTGACG AGATTGACA AGAATTGACA	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PNSQQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA 31 CTCAGCCAGT CCTCAGCCAGT CCTCTTCTGG TGGCTTTGGT TGGTTTAGAGCT AGATGATGAT AGATGATGATT TGGAGCCATC GTGTGAGGCT CGTGTGAGGCT CGGGAGCCAAC CATGAAGGTT	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CORGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGQL EGPELVADSN 41	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGSGCT CTCTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT	120 180 240 300 360 420 540 600 720 60 120 120 120 1240 300 360 420 540 600 720
5055606570	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding sequ 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTGAACCT AGGCTTGGTC CAGAGGCAGG CAAGGGCAGG CAAGGGCAGT CACAGTGTC CACAGTTGTC CACAGTTGTC CACAGTTGTC CACAGTTCACC TACCGTTTCACCT CACAGTTGTC CACAGTTGTC CACAGTTGTC CACAGTTCACC TACCGTTCACC TACCCC TACCC TACCC TACCCC TACCC TACC	LILLAALGASG ACGMQGVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GOEDADGDG GOEDAGGC VIVINGGREI VMMKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA sequid Accession Lence: 71 11 GGAAGGCAGC GGAAGGCAGC GGAGGCATCC GACACTCACAG GCAACCTCACAG GCCAACCTCAG GCCACCTCAG TGGGCATCCC CTGAACTCTG AACACATACT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPT HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE Uence n #: NM_024 919 21 GGCAGCTCCA TCAGCAGAA TTCTGATAT AAGAAGGCAA TTTCTGATAT AAGAAGGCAA ATTGCTGATCA AGACTTAGAC AGACTTAGAC AGACTTAGAC AGACTTAGAC AGACTTAGAC CAGTTAGAAC CAGTTAGAC CCTGTATGAT	GPOMLRELQE CAPGPCPPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PMSDQKDSDG VPMSAQEDSD DKVVDKIDVC AVGYTAFMGV AVGYTAFMGV AVGYTAFMGV ACPGIQLKAV QVGYIRVRFY THQLRQA 31 CTCAGCCAGT CCTCAGCCAGT CCTCATCGGAGC CGTGATACAA AGATGAGCTG AGTGATAGTT TGGAAAATGT GGGAGCCAGT TGGAGGCTT TGGAAGTT TGAAAATGAC TGGAGAGCCT TTGAAAATGAC TGGAGAGCCT TTGAAAATGAC	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDDC DGIGDACDDC PENAEVILTD DFEGTFHVNT KSSTGPGQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGATCCT TATACATCA AGCATACTA AGCATGCATCCT TATACATCA AGCATGCATCC AGCTGCTGCCTATACTA AGCATGCATCC AGCATGCTTATCATCA AGCATGCATCC AGCATGCTTATCATCA AGCATGCAGC GGCATGCT TATACCATCA AGCATGCAGGC CCCCGATGGT TTCTCGGAAGG CTGTCTGTGCC ATTGCCAAAG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEN NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTT ATGAAATGTT CTTCTAAAGG AAGTGATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGGA	120 180 240 360 420 540 660 720 60 120 180 240 300 420 480 540 600 660 720
505560657075	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQIN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequil GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTGAACCT TTGAACTG CAGGGGCAGG GAAAAACGTG CAGGTGATAAC CAGGTGATC CAGGTGTCACAAGTGTC CAGGTTGAGC TATCAAAGTG TACCAAAGTG TATCAAAGTG TATCAAAGTG	LILLAALGASG ACGMQGSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVULNGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA Seqiid Accession Lence: 71 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE UENCE 1 #: NM_024 919 21 GGCAGCTCCAT CAGCTGAGAA TTTCTGATAT CAGCTGGGAA TTTCTGATAT AGAAGGCAC AGTATAAAAC AGTCTGGCAC AGACCTTGCG AGACTTGCG AGACTTGCG AGACTTGCAC CCTGTATGAT AGAATGACAA	GPOMLRELQE GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGGC GTGTATACAA AGATGAGCTT GGAGCCTTC GTGTGAGGCT GGGGGCCAAC CATGAAGGTT TGAAAATGT TGAAAATGT TGGAGCCTAC GGGGGCCAAC CATGAAGGTT GGAGCTCAC GCGGAGTCAC	TMAALQDVRD TMAALQDVRD TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDNC HDGQGDACDN ESTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGAGATCC TGGCTGAAGG TCGGAGCAGG TCGGACCAGG TCATATCATCA AGCATGCTGT TATATCATCA AGCATGCTGT TTCTCGGAAG GTGTTTTTCCCAAAG CTTCTGCCAAG CTTCCAGAC CTTCCAGAC CTTCCAGAC CTTCCCAGAC CTTCCCAGAC CTTCTCCCAAG CCTACACTGCCG CTCCAAGC CTCCAAGC CTACAACTGCCG CTCCAAGC CTACAACTGCCG CTACAACTGCCG CTCCAACC CTACAACTGCCG CTACAACTGCCG CTACAACTGCCG CTACAACTGCCCG CTCCAACC CTACAACTGCCCAC CTACAACTGCCAC CTACAACTGCCCAC CTACAACTGCCCAC CTACAACTGCCAC CTACAACTACAC CTACAACTGCCAC CTACAACTCCAC CTACAACTCAC CTACAACTCCAC CTACAACTCCAC CTACAACTCCAC CTACAACTCCAC CTACAACTCAC CTACAACTCCAC CTACAACTCCAC CTACAACTCCAC CTACAACTCCAC CTACAACTCAC CTACAACTCCAC CTACAACTCAC CTACAACTCAC CTACAACTCAC CTACAACTCAC C	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGACACTCCAT TGACCTCCAT CTTTAGAATGTT CTTTGGGGT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTCCAATAC TCTACAATGT TCACAAGGGA TAAACTCAAA	120 180 240 300 360 480 540 600 720 60 120 180 240 300 480 540 660 720 780 840
5055606570	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Accoding sequency GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGGGCCAG GAAAAACGTG CAAGGGCAG CAAGGCCAG TACCACT CACAGTCACT TTTTGAACCT AGGCTTGGAC CACAGTCACT CACAGTCACT TATCAAAGTG GGCTTCTCTGGGCT TATCAAAGTG GGCTTCTCTGGGCTCTTCTCTGGGCTCTCTCTTCTTCTTC	LILLANGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV VVMKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA sequitable LII GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGTCGCCT GACATCAAAC CATGAGTTCA CAGCAGTCAG GCTAACCTTG GCCAGCTCAG GCTAACCTTG GCCAGCTCAG TGGGCATCCG CAGAATCGG TGGGATCCC CTGAATCGG TGGGATCCC CTGAATCGG TGGGATCCT ACAGAATCGG TGTGTCTCTT ACAGAATCGG TGTCTCTTT ACAGAATCGG TGTGTCTCTTT ACAGAATCGG TGTGTCTCTTT ACAGAATCGG TGTGTCTCTTT TCAATTCGTT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VOYMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE 1 GGCAGCTCCA TGGGCAGAT CAGCTGGAA TTTCTGATAT AAGAAGGCAA TTGCTGATCA AGTATAAAAC AGACTTGCGA AGTATAAAAC AGACTTGCGAC AGTATAAAAC AGACTTGCGCAC AGTATAAAAC AGACTTGCGCAC AGAATGTGAC AGAATGTGAC AGAATGTGAC AGAATGTGAC AGAATGTGAC AGAATGTGAC AGAATCAAAAG CCTTTCTTTGCC	GPOMLRELQE GPOMLRELQE GPOMLRELQE CAPGPCPPGY CEACPPGYSG PGFYGDQASG PGFGATACAA PGGAGCCAGC CATCAGCCAGC CATCAGCTAGG CGGGGAGTCAC CATCAGCTGG CCATCAGCTGG CATCAGCTGG CATCAGCTG CATCAGCTGG CATCAGCTG CATCAGCTGG CATCAGCTG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTG CATCAGCTG CATCAGCTG CATCAGCTG CATCAGC CATCAGCTG CATCAGCTG CATCAGCTG CATCAGCTG CATCAGCTG CATCAGCTG CAT	ITMAALQDVRD ACIQTESGGR PTHQGVGLAF CORGAQRFCP PCPEQCRC EDKWGDACDN DGIGDACDNC HDGQGDACDNC HDGQGDACDNC EGFEVANT KSSTGPGGL EGFELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GGCATGCCGG CCCGATGGT TTCTCGGAAG GTGTCTGGC ATTGCCAAAG CTACACGCG CCTAAATTA CACCAGATAC AGCATGCCGG CCCCATGGT CCGATGGT CCGATGGT CCGATGGC CCCAATGGT CCGATGCCGATGGT CCCAATGGT CCCAATGCCGG CCCCAATGGT CCCAATGCCGG CCCCAATGGT CCCCAATGGT CCCAATGCCGG CCCCAATGGT CCCAATGCCGG CCCCAATGGT CCCAATGCCGG CCCCAATGGT CCCAATGCCGG CCCCAATGGT CCCAATGCCGG CCACTGCCCAATGCCGG CCACTGCCCAATGCCGG CCACTGCCCAATGCCGG CCACTGCCCAATGCCGG CCACTTCCCCAAGGT CCCAAACCTCCCCAATGCCGG CCACTTCCCCAACGCTGCC GCACTTCCCCCACTGCCCGCCCCCCCCCC	WLRQQVREIT CSPCPAGFTG AKANKQVCTD DSSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 600 660 720 60 120 300 360 420 480 540 660 720 780 840 900
505560657075	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Accoding sequil GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTGAACCT AGGCTTGGTC CAGAGGCAGG GAAAAACGTG GAGTCACAA GAGTTATAAT CACAGTTGTG CACAGTTCAC TATCAAAGTG GGCTTCACTG TTACAAAGTG GGCTTCATG TTACCCTATG	LILLAALGASG ACGMQGVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GOEDADGDG GOEDAGG GOEDAGGC VIVINGGREI VMMKQMEQT PRNVGWKDKK NIWANLRYR 71 DNA sequid Accession Lence: 71 11 GGAAGGCAGC GGAGGCAGC GGAGGCAGC GGAGCTACAC GCAGCTCAG GCAGCTCAG GCAGCTCAG GCAGCTCAG GCAGCTCAG GCAGCTCAG TGGGCATCCC ACAGAATCGG ACACATACT ACAGAATCGG TGTGTCTCTT CTAAAATAAT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPT HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWPLQHRP CNDTIPEDYE Uence n #: NM_024 919 21 GGCAGCTCCA TCATCAT CAGCTGGGAA TTTCTGATAT AAGAAGGCAA TTTCTGATAT AAGAAGCAA ATTGCTGCAC AGTATAAAAG CCTGTATGAT AGAATGTGAC CCTGTATGAT AGAATGTAA CCTGTATGAT CCTGTATGAT CCTGTATGAT CAGTTGATAT CAGTTTATAT CAGTTGATCA CTGTTATTAT CGTGCCTCGGG CGTGCCTCGGG GGGCCTCGGG GGCCTCGGG GGGCCTCGGG GGCCCTCGGG GGCCCTCGGG GGCCCTCGGG GGCCCTCGGG GGCCCTCGGG GGCCCTCGGC GGCCCCCGGC GGCCCCCGC GGCCCCCC	GEGGAGTCAAA	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDD PENAEVILTD DFEGTFHVNT KSSTGPGQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGCATACTA AGCATACTG TGTATACATCA AGCATACTG TATATCATCA AGCATGCG CCCCGATGGT TTTCTGGAAGG CTGTCTTGTGC ATTGCCAAAGC CTACAGCTGC CATCCAAGTC CATCCAAGTC CCATCCAAGTC CATCCAAGTC CATCCAAAGTC CATCCAAAGTC CATCCAAAGTC CATCCAAAGTC CATCCAAAGTCACTGC CATCCAAAGTCACTGC CATCCAAAGTCACTGC CATCCAAAGTCACTGC CATCCAAAGTCACTGCC CATCCAAAGTCACTGCC CATCCAAAGTCACTGCC CATCCAAAGTCACTGCC CATCCAAAGTCACCTGCC CATCCAAAGTCACCTGCC CATCCAAAGTCACCTGCC CATCCAAAGTCACCTGCC CATCCAAAAGTCACCAACTGCC CATCCAAAAGTCACCAACACTACCAACACTACCAACACTACCACACACA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGG CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTT ATGAAATGTT CTTCTAAAGG AAGTGATGT TCCCCCAGCC TCTCCAATGC CCACAGGGGA TAAACTCAATG CACAGGGGA TAAACTCAATG CCACAGGCGC CATCTCAATGC CACAGGGGA TAAACTCAAAG CTCTCAGATGC CCATCGCC CATTGTTACA	120 180 240 300 360 420 600 660 720 60 120 180 300 360 420 540 600 720 780 840 900 960
505560657075	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDDDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequil GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGGGGAAA CAGGGGAAT CAGGTTTGAG TACCAGTTCACT TACACAGTCACT TATCAAAGTG GGCTTTTTGA TACCAGATCACT TATCAAAGTG GGCTTTCTCTG GGCTTTCAGC TATCAAAGTG GGCTTCTCTG TTACCTGATG ACAGGGGATCT	CESSION #: 11 LILLAALGASG ACGMQGVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDGI CDDDIDGDGI DDDQDQDGDG GQEDADRGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA sequid Accession LUCTURE ACCESSION	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL HQDSRDNCPT HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE UENCE I #: NM_024 919 21 GGCGGCAGAT CACTCATCAT CAGCTGGGAA TTTCTGATAA TTGCTGATCA ATGCTGGCAC AGAACTTGACC AGACTTTCTGTAG AGATTGACCA CCTGTATGAT AGAATGACCA GGTGCAAAAG CCTTTTCTTTGGC CCTGTATGAT AGATCAAAAG CTTTCTTTGGC GGGCCTCGGC GGGCCTCCA GGAATTGACCA GGAATTGACCA CCTGTATGAT GGTGCCTCGGC TTCACCACCA	GPOMLRELQE GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 31 CTCAGCCAGT CATCAGCCAGT CATTCGCGAG CGTGATACAA AGATGAGCTT TGGAGCCTTT GGGGCCTTC GGGGAGCCAAC CATGAAGGTT TGAAAATGT TGAAAATGT TGAGACCTT TGAGACCTT GGGAGCCAAC CATGAAGGTT TGAAAATGAC GCGGAGTCAC GCGCAGTCAC GCGCAGTCAC GCGCAGTCAC GCGCAAAAAGGT GCACAAAAAGG GCACAAAAAGG GCACAAAAAGG GCACAAAAAGG GATTGCCACACAAAAAGG GCACAAAAAAGG GATATGACCT	I TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECPPQCRKD EDKWGDACDN DGIGDACDNC DGIGDACDNC DGIGDACND DFERMEVILID DFEGTFHVNT KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGGAATCC TGGTGAGGG GGCAATGCCT TATATCATCA AGCATGCTGG TTCTCGGAAG CTCCGATGGT TTCTCGGAAG CTACAGCTGC ATTGCAAAGT ATTACATCA AGCATGCTGAAGG CTACAGCTGC CATGCAAAGT AGTTTTATAT	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT AGGACACTCCAT TGAGCTGCAC CATGATGAT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGGA TAAACTCAAA CTTCTACAATGT CAACAGGGGA TAAACTCAAA CTTCTAGACCC CATTGTACA	120 180 240 360 480 540 660 720 60 120 180 240 300 420 480 540 660 720 840 900 900 1020
505560657075	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Accoding sequ GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGGGCAGAA GGACTATAAT CACAGTGCACT TATCAAAGTG TACCAGTCACT TATCAAAGTG GGCTTCTCTG TTACCTCAGT AAATGAATTC AAATGAATTC AAATGAATTC AAATGAATTC AAATGAATTC MVPDTACVINE	LEASION #: 1 LILLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GOEDADRGDG GOEDADRGDG GOEDADRGDG UDDIDGDRI DSDQDQDGDG GOEDADRGV VVVLNQGREI VVMWQMEQT PRNVGWKDKK NIIWANLRYR 10 DNA sequid LONG SCORT SC	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VOTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE LEENCE I #: NM_024 921 GGCAGCTCCA TCAGCAGAA TTGCTGATCA AGAAGGCAA TTGCTGATCA AGGACTTGCGA AGTATAAAAC AGACTTGCGA AGTATAAAAC CCTGTATGAT AGAACGCAA AGAATGTGCA CCTGTATGAT AGAATGTCAC CCTGTATGAT AGAATGTCAC CCTGTATGAT AGAATCAAAAG CCTTTCTTTGC GGCCTCGGC TTCACCACC GGTCCCGGC TTCACCACC GGTCTCGGAGT TTCACCACC GGTCTCGGAGT	GPOMLRELQE GPOMLRELQE GPOMLRELQE CAPGFCPGYSG PGFYGDQASG PGFYGDQA PGFYGDQA PGFYGDASG PGFYGGAGGCTTCG PGGAGCCAGC PGGAGCAGC PGGAGCCAGC PGGAGCAGC PGGAGCACC PGGAGCAGC PGGAGC PGGAGC PGGAGC PGGAGC PGGAGC PGGAGC PGGAGCAGC PGGAGC PGGAGC P	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CORGAQRFCP PCPEQCRKD EDKWGDACDD DGIGDACDDC DGIGDACDDC DGIGDACDC DGIGDACDC DGIGDACDC EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGAA GGTGAATCC TGGCTGAAGG TCGGAGCAGG GGCATTCTCGGAAG CTACAAGTAC AGCATTCAGAAG AGTGCTAAAGT AGCATGCCAAAGT AGCATGCCAAAGT AGCATGCCAAAGT AGCATGCCAAAGT AGTTTTATAGT AGTTTTATAGT AGTTTTATAGT AGTTTTATAGT AGTTTTATAGT AGTTTTATAGT AGTTTTATATAGAAGT AGTTTTATAGT AGTTTAGAAGT AGTTTTATAGT AGTTTAGAAGT AGTTTTATAGT AGTAAGAAAAC AGCAAGAAAAC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT ATGAAATGTT TCTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGGA CTACACGCAT CAACAGGGGGA CTCTCAATAC TCTACAATGT CAACAGGGGA CTCTCAGCCC CATTGTTACA CTCTCAGCCC CATTGTTACA CTCTCAGCCC CATTGTTACA TTCTGGGAGG AAAAAGAAGG	120 180 240 300 360 480 540 660 720 60 120 360 480 540 660 720 780 960 960 900 900 900 1080
50 55 60 65 70 75	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACT AGGCTTGGTC CAGGGGGAAT GGACTATAAT CACAGTGGTC CAGCTTTGGG TACGATCACC TATCAAAGGGATCAC TATCAAAGGGGATCAC TATCAAAGGGGATCAC ACAGGGGTTCAC GGCTTCTGG GCCTTCTGG TTACCTGATG ACAGGGGATCT AAATGAATTC CAAAAGCAGA	LEASION #: 11 LITLAALGASG ACGMQGSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio. 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPT ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL VYMQANPFRAV SYRWFLQHRP CNDTIPEDYB 1 GGCAGCTCCA TGGGGCAGAT CACTCATCAT CAGTTGGAC ATGATGACA ATGCTGGCA ATGTTGATCA AGAATTGACC CCTGTATGAT AGAACTAGAC CCTGTATGAT AGAACTAGAC CCTGTTAGAT AGAACTAGAC CCTGTTAGAT CCTGTCTGGG CTTTCACCACCA CTTCACCACCA CTTTCACCACCA CTTTCACCACCA CTTTCACCACCA CTTTCACCACCA CTTC	GAGAGATAAA GAGAARAAAA GARAGAGA GARAGAGAG GARAGAG GARAGAGAG GARAGAG	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDD DFENAEVILTD DPEGTFHVNT KSSTGPGQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA AGATGCCT TGAGTGAGAGGCGG GCACTTCTGGAGGGTTTCTGGAGGGAGGGGAG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDDDGVPDS FRAFQTVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG GCTGGGAACC GCATCATCAT GACACTCCAT AGAGTGTTTT ATGAGATGT TCTTTGCGGCT CTCTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGGA TAAACACAGA TAAACTCAA TTTTGGGAGG AAAAAGAAG TATTTGAGT AAAAGATGT TTTTGGGAGG AAAAAAAGATGT TTTTGGGAGG AAAAAAAGATGT TTTTTGGGAGG AAAAAAAGATGT TTTTTGGGAGG AAAAAAAGATGT TTTTTTTT	120 180 240 300 360 420 600 660 720 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140
505560657075	Protein Acci MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac. Coding sequ GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACT AGGCTTGGTC CAGGGGGAAT GGACTATAAT CACAGTGGTC CAGCTTTGGG TACGATCACC TATCAAAGGGATCAC TATCAAAGGGGATCAC TATCAAAGGGGATCAC ACAGGGGTTCAC GGCTTCTGG GCCTTCTGG TTACCTGATG ACAGGGGATCT AAATGAATTC CAAAAGCAGA	LEASION #: 11 LITLAALGASG ACGMQGSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio. 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RCSFQCGPCQ GNGILCGRDT VPNEKDNCPT ENQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL VYMQANPFRAV SYRWFLQHRP CNDTIPEDYB 1 GGCAGCTCCA TGGGGCAGAT CACTCATCAT CAGTTGGAC ATGATGACA ATGCTGGCA ATGTTGATCA AGAATTGACC CCTGTATGAT AGAACTAGAC CCTGTATGAT AGAACTAGAC CCTGTTAGAT AGAACTAGAC CCTGTTAGAT CCTGTCTGGG CTTTCACCACCA CTTCACCACCA CTTTCACCACCA CTTTCACCACCA CTTTCACCACCA CTTTCACCACCA CTTC	GAGAGATAAA GAGAARAAAA GARAGAGA GARAGAGAG GARAGAG GARAGAGAG GARAGAG	TMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDD DGIGDACDD DFENAEVILTD DPEGTFHVNT KSSTGPGQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA AGATGCCT TGAGTGAGAGGCGG GCACTTCTGGAGGGTTTCTGGAGGGAGGGGAG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT ATGAGTGTTTT ATGAGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGGA TAAACTCAAA CTCTACAATGT CAACAGGGGCA TATTAGAAGT TATTGGGACG AAAAAGAGC TATTAGAAGT TATTAGAAGT CCCTGGTTTT	120 180 240 300 360 420 540 600 660 720 60 120 360 420 480 540 660 720 780 960 960 960 960 960

5	CATTGGCAAA TATCGGGCAC CTGATGGGAT CAAGCCAAGT TAGATCTCCA TGAAGCACAC AATGAAGCTT GTTAACCACT	TAAGCATTCT CAGGATAACA TATCTTCAGC TCTGTAAGAG GACCCTGCCT ACAGACTTTT TGAAGGAAAA GCCTTCCTGG TAGAGTTCTG	AGAGGGGAGC GTCTCTTTGG TCTCTCAGTG TCTCTCAGTG TGTTGAGCT TAATGCCTGA GGCCACAATT GAAAGCAAGG GAATACTTTG ACCTTGGAGC ATCGTTCAAG	CTGCTGCCTC AACAGAGTTG TCTAAGTTTC GTTCTAGCTC CAAATTAAGG ACAATGACTG TTTCCAGCCC CACGGTGACT	AGCACAGAGA ACAAGGCCTA TTTCCCTTCA AGGTTTTCTT CAACAAACAT CTTGAATTGA CCTTCCCACA GTATTACATG	GCCAGAACTC TGGGAAATGC TTCTACCCTG ACTCTGAAT ATACCTTCCA GGCCTTGAGG CTCTTCATGT TTGTTATAGA	1260 1320 1380 1440 1500 1560 1620 1680 1740 1800
	Seq ID NO:	72 Protein	sequence				
15	Protein Acc	ession #: 1 11	TP_078902 21	31	41	51	
	i	1	1	1	1	1	
20	DIKLSDIVIQ QLTDAGTYKC WASQVDQGAN	WLKEGVLGLV YIITSKGKGN FSEVSNTSFE	GAIALIIGFG HEFKEGKDEL ANLEYKTGAF LNSENVTMKV CVSSFFAISW	SEQDEMFRGR SMPEVNVDYN VSVLYNVTIN	TAVFADQVIV ASSETLRCEA NTYSCMIEND	GNASLRLKNV PRWFPQPTVV	60 120 180 240
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	1	11	21	31	41	51	
	GGGAGGGAGA	GAGGCGCGCG	GGTGAAAGGC	GCATTGATGC	AGCCTGCGGC	GGCCTCGGAG	60
20	CGCGGCGGAG	CCAGACGCTG	ACCACGTTCC	TCTCCTCGGT	CTCCTCCGCC	TCCAGCTCCG	120
30			CCATGCGACC TGCTGCTGCA				180 240
			CGCAGCTCCG				300
			CAGGAGTGCC				360
35			TCCCAGGTCG AGTCCTGGAC				420 480
55			TTGGGAAAAT				540
			TGTTCAGTGG				600
			CATTCAATGG AAGGAAGCCC				660 720
40			TTTGTGAAGG				780
			ATTACCCAAA				840
			AACTACCAAA ATGGTTCACT				900 960
4.0	CATCTGAATG	AAAAGCAAAG	CTAAATATGT	TTACAGACCA	AAGTGTGATT	TCACACTGTT	1020
45			TTTTGCTTCA				1080
			TAGTCACATT AGTATAGCAT				1140 1200
			AGAATTTTTT				1260
50	CAACCTTAAA	ААААААААА	AAAA				
20	Sea ID NO:	74 Protein	semience				
		cession #: 2					
	1	11	21	31	41	51	
55	MPPOGPAASP	ORINGIALIA	LLQLPAPSSA	SEIDKGKOKA	OLEOREVVDI.	YNGMCLOGPA	60
			PGRDGFKGEK				120
			FSGSLRLKCR				180
	LPK	THRTSSVEGL	CEGIGAGLVD	VAIWVGTCSD	YPKGDASTGW	NSVSRIIIEE	240
60							
		75 DNA seq	uence n #: BC0104	23			
		uence: 248.		23			
65	1	11	21	31	41	51	
05	CACAGOGTGG	CARGCAGCTC	TCCCCCACCT	CCCACCTCCC	 Gather Coolet	TCTTGGGGGT	60
						AGTGGAGACC	120
						CTTATTCAAG	180
70						CAGTCTGCCT	240 300
, •						AGACCTCAGA	
						GAGGGGACTC	420
						GCGCCCAGGA AGGGCCGCGT	
75						GCAACGCAGT	
	GCAGGCGGAT	GAGGGCGAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCCCCCCC	GCAGCTTCCA	660
						CTGGTCCAGC GCAGCCCAGC	720 780
0.0						CCTTCAAGCA	
80	CTCCCGCTCT	GCTGCCGTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
						GGATCACCCA	960 1020
						AGCCCCTCC	1080
05	CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCCAGT	GGGGTACGAG	TGGATGGGGA	1140
85	CACTTTGGGC	TTTCCCCCAC	TGACCACTGA	GCACAGOGGC	ATCTACGTCT	GCCATGTCAG	1200

	CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTTCTTGACC	CCCAGGAAGA	1260
	CTCTGGGAAG	CAGGTGGACC	TAGTGTCAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCGC	1320
		TGCCTTCTGG					1380
_		ATGACCCAGA					1440
5	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
		GGCCACCCTG					1560
		GGCCGCAGTT					1620
	TGAACTGCTG	TCTCCAGGCT	CTGGGGGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
	CAAACAGGCC	ATGAACCATT	TTGTTCAGGA	GAATGGGACC	CTACGGGCCA	AGCCCACGGG	1740
10		TACATCAATG					1800
10							
		CTCCTTCTGT					1860
	ACACCCCCAT	TTCTTGCGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
		TTCATCGGGA					1980
1.5		GTGCATGTGT					2040
15	TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
	AACTCAACTC	TGGTGTATGT	CCCACCCCAT	THYSAGTYSGTT	GOGTGGGCAA	CACTGTCAGG	2160
		TGTGTCATGT					2220
	CAGACCCCAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
	CAGACCCAGG	TGTGCGGGCA	TAGCTGGAGC	TEGAATETEE	CTCCCCTCTC	AGGGAACCTG	2340
20							
20		CTTCGGAGCC					2400
	GAGGCTTGAA	CTGTTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
		TGTAAATATA					2520
		TTTTTCTTTT					2580
~ ~	TTTTATTTT	ATTTTTTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCCTGT	2640
25	CTCTDAAAAA	ACCAAAACCC	AAAAAAAAA	AAAAAAAAA			
	0.01.0100.			***************************************			
	Seq ID NO:	76 Protein	sequence				
	Protein Acc	ession #: A	AH10423				
		11	21	31	41	51	
30	1	<u>†</u>	21	-	41	7.	
<i>3</i> 0	1	1			1	1	
	MPLSLGAEMW	GPEAWLLLLL	LLASFTGRCP	AGELETSDVV	TVVLGODAKL	PCFYRGDSGB	60
		DAGEGAOELA					120
		TFPAGSFQAR					180
	VTWDTEVKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPGL	LQDQRITHIL	240
35		RGLEDONLWH					300
55							
	GFPPLTTEHS	GIYVCHVSNE	FSSRDSQVTV	DVLDPQEDSG	KQVDLVSASV	VVVGVIAALL	360
	FCLLVVVVVL	MSRYHRRKAQ	OMTOKYEEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
		SSCSVMSEEP					480
				41/01/12/100	201 000.000	PPPERPORUE	
40	AMNHFVQENG	TLRAKPTGNG	IYINGRGHLV				
40							
	Sea ID NO:	77 DNA sequ	ience				
				474 7			
	NUCTET C VC	rd wcceseron	n.∦: NM_003∘	4/4.2			
	Coding sequ	ence: 37					
	Coding sequ			31	41	51	
45		ence: 37	3036		41 	51 l	
45	1	ence: 37 11 	3036 21 	31 	1	1	60
45	1 CACTAACGCT	ience: 37 11 CTTCCTAGTC	3036 21 CCCGGGCCAA	31 CTCGGACAGT	 TTGCTCATTT	 ATTGCAACGG	60
45	1 CACTAACGCT	ence: 37 11 	3036 21 CCCGGGCCAA	31 CTCGGACAGT	 TTGCTCATTT	 ATTGCAACGG	60 120
45	1 CACTAACGCT TCAAGGCTGG	lence: 37 11 CTTCCTAGTC CTTGTGCCAG	21 CCCGGGCCAA AACGGCGCGC	31 CTCGGACAGT GCGCGACGCA	 TTGCTCATTT CGCACACACA	 ATTGCAACGG CGGGGGGAAA	
45	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC	3036 21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC	TTGCTCATTT CGCACACACA GCGGGCCGTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT	120 180
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA	lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG	3036 21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC	120 180 240
45 50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG	3036 21 CCCGGGCCAA AACGGCGCC TAGAAGAGCT CAGGAATCC CGCTCGCCGC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG	120 180 240 300
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG	3036 21 CCCGGGCCAA AACGGCGCC TAGAAGAGCT CAGGAATCC CGCTCGCCGC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG	120 180 240
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCCCGCGTGG GCGACGATGG	ience: 37 11 CTTCCTAGTC CTTGTGCCAG CATGAAAGGC CTCGCGAGG GATGGTGCAG CAGCGCGCCC	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG	120 180 240 300 360
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACGATGG GCCGGTGCTC	ience: 37 11	3036 21	31 CTCGGACAGT GCGCGACGCA CAGCGGCGCGC CTCCGGTCGC CGGGCCCGAC TCCCCCGCCC CGAGGGGTGA	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA	120 180 240 300 360 420
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCGCGTGG GCGACGATGG GCCGGTGCTC GCTGATGAAG	lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TGCTGGCGCC TTGTCAGTGC	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTC CTGCAGGCC CTCTGTTCGG	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGGCCCGAG TCCCCGCCC CGAGGGGTGA AGTGGGGACC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGCC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGTGGCCTG CGAAGGAAGA AGTGAAGACG	120 180 240 300 360 420 480
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCGCGTGG GCGACGATGG GCCGGTGCTC GCTGATGAAG	ience: 37 11	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTC CTGCAGGCC CTCTGTTCGG	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCGCCC CGAGGGGTGA AGTGGGGACC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGCC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGTGGCCTG CGAAGGAAGA AGTGAAGACG	120 180 240 300 360 420
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCGCGTGG GCGGTGCTC GCTGATGAAG TTCGACTCCA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCGAGG GATGGTGCAG CAGCGCCC TGCTGCGCCC TTGTCAGTCC AGAATCATCCC	3036 21	31 CTCGGACAGT GCGCGACGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCC CGAGGGTGG AGTGGGGACC AATATTCGAC	TTGCTCATTT CGCACACACA GCCGGCCGGG GACGCCCGGC AGCTGCTGCA GCCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA	ATTGCAACGG CGGGGGAAA CGCGAGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG GCAAGGAAGA AGTGAAGAAGA AAGCAAAGAA	120 180 240 300 360 420 480 540
	1	ience: 37 11	3036 21	31 CTCGGACAGT GCGCGACGCA CAGCGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCC CGAGGGGTGA AGTGGGGAC AATATTCGAC CTCATTGCCA	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC	ATTGCAACGG CGGGGGAAA CGCGAGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAGA AGTGAAGAGA GGAAACCCAC	120 180 240 300 360 420 480 540 600
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCGGTGCTC GCTGATTGAAG TTCGACTCCA TTGACTCAA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTGGCGCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGCTCGCGG GCTGCCGTG CTGCAGGGC CTCTGTTCGG AAAATGATGCTG AAATGAAGGT TGTCTCCTC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGCC CGGGCCCGAG TCCCCGCC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCCA GCTCGAAATT	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAGC AAGCAAAGA TCTGGGTCAC TCTGGGTCAC	120 180 240 300 360 420 480 540 600 660
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCGGTGCTC GCTGATTGAAG TTCGACTCCA TTGACTCAA	ience: 37 11	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGCTCGCGG GCTGCCGTG CTGCAGGGC CTCTGTTCGG AAAATGATGCTG AAATGAAGGT TGTCTCCTC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGCC CGGGCCCGAG TCCCCGCC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCCA GCTCGAAATT	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAGC AAGCAAAGA TCTGGGTCAC TCTGGGTCAC	120 180 240 300 360 420 480 540 600
50	CACTAACGCT TCAAGGCTGG CTITITITAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCGGTGCTC GCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCGAGG GATGGTGCAG CAGGGGCCC TGCTGGGGC TTGTCAGTGC AGAATCATCC ATGTGAAAG ATGGACAG ATGGACAGA ATGGACATGT	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG CTGCTGAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT	31 CTCGGACAGT GCGCGACGCC CTCCGGTCGC CGGGCCCGAC TCCCCCGCCC CATGGGGACA AGTGGGGAC AATATTCGAC CTCATTGCCA GCTCGAAATT TCTGAATCAG	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCCGCC AGCTGCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTTCTC	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAAG AGTGAAGAA GGAAACCAA CGCACGTCT CCTGGGTCAC CAGCACGTGT	120 180 240 300 360 420 480 540 600 660
50	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGACCTGA GCCGCGTGG GCGACGATGG GCGACGATGA GCCGGTGCTC GCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACC TCTGGTCTCA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCGCAGG GATGGTGCAG CAGCGCCC TGCTCAGCGCC ATCTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACAGTA GGGACTTAT	3036 21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTGCCGCG CTTGCCGGG CTTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCT ACGGGGATAT TGTGTTTGAA	31 CTCGGACAGT GCGCGACGCG CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCCC CGAGGGGTGC AATATTCGAC CTCATTGCA GCTCGAATAT TCTCGATTCAG AATGAAAGCT	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCTAGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAGA AGTGAAGAGC TCTGGGTCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA	120 180 240 300 360 420 480 540 600 660 720 780
50	1	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCCCC TTGTCAGTGC AGAATCATCC ATCTGGAAA ACGCTACTGAAAG ACGGTACTGA ACGGACTTAT ACAGATACAA	3036 21 CCCGGGCCAA AACGCGGGC TAGAAGAGCT CAGGAAATCC GCTCGCGG GCTGCCGTG CTGCAAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTCCCAA	31 CTCGGACAGT GCGCGACGCA CAGCCGGCCCGAG TCCCCGCCC CGAGGGGGAAC AGTGGGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCACTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGA TGAAAAGCGT	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCT CGAAGGAGA AGTGAAGAGA AGTGAAGAGA AGGAAAGA AGGAAAGCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA	120 180 240 300 360 420 480 540 660 720 780 840
50	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGTGCTC GCTGATGAAG TTCGACTCCA TGTTCTGCAC TGTTACTACC TCTGGTTCTCA AGTGCAACCA TGTGCAACCA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTCCCGG GCTGCCGGG CTGCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTCCCAA ACCAAACCTC	31 CTCGGACAGT GCGCGACGCA CAGCAGCA CAGCGCGCC CGAGGGCCAA AGTGGGACC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAAGC GCTCAAAGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCTCATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCA ACACGGTAAT CAGTCAGTCT ATGTCTTAGA ATGAAAAGGGT ATGTGTTTCC	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAGA AGTGAAGAGC TCTGGGTCAC TCTGGGTCAC CAGCACGTGT ACCAATGAA ACCACCTCT	120 180 240 300 360 420 480 540 660 720 780 840 900
50	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGTGCTC GCTGATGAAG TTCGACTCCA TGTTCTGCAC TGTTACTACC TCTGGTTCTCA AGTGCAACCA TGTGCAACCA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTCCCGG GCTGCCGGG CTGCTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTCCCAA ACCAAACCTC	31 CTCGGACAGT GCGCGACGCA CAGCAGCA CAGCGCGCC CGAGGGCCAA AGTGGGACC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAAGC GCTCAAAGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCTCATGGAA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCA ACACGGTAAT CAGTCAGTCT ATGTCTTAGA ATGAAAAGGGT ATGTGTTTCC	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAGA AGTGAAGAGC TCTGGGTCAC TCTGGGTCAC CAGCACGTGT ACCAATGAA ACCACCTCT	120 180 240 300 360 420 480 540 660 720 780 840
50	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCGGGTGGG GCGACGATGGT GCTGATGAAG TTCGACTCAAA TATCTGCAAG TGTTACTACA TGTGGATCAC TCTGGTCTA AGTGCAACCA AGTGCAACCA CCAGACATGGG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGG CTCGCCGAGG GATGGTGCAG CAGCGCCCC TGCTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGCACTAT ACAGCACAC CAGGAAGGC CAGAGAAGGC	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGT GCTGCCGGT AGAAGAGT TGTCTCCGAAGGCC TGTCTCGGAAGT TGTCTCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCAC TAAAAGAGAG	31 CTCGGACAGT GCGCGACGCA CAGCGCGGG CTCCGGTCGC CGGGCCCGAC AGTATTCGAC ACTATTCGAC GCTGCAATAT TCTGATTCAG AATGAAAGCT GCGAAGAAGA ACCCTCAAGG	TTGCTCATTT CGCACACAC GCGGCCGCGG AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCATTCAC ACACGGTAAT CAGTCATCT ATGTCTTAGGA TGAAAAGCGT TGAAAAGCGT TGAAAAGCGT ATGTCTTCCC CAACTAAGTA	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG GGAAGGAAGA AGTGAAGAAG AGTGAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAACTGAAA ACCACCCTCT TGTGGAGCTG	120 180 240 300 420 480 540 660 720 780 900 960
50	1	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CAGCGCCC TGCTGCGCCC TTGTTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATTAT ACAGATACAA ATCACAACAC CAGACAACCC CAGCACACCC CAGACACCC CAGACACCC CAGACACCC	21 CCCGGGCCAA AACGCGGCCAA AACGCGGCGC TAGAAGAGCT CAGGAAATCC CCTCTCGCGG CTGCAGGCC CTCTGTTGGA AGAAGTGCTG AAATGAAGGT TGTCTCCCTA ACGGGGATAT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG	31 CTCGGACAGT GCGCGACGGC CAGCGGGGGC CTCCGGTCGC CGGGCCCGAG TCCCCGGCC AATATTCGAC CTCATTGCA GCTCGAAATT TCTCATTCAG AATGAAAGCT GCGAAGAAGC GCTGAAAGAA ACCCTCAAGGA ACCCTCAAGGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGTCATTCAC ACACGGTAAT CAGTCATTAGAA TGAAAAGGGT ATGTCTTAGA ACACTAAGTA AAGATCTGGAA AAGATCTGGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGCTCGGC CTGAAGGCCG GCTGACGCCTG CGAAGGAAGA AGTGAAGACA AGCAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCCTCT TGTGGAGCTC AAAAGTTAAG	120 180 240 300 420 480 540 660 720 780 900 960 1020
50	CACTAACGCT TCAAGGCTGG CTTTTTTAAA GCCCGCGTGG GCCGCGTGCT GCTGATCAAG TTCGACTCCA TGTCCAAG TGTTACTACC TCTGGTTCTCA AGTGCAACCA TGTGCATCACC CGACATGGG CGACATGGG CGACATGGG CAGCATGGG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TTGTCAGTGC ATGTAGTAGCA ATGTAGTAGTAGCA ATGTAGTAGCA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGCAG CAAGAAGCCG TAGAGATGCCG TAGAGATTGC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGCTGCCGTG CTGTGCCGTG AGAAGTTCTG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTGTTTCAA ACTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG TAATCACGTT	31 CTCGGACAGT GCGCGACGCA CAGCAGCA CAGCCGCGCC CGAGGGGGACA AGTGGGGACC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAG GCTCAAAGA ACCCTCAAGA ACCCTCAAGA ACCCTCAAGA ACCATCAAGAA	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCCGCC AGCTGCTAC GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCAGTCA ACACGGTAAT CAGTCATCTA ATGTCTTAGA ATGTCTTAGA ATGTCTTAGA AGACTACGCA ACACTAAGTA AAGATCTGGA AAGACCACT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CGAAGGAAGA AGTGAAGACGA AGTGAAGACCA TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCACCTCT TCTGGAGCTCA TCTGGGGATCA ACCACCTCT TCTGGAGCTG AAAAGTTAAG GAACATTCGG	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080
50 55 60	CACTAACGCT TCAAGGCTGA CCGAGCTGA GCCGCGTGGG GCGACCATGG GCGACCATGG GCGACCATGG TTCGACTCCA CTGATCAAAG TATCTGCAAG TGTTACTACA TGTGGATCAC TCTGGTCTAA AGTGCAACCA CGACATGGG CGACCATTGA CAGACATGGG CAGCCATTGA ATCCTCTGG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCGAGG GATGGTGCAG GATGGTGCAG CAGGGGCCC TTGTCAGTGC ATCTGGAAAA ATCATCAT ACAGTACTA ACAGTACTA ACAGATACAA CAAGAAACAG CAAGAAACAG CAAGAAACAG TAGAGATTGC TAGGACAACCG TAGAGATTGC TAGGACATCG TAGGAGATTGC TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATTGC TAGGCGTGGA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTTGCCGGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATTTTGAA ACTCTTCCCA TAAAAGAGAG TAATCACGTT AGTGTTGAA	31 CTCGGACAGT GCGCGACGC CAGCGCGGC CTCCGGTCGC CGGGCCCGAC CGAGGGGTGA AGTGGGGTA AGTGGAGAC ATATTCAC ATTGATTCAG ATTGAATT TCTGATTCAG AATGAAGAGC GCTGCAAGAG GCTGCAAGAG ACCCTCAAGG AGCAGGAAGAGC AGCAAGTTTT GACAAGACT	TTGCTCATTT CGCACACACA GCGGCCGCGG GACGCCCGGC AGCTGCTGCA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTTTA ATGTCTTAGA TGAAAAGGT ATGTCTTAGA ACAGACCACT AAGACCACT AATGCCACT AATGCCACT AATGCCACT AATGCCACT AATGCCACT AATGCCACT	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTAGCCCTG GCAAGGAAGA AGTGAAGAA AGTGAAGAA AGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCACCCTCT TGTGGGGATCA AAAGTTAAG GAAATTCGG AAGTTCAGAAC AAGTTAAG	120 180 240 360 420 480 540 600 720 780 840 900 900 1020 1080
50 55 60	CACTAACGCT TCAAGGCTGA CCGAGCTGA GCCGCGTGGG GCGACCATGG GCGACCATGG GCGACCATGG TTCGACTCCA CTGATCAAAG TATCTGCAAG TGTTACTACA TGTGGATCAC TCTGGTCTAA AGTGCAACCA CGACATGGG CGACCATTGA CAGACATGGG CAGCCATTGA ATCCTCTGG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCGAGG GATGGTGCAG GATGGTGCAG CAGGGGCCC TTGTCAGTGC ATCTGGAAAA ATCATCAT ACAGTACTA ACAGTACTA ACAGATACAA CAAGAAACAG CAAGAAACAG CAAGAAACAG TAGAGATTGC TAGGACAACCG TAGAGATTGC TAGGACATCG TAGGAGATTGC TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATCG TAGGACATTGC TAGGCGTGGA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTTGCCGGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATTTTGAA ACTCTTCCCA TAAAAGAGAG TAATCACGTT AGTGTTGAA	31 CTCGGACAGT GCGCGACGC CAGCGCGGC CTCCGGTCGC CGGGCCCGAC CGAGGGGTGA AGTGGGGTA AGTGGAGAC ATATTCAC ATTGATTCAG ATTGAATT TCTGATTCAG AATGAAGAGC GCTGCAAGAG GCTGCAAGAG ACCCTCAAGG AGCAGGAAGAGC AGCAAGTTTT GACAAGACT	TTGCTCATTT CGCACACACA GCGGCCGCGG GACGCCCGGC AGCTGCTGCA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTTTA ATGTCTTAGA TGAAAAGGT ATGTCTTAGA ACAGACCACT AAGACCACT AATGCCACT AATGCCACT AATGCCACT AATGCCACT AATGCCACT AATGCCACT	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTAGCCCTG GCAAGGAAGA AGTGAAGAA AGTGAAGAA AGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCACCCTCT TGTGGGGATCA AAAGTTAAG GAAATTCGG AAGTTCAGAAC AAGTTAAG	120 180 240 360 420 480 540 600 720 780 840 900 900 1020 1080
50	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGACCTGG GCGACGATGG GCGCGGTGGT GCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA CTGGTCTCA AGTGCAACCA TGTGGATCAC CAGACATGAG GTGATCATCA CAGGCATTAA ATCGTGTTGG CCATTAG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCGAGG GATGGTGCAG CAGCGCCCC TGCTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGACATTAT ACAGATACAA ATCACAACAC CAAGAAGGCA CAGACAACCG TAGGCGTGGA CAGACAACCG TAGAGATTGC TAGGCGTGGA AGCCTCCATGA	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGGC CTGTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTCAA ACCAAACCTC TAAAAGAGAG AGAGTTTCAG TAATCACGTT TAGTGTGGAAT ATTTCTGGAC	31 CTCGGACAGT GCGCGACGCA CAGCGCGGC CTCCGGTCGC CGGGCCCGAG AGTGGAGAGT AGTGGGGACC AATATTOGAC CTCATTGCA AGTGAAAGT TCTGAATCAG AATGAAAGCT GCGAAGAAGA ACCCTCAAGG AGCCAAGGAA ACCCTCAAGG AGCAAGTTT GACATGAACA TGGAAGAAGA TGGAAGGAAGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGTCATTACAC ACACGTAAT TGAAAAGGGT ATGTCTTAGA ATGACTATGATACC CAACTTAAGA AAGACCACT AATGCTCTG AATGCTCT AATGCTCTT AATGCTCTT AATGCTCTT TGAAGACCACT TGAAGACCACT TGAAGCTCTT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCT TGAAGCTTCTT TGAAGCTTCT TGAAGCTTCTT TGAAGCTTCTT TGAAGCTTCTT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTGACGCCTG CGAAGGAAGA AGTGAAGAGA AGGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCTCT TCTGGGGCTG AAAAGTTAAG GAACATTCAG GAACATTCAG AACATTCAG AACATTCAG AACATTCAG AACCATCC ACCACCCTCT AAAAGTTAAG GAACATTCAG AACATTCAG AACATTCAG AACCATCC ACCACCCTCT AAAAGTTAAG AACATTCAG AACATTCAG AACATCAGAAA	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1200
50 55 60	1	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCCCC TTGTCAGTC ATGTACATC ATGTACATC ATGTACATC ATGTACATC ATGGACATT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGACATGT TAGGACATGT ACAGATACAA ATCACAACAC TAGAGATGCA ATGCCCAGCT AGAGATTGC TAGAGATGCA ATGCCCAGCT AGAGATGCA ATGCCCAGCT AGAGATGCA ATGCCCAGCT AGAGATGCA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTGCCGTG CTGCCGTG CTGCTATCGG AAATGCTT AAATGAAGT TGTCTCCCT ACGGGGATAT TGTGTTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG TAATCACGT AGTGTTGAAT AGTGTTGAAT ATTCTCGAA	31 CTCGGACAGT GCGCGACGCA CAGCCCGGCCCCGACGGA AGTGGGGGCCAA AGTGGGGACC AATATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAG ACCCTCAAGG ACGCAAGAAG ACCATCAAGG AGCAAGAAG AGCAAGAAG GACAAGTTTT GACATGGACA GGTTAATTCA	TTGCTCATTT CGCACACA GCGGCCGGG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCAGTCT ATGTCTTAGA TGAAAAGGGT ATGTGTTTCC CAACTAAGT AAGATCTGGA ACAGACCACT AATGCTCTGT TGAAACTAA AAGATCTGGA ACAGACCACT AATGCTCTGT TGAAGCTTCTT AAGGCACCC AATGCTCTGT AAGGCACCAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCT CGAAGGAGA AGTGAAGACC AAGCAAGAAG AGCAACGAA CCAGCCTCT TGTGGGTCAC TGTGGGTCAC ACCACCTCT TGTGGAGCTC AACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AAGTCAAGAA CACCCCACACCTCT CTGGAGCTG AAAGTTAAG CACCCCACCACCACCACCCACCCACCCACCCACCCCCT TGTGGAGCTG AAAAGTTAAG CAACCACCCACCACCCACACCACCCACCCACCCACC	120 180 240 300 360 420 540 600 660 720 780 840 900 1020 1080 1140 1260
50 55 60	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCCGCGTGG GCGACCATGG GCGACCATGG TTCGATCATAA TATCTGCAAG TGTTACTACC TCTGGTCTA AGTGCAACA CGGACATGGG CTGATCAGA ATGCGATCAC CAGACATGGG CAGCGATTAA ATCGTGTTCCACA CAGCATTAA CCCATGACA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGCGCGCC TTGTCAGTGC ATGTCAGTGC ATGTCAGTAG ATGGACATGT ACAGATACTA ACAGATACAA ATCACAACAC CAAGAAGGCA CAGACAACCG TAGGCGTGGA TAGGCATGGA ATGCCATGA ATGCCATGA ATGCCATGA ATGCCATGA ATGCCATGA TAGGCCATGTG TGAGCCATGTG	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTCGCGGC GCTGCCGGG CTGCTGTTCGG AGAAGTTCTG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACTGTTCGAAGGT TAAAAGAGAG TGAATGAGT TAGTTTGGAAT ATTTCTGGAAT CTTCAGTGGAAT ATTTCTGGAGG	31 CTCGGACAGT GCGCGACGCC CGGCGCCCCC CGAGGGTGA AGTGGGGAC AATATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGCT TCTGATCAG ACCTCAAGG ACCCTCAAGG ACCTCAAGG ACCACAAGA ACCTTCAAGG ACGACAAGAAGC CGTGCAAAGT TCTGATTTAT TCTGATTTAG ATTGAAAGCT TCTGATTTAG ATTGAAAGCT TCTGATTTATTCAG AGCAAGGAAGA CCTTCAAGG AGCAAGGAAGA CCTTCAAGG AGCAAGGAAGT TTTATTTTCC CAGTCTTGGGG CAGTCTGGGG CAGTCTTGGGG CAGTCTGGGG CAGTCTGGGGG CAGTCTGGGGGGGGGG	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCAGTCA ACACGGTAAT ATGTCTTAGA ATGTCTTAGA AAGATCTGGA AAGATCTGGA AAGATCTGGA AAGACCACT AATGCTCTT TGAAGCTCT TGAAGCTCT TGAAGCTCT AAGGCACC GAATTGTCAT	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGACC AGCAACGAC TCTGGGTCAC CCAGCACGTCT ACCAATGAAA ACCACCTCT TCTGGGGTCA AACCCACT TCTGGGGTCA AACCCACT TCTGGAGCT AAAAGTTAAG GAACATTCGG AAGTCAGGAC ACCTCCCCAA ACCTCCCCAA CCTCCGCAAT CATCGGCATG AAAAGTTAAG GAACATTCGG AAGTCAGGAC ACCTCCCCAAT ACCACCCTCT CGGACATCAGGAC ACCTCCCCAAA ACCTCGCCAAT CATCGGCATT GGACCATTCA	120 180 240 300 360 420 480 540 660 720 840 900 960 1020 1080 1140 1200 1260 1320
50 55 60	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCCGCGTGG GCGACCATGG GCGACCATGG TTCGATCATAA TATCTGCAAG TGTTACTACC TCTGGTCTA AGTGCAACA CGGACATGGG CTGATCAGA ATGCGATCAC CAGACATGGG CAGCGATTAA ATCGTGTTCCACA CAGCATTAA CCCATGACA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG GATGGTGCAG CAGCGCGCC TTGTCAGTGC ATGTCAGTGC ATGTCAGTAG ATGGACATGT ACAGATACTA ACAGATACAA ATCACAACAC CAAGAAGGCA CAGACAACCG TAGGCGTGGA TAGGCATGGA ATGCCATGA ATGCCATGA ATGCCATGA ATGCCATGA ATGCCATGA TAGGCCATGTG TGAGCCATGTG	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTCGCGGC GCTGCCGGG CTGCTGTTCGG AGAAGTTCTG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACTGTTCGAAGGT TAAAAGAGAG TGAATGAGT TAGTTTGGAAT ATTTCTGGAAT CTTCAGTGGAAT ATTTCTGGAGG	31 CTCGGACAGT GCGCGACGCC CGGCGCCCCC CGAGGGTGA AGTGGGGAC AATATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGCT TCTGATCAG ACCTCAAGG ACCCTCAAGG ACCTCAAGG ACCACAAGA ACCTTCAAGG ACGACAAGAAGC CGTGCAAAGT TCTGATTTAT TCTGATTTAG ATTGAAAGCT TCTGATTTAG ATTGAAAGCT TCTGATTTATTCAG AGCAAGGAAGA CCTTCAAGG AGCAAGGAAGA CCTTCAAGG AGCAAGGAAGT TTTATTTTCC CAGTCTTGGGG CAGTCTGGGG CAGTCTTGGGG CAGTCTGGGG CAGTCTGGGGG CAGTCTGGGGGGGGGG	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCAGTCA ACACGGTAAT ATGTCTTAGA ATGTCTTAGA AAGATCTGGA AAGATCTGGA AAGATCTGGA AAGACCACT AATGCTCTT TGAAGCTCT TGAAGCTCT TGAAGCTCT AAGGCACC GAATTGTCAT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCT CGAAGGAGA AGTGAAGACC AAGCAAGAAG AGCAACGAA CCAGCCTCT TGTGGGTCAC TGTGGGTCAC ACCACCTCT TGTGGAGCTC AACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AAGTCAAGAA CACCCCACACCTCT CTGGAGCTG AAAGTTAAG CACCCCACCACCACCACCCACCCACCCACCCACCCCCT TGTGGAGCTG AAAAGTTAAG CAACCACCCACCACCCACACCACCCACCCACCCACC	120 180 240 300 360 420 540 600 660 720 780 840 900 1020 1080 1140 1260
50 55 60	CACTAACGCT TCAAGGCTGA CCGAGCTGA GCCGGGTGGG GCGACGATGA GCCGGTGCTCCA CTGATCATAA TATCTGCAAC TCTGGTCTA AGTGCAACCA TGTGGATCAC CGAGCATTAAC CGAGCATTAC CGAGCATTAC CAGACCATCA CAGCCATTAC CCCATCACCA CCCATCACCA CCCCATCACCA CCCCAATCA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCGAGG GATGGTGCAG GATGGTGCAG TGCTCAGTGC AGAATCATCC AGAATCATC ATCTGAAAG ACGGACTTAT ACAGATACAA CAAGATACAA CAAGAAGCA TAGAGATACAG TAGAGATTGC TAGGCGTGGA GCCTCCATGA ATGCGCAGCT TGAGCATGT TGAGCATGT TGAGCATGT	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGG CTTGCCGGG CTTGCTCGG AGAAGTGCT AGAAGAGT TGTCTCCCT ACGGGGATAT TGTCTTCCGT ACGGGGATAT TGTCTTTGAA ACTCTTCCCT TAAAAGAGAG TAATCACGTT AGTGTGAAT ATTTCTGGAC TGGTGGAAT ATTTCTGGAC CGCGCAGAC CGTGACCCTG	31 CTCGGACAGT GCGCGACGCC GCGCCCCCC CGGGCCGAC AGTATTCGAC AGTGGAAATT TCTGATTCAG AATGAAAGCT GCGCAAGAAATT TCTGAAAAGCT GCTCAAAGA ACCCTCAAGG AGCAAGAAATT GACATGAAGA CCTCTAAGG CCTCTCAAGG CCAGTCTCGGG CCAGTCTCGGG CCAGTCTCGGG CCAGTCTCGGG CCAGTCTCGGG CCACTTCAGG CCAGTCTCGGGG CCACTTCAGGG CCACTTCAGGC CCACTTCAGC CCACTTCAGC CCACTTCAGGC CCACTTCAGGC CCACTTCAGGC CCACTTCAGC CCACTTCAGGC CCACTTCAGC CCAC	TTGCTCATTT CGCACACAC GCGGCCGGC GACGCCCGGC GCTTATGGAA TCTGGATCC TACAACGGGA GCAGTTTCAC ACACGGTAAT TCAGTCATCAC ACACGGTAAT TAGTCATCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT TGAAGCCACT TGAAGCTCT AATGCTCTT AATGCTCTT AATGCTCTT CAACTAGTA ACAGACCACT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT AAGGGACCAC GAATTGTCAA	ATTGCAACGG CGGGGGGAAA CGCGGGGGGAAA CGCGGCCCTG CGAAGGCCG CGAAGGAAGA AGTGAAGACA AGTGAAGACA CCACCACTCTGGGTCAC ACCACTCTTTGGGACTCA ACCACCCTCT TCTGGAGCTCA AAAGTTAAG GAACATTCAG AACTTCGGCATG ACTCGCAAT ACTCGCAAT ACTCGCAAT CATCGCATG	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1260 1320 1380
50 55 60	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCGACGATGG GCGCGGTGGT GCTGATGAAG TTCGACTCCA TGATCATAA TATCTGCAAG TGTTGATCACC AGTGCACTCCA AGTGCAACCA TGTGGATCAC CAGACATGAG GCGATTAA ATCGTGTTGG CCATTGAC TCCCATGACA ACCCCAATCACA ACCCCAATCACA ACCCCCAATCACA ACCCCCAATCACA ACCCCCAATCACA ACCCCAATCACA ACCATGACA ACCATGACA ACCAATCACCA AATCATGACA AATCATGACA AATCATGACA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG ATGAAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCCC TTGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTAC ACGGACTTAT ACAGAACAC CAAGAAGGCA CAGACAACAC TAGAGATCC CACTCCATGA ATCCCCATGA ATCCCCATGAC CACTCGACAG	3036 21 CCCGGGCCAA AACGCGGGC TAGAAGAGCT CAGGAAATCC GCTCGCGGG GCTGCCGTG CTGCAAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGATAT TGTGTTTCCCA ACCAAACCTC TAAAAGAAG TAATCAAGGT TAGTGTTAGA TAGTGTGGAA TGTGTGGAA CTCTTCCCA CCAAACCTC TAAAACAGAG TAATCAGGT TAGTGTGGAA TGTCTGGAC TGTCAGTGGG CACGGCAGAC CGTGACCCC GGGCTGTAGC	31 CTCGGACAGT GCGCGACGCA GCA CAGCGGCCCGAG TCCCCGCCC CGAGGGCCAA ATATTCGA CTCAATTCCA GCTCGAAATT TCTGATTCAG GCTGAAGAAG ACCTCAAGG ACCTCAAGG ACCACAGGAAGAAG GCAAGTTT GACATGGCA GCACAGTTT GACATGGACA GCACATTT GACATGACA GCACATTT GACATGACA GCACATTT GACATGACA GTTATTCCC CAGTCTGGAG GCACATAGGC TGTCAAATGG TGTCAAATGG	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGTCATTCAC ACACGGTAAT CAGTCATTTAGA TGAAAAGCGT ATGTCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTGT TGAAGCTCT AAGGCACAC CGAATTTCAC CGAATTTCAC CGAATTGCAC CGAATTGCAC CGAATTGCAC CGAATTGCAC CGAATTGCAC CGAATTGCAC CGAATTGCAC CGAATTGCAC CGACTAGAAA CGGTTGAGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTTCAG AACTTCAG AACTTCAG CAGCACATTCAA CACCCCTCT TGTGGAGCTG AAAAGTTAAG GAACATTCAG CACCACCTCT AAAAGTTAAG GAACATTCAG CACCACCTCT AAAAGTTAAG GAACATTCGGAAA CATCGGCATG AACCATCGGCATG AAGACCATTCG GAACCATTCG	120 180 240 300 480 540 600 660 780 840 906 1020 1080 1140 1260 1380 1440
50 55 60	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCCA TTCGATCAAA TTCGATCAAA TGTTACTACC TCTGGTTCAC AGTGCAATCAC CAGACATGG GTGATCACA AGTGCAACCA TGTGCATCAC CAGACATGG CAGCCATTCACCA ATCCTGATCACCA GCCCCAATCA GCCCCAATCA ATCATGACA ATCATGAACG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TTGTCAGTC ATCTGGAAAG ATCACATC ATCTGGAAAG ATCGACATT ACAGATACAA ATCACAACAC CAACAACAC TAGGACTAGT TAGGACTAGT ACAGATACAA ATCACAACAC TAGGACTAGT TAGGACTAGT TAGGACTAGT TGGGCTGGAC TTGGGCTGGAC TTGGGCAGGCT TGAGCATGCC TCGCCACGC TCCACCGC CTTCCACCGC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTGCCGTG CTGCTGTTCGG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTGTTCCTC ACGAGGCTTGTTTTTTTGAA ACCTATTTTTTTAAAACAGAG AGAGTTTCAG TAAATCAGTT AGTGTGGAAT ATTTTCTGGAC CGTGACCCTG CACGGCAGAC CGTGACCTG	31 CTCGGACAGT GCGCGACGCA CAGCAGCA CAGCCGCGCCCCAGCGGACCCA AGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAG ACCTCAAGG AGCAAGAAG AGCAAGAAG AGCAAGAAG TCGACTTTTTCGACTAAGG AGCAAGAAG AGCAAGTTTT GACATGGACA TGGAGAAG GTTTATTCCC CAGTCTGGGG GCACATTAGGC TGTCAAATGG CCCATGGTGT	TTGCTCATTT CGCACACACA GCGGGCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCAGTCA ACACGGTAAT ATGTCTTAGA ATGTCTTAGA ACAGTAGTA ATGACTAGTA AAGATCTGGA ACAGACCACT AATGCTCTGGA ACAGACCACT CGATTCTCAC GAATTCTCAT TGGGCACACA CGGTTAGGAA TCAGCAGTTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAGA AGTGAAGACG AAGCAAGAA GGAAACCCAC TCTGGGTCAC CCAGCAGTTT ACCAATGAAA CCGGGGATCA ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGGAAT CACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AATTCGGAAT CACCGCATTCGCAAA CACCGCAAT ACCACCCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AAGTCAGGAC ACTCGCAAA CATCGGCAAT CATCGGCATG GGACCATTCA TTTCGGGATG AGGAGGCTGC CAGCAGGAAG	120 180 240 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500
50 55 60	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCCA TTCGATCAAA TTCGATCAAA TGTTACTACC TCTGGTTCAC AGTGCAATCAC CAGACATGG GTGATCACA AGTGCAACCA TGTGCATCAC CAGACATGG CAGCCATTCACCA ATCCTGATCACCA GCCCCAATCA GCCCCAATCA ATCATGACA ATCATGAACG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TTGTCAGTC ATCTGGAAAG ATCACATC ATCTGGAAAG ATCGACATT ACAGATACAA ATCACAACAC CAACAACAC TAGGACTAGT TAGGACTAGT ACAGATACAA ATCACAACAC TAGGACTAGT TAGGACTAGT TAGGACTAGT TGGGCTGGAC TTGGGCTGGAC TTGGGCAGGCT TGAGCATGCC TCGCCACGC TCCACCGC CTTCCACCGC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTGCCGTG CTGCTGTTCGG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTGTTCCTC ACGAGGCTTGTTTTTTTGAA ACCTATTTTTTTAAAACAGAG AGAGTTTCAG TAAATCAGTT AGTGTGGAAT ATTTTCTGGAC CGTGACCCTG CACGGCAGAC CGTGACCTG	31 CTCGGACAGT GCGCGACGCA CAGCAGCA CAGCCGCGCCCCAGCGGACCCA AGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAG ACCTCAAGG AGCAAGAAG AGCAAGAAG AGCAAGAAG TCGACTTTTTCGACTAAGG AGCAAGAAG AGCAAGTTTT GACATGGACA TGGAGAAG GTTTATTCCC CAGTCTGGGG GCACATTAGGC TGTCAAATGG CCCATGGTGT	TTGCTCATTT CGCACACACA GCGGGCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCAGTCA ACACGGTAAT ATGTCTTAGA ATGTCTTAGA ACAGTAGTA ATGACTAGTA AAGATCTGGA ACAGACCACT AATGCTCTGGA ACAGACCACT CGATTCTCAC GAATTCTCAT TGGGCACACA CGGTTAGGAA TCAGCAGTTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTTCAG AACTTCAG AACTTCAG CAGCACATTCAA CACCCCTCT TGTGGAGCTG AAAAGTTAAG GAACATTCAG CACCACCTCT AAAAGTTAAG GAACATTCAG CACCACCTCT AAAAGTTAAG GAACATTCGGAAA CATCGGCATG AACCATCGGCATG AAGACCATTCG GAACCATTCG	120 180 240 300 480 540 600 660 780 840 906 1020 1080 1140 1260 1380 1440
50 55 60	CACTAACGCT TCAAGGCTGA CCACTACACGCTGCA CCGGAGCTGA GCCCGGTGGG GCGACCATGG GCCACTACACA TATCTGCAAC TCTGGTCTAA AGTGCAACA TGTGGATCAC CAGACATGG GCGATTAC CAGACATGG GTGATCACA ATCCTCTGG CAGCATTAC CAGACATGG CAGCATTAC CCATGACA ATCATCACA ATCATGAACA GCCCCAATCA GACAATCACA ATCATGAACA GACTTGGAAA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCCCC ATCTGGAAAG ATGACACAC ATCTGGAAAG ATGACATACA ATGACAACAC CAAGAAGGCA CAAGAAGGCA TAGGCAGTGT TAGGCATGCA ATGCCATGA ATGCCATGA ATGCCATGA CAGCATCCAGG CACCTCCATGA CAGCATGCAGC CACCTCCATGA CACCTCCACCG CCACCCTCGACAG CCTCCACCG	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGGG CTGCCGGG AGAAGTGCTG AGAAGTGCTG AGAAGTGCTG ACGGGGATTTGAC ACCAAACCTC TAAAAGAGAG AGAGTTTCAG TAATCAGTT AGTGTGGAA CTCTTCCCA TAGAGGAGA CGTGCCGAGC CGCGCAGAC CGTGACCTG GGGCTGTAGC GGGCTGTAGC GGGCTGTAGC GGGCTGTAGC GGGAGAT GGAAAGGAATG GGAACCTG CAGGCAGAC CGTGACCTG GGGCTGTAGC GGGAACCTG GGAACCTG GGAACCTG GGAACCTG GGAACCTG GGGCAGAC CGTGACCTG GGGCAGAC CGTGACCTG GGAACGAATG	31 CTCGGACAGT GCGCGACGCA CAGCACGCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCCGGG GACGCCGGC AGCTGCTAGGAA TCTGGATCCC TACAACGGA ACACGGTAATC ACACGGTAAT CAGTCAGTCA ACACGGTAAT AGGTCATCTA ATGTCTTAGA AAGATCTCC AACTAAGTA AAGATCTCGA ACACGACTA TGGAACCACT TGAAGCTCT TGAAGCTCT AAGGACCACT AAGGACCACT AAGGACCACT AAGGACCACT AAGGACCACT TGGAGCACTA TCGGACTAGT TGGGCCACAA CCGTTGAGAC TCGGATTGCCT TGGGCACTAC TCGCACTTG	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGACC AGCAACGACA TCTGGGTCAC TCTGGGTCAC CAGCACGTAT ACCAACTCAC ACCACCTCT TGTGGAGCTA AAAAGTTAAG GAACATTCAG AAATTCAG AACTCCAC ACCTCGCAAA CACCGCATC ACCACCTCT TGTGGAGCT AAAAGTTAAG GAACATTCAG ACCTCGCAAA CATCGCATC ACCTCGCAAA CATCGCATC ACTCGCATC ACTCGCATC CAGCAGGATC ACGAGGCTC CAGCAGGAAGC CACCAGGAAGC CCCGGAAGTC	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560
50 55 60	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCCGCGTGG GCGACGATGG GCCGCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA TGTGGATCAC CAGACATGAG GCGATTAA ATCTGTGATCAC TCTGGTTCAC TCTGGTTCAC TCTGGTTCAC TCTGGTTCAC GCGATTAA ATCGTGTTGG CCATTCACA TCCCATGACA GCCCAATTCA GCCCAATTCACA GCCCAATGACA GCCCAATGACA GCACTCACA ATCATGACA GACAATCCCC AATCATGACA ATCATGACA ATCATGACA ATCATGACA AGGGAGTTTT	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGG CTCGCGAGG GATGGTGCAG GATGGTGCAG TGCTCAGTGC AGAATCATCC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGACACAC CAGACAACAC CAGACAACAC CAGACAACAC TAGGCGTGGA TAGGCATGG ATGCGCAGCT TGAGCATGG CACTGGAAG CTTCCACGG CCACTGGACAG CTTCCACCGG CCACGGGCCTGGA TCGGCGGCCTGGA TCGGCGGCCCAGCACCC	3036 21 CCCGGGCCAA AACGGCGGC TAGAAGAGC TAGAAGAGC TAGAAGAC CGTCGCCGG GCTGCCCGTG CTGCAGGGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCAC TAAAAGAGAG TAATCACGTT AGTGTGGAAT ATTTCTGGAC TGTCAGTGGACCTC GGGCTGTAGC GGGCTGTAGC GGACCATTT GAAAGGAATG GAAAGGAATG GAAGGTATGGG	31 CTCGGACAGT GCGCGACGCA CAGCGCGCGC CGGGCCCGCC CGGGGGGGACA AGTGGGGACA AGTGGGACA AGTGGAAATT TCTGATTCAG ATGAAAGCT GCGCAAGAA ACCTCAAGG AGCAAGAAGA GCAAGATTT TGCATTTT GCATTGCA CGTGCAAGA CGCTGCAAGA CGCTGCAAGA CGCTGCAAGA CGCTGCAAGA CGCATGAAGA CGCTCAAGG GGCACATGACC CAGTCTGCG GCACATGAGC GCACATGAGC GCACATGAGC GCACATGAGC GCACATGAGC GCACATGAGC GCACATGAGC GCACATGAGC AGCACATTTG	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGCGTATTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTT AATGCTCTGA TGAAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCTC TGGAACAAGG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTGACGCCTG CGAAGGAAGA AGTGAAGACA AGGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCAGCACGTT TGTGGGGCTG AAAAGTTAAG GAACATTCAG GAACATTCAG CATCGCAAA CATCGCATT ATTCGGGATC ATTCGGATC AGGAGGCTGC AGCAGGAGT AGGAGGCTGC AGCAGGAAGT AGGAGGCTGC AGCAGGAAGT AGGAGGAGTGT AGGAGGAGTGT AGGAGGAGTGT AGGAGGAGTGT	120 180 240 360 420 540 660 780 960 1020 1140 1200 1260 1320 1440 1560 1620
50 55 60	1	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TTGTCAGTC TTGTCAGTC ATGAAATCATC ATGACATACTAC ATGACATACTAC ATGACATACTAC ATGACATACTAC CAAGAAGACA TAGACATACTAC TAGACATCAC TAGACATCAC TAGACATCC TAGACATC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGG GCTGCCGTG CTGCTGTTCGG AAATGCTG AAATGCTG AAATGCTG TGTCTCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGAG TAATCAGGT TAATCAGGT AGTGTGGAA CCGCAGCAGAC CGTGGCCGAGAC CGTGACCTG GGGCTGTAGC GGAAGGATTAGGAAGGATG GAAAGGAATG GAAAGGAATG ATGTAGAAGAAGAGAGATG CGTACCCATTT GAAAGGAATG GAAAGGAATG GAAAGGTAGTGGAACTGTAGAAGGAATG ATGTAGAAAGAAAGAATG GAAAGGAATG AATGTAGAAA	31 CTCGGACAGT GCGCGACGCA GCGGCGCGCGC CGGGCCCGAG TCCCCGCC CGAGGGGGC AGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCAAAGAAG ACCCTCAAGG AGCAAGAAG GACAAGTTTT GACATGGACA GTTTATTCGC CAGTCTGGGG TGTCAAAGA GCTCAAGGA GCAATAGGC AGCAAGAGA GCAATAGGC CAGTCTGGGG GCACATGGGC AACAGATTTG CAACAGATTTG CAACAGATTTG CAACAGATTTG CAACAGATTTG CACAGATTTG CACAGATTGCA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGC AGCTGCTGC GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGTCAGTCAT ATGTCTTTAGA TGAAAAGGGT ATGTGTTTCAC CAACTAAGTA ACAGTAAGTA ACAGTAGTA TGAAAGCGT TGAAGCTTCT TGGAAGGAGG ATGCCACAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAGA AGTGAAGAGA AGTGAAGACC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTC AACCACCTCT TGTGGAGCTC AAAAGTAAA CCGGCGATCA ACCACCTCT TGTGGACTC AAAAGTAAAG CATCGGCATC AACTCAGCAAA CATCGGCATC ACTCGCAAA CATCGGCATC ACTCGCAAA CATCGGCATC CAGCAGGATC CAGCAGGAAG CCCCGGAAGT CAGCAGGAGG CCCGGAAGT CAGCAGGAGG CCCTCT CTTACCCTG	120 180 240 300 480 540 600 600 780 840 900 1020 1140 1200 1260 1380 1440 1500 1500 1620 1680
50 55 60 65 70	1	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCC TTGTCAGTC TTGTCAGTC ATGAAATCATC ATGACATACTAC ATGACATACTAC ATGACATACTAC ATGACATACTAC CAAGAAGACA TAGACATACTAC TAGACATCAC TAGACATCAC TAGACATCC TAGACATC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGG GCTGCCGTG CTGCTGTTCGG AAATGCTG AAATGCTG AAATGCTG TGTCTCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGAG TAATCAGGT TAATCAGGT AGTGTGGAA CCGCAGCAGAC CGTGGCCGAGAC CGTGACCTG GGGCTGTAGC GGAAGGATTAGGAAGGATG GAAAGGAATG GAAAGGAATG ATGTAGAAGAAGAGAGATG CGTACCCATTT GAAAGGAATG GAAAGGAATG GAAAGGTAGTGGAACTGTAGAAGGAATG ATGTAGAAAGAAAGAATG GAAAGGAATG AATGTAGAAA	31 CTCGGACAGT GCGCGACGCA GCGGCGCGCGC CGGGCCCGAG TCCCCGCC CGAGGGGGC AGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCAAAGAAG ACCCTCAAGG AGCAAGAAG GACAAGTTTT GACATGGACA GTTTATTCGC CAGTCTGGGG TGTCAAAGA GCTCAAGGA GCAATAGGC AGCAAGAGA GCAATAGGC CAGTCTGGGG GCACATGGGC AACAGATTTG CAACAGATTTG CAACAGATTTG CAACAGATTTG CAACAGATTTG CACAGATTTG CACAGATTGCA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGC AGCTGCTGC GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGTCAGTCAT ATGTCTTTAGA TGAAAAGGGT ATGTGTTTCAC CAACTAAGTA ACAGTAAGTA ACAGTAGTA TGAAAGCGT TGAAGCTTCT TGGAAGGAGG ATGCCACAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTGACGCCTG CGAAGGAAGA AGTGAAGACA AGGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCAGCACGTT TGTGGGGCTG AAAAGTTAAG GAACATTCAG GAACATTCAG CATCGCAAA CATCGCATT ATTCGGGATC ATTCGGATC AGGAGGCTGC AGCAGGAGT AGGAGGCTGC AGCAGGAAGT AGGAGGCTGC AGCAGGAAGT AGGAGGAGTGT AGGAGGAGTGT AGGAGGAGTGT AGGAGGAGTGT	120 180 240 360 420 540 660 780 960 1020 1140 1200 1260 1320 1440 1560 1620
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCGACCATGG GCGACCATCA TCGACCACA TCGATCAAAA TATCTGCAAG TGTTACTACC CTGATCAACA AGTGCAACCA CAGACATGGG CTGATCACA ATCATGACA ACCCATCACA GCCCCAATCA GACAATCCCC AATCATGACA GCCCCAATCA ATCATGACA GACATTCACCA AATCATGACA GACATTCACCA AATCATGACA GACATTCACCA AATCATGACA GACATCTCGGGGAAACCACA AACCATGACA GACATTCACCA AATCATGACA GACTTGGAGA AGGGAGTCTT GACTGTGGGGAAGCCGGACG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTGC ATGTAGTAC ATGTACATC ATCTGAAAG ATGGACATTAT ACAGATACAA ATCACAACAC CAAGAAGCAG CTGCAGGA TTGGTGCAGG TTGGTGCAGG CTTCCACCGG CCAGCCTGGA TCGGGGGCCTGGA AGCCAGCAGA CTGGGGGCCAGA CTGGACAG CTTCCACCGG CCAGCCTGGA AGCCAGAGA CTGTGGGGGCCAGA CTGGACAG CTGGACAG CTGGACAG CTGGACAG CTGGACAG CTGGACAG CTGGACAG CTGGACAG CTGGACAG CTGTGTGGG	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT TAGAAGAGCT CAGGAAATCC GCTCGCGGG GTTGCCGTG CTGTTCGG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA AGAGTTTCAG AGAGTTTCAG TAATCAGGT AGTGTGGAAT ATTTCTGAAT AGTGTGGAAT ATTTCTGAAT AGTGTGGAAT ATTTCTGGAAT ATTTCTGGAAT ATTTCTGGAAT ATTTCTGGAAT ATTTCTGGAAT ATTTCTGGAAT ATTTCTGGAAT ATTTCTGGAAT GAAAGGAAT GAAAGGTATCAG GAACTCTGGAAT ATTTATGAAT ACATGGGCTG	31 CTCGGACAGT GCGCGACGCA CAGCAGCA CAGCGCGCGCC CGGGCGCAGCA AGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCA GCTCAAAGA ACCTCAAGG AGCACGAAGAGA AGCAAGAGA GCAAGAGAG GCTGCAAAGA ACCTTCAAGG AGCAAGAGA GCAAGAGAG GCTGCAAAGA GCAAGTTTT GACATGGACA GTTTATTCCC CAGTCTGGGG GCACATTGAG GCACATGAGA GCCATGAGAG CCCATGGTGT AACAGATTTC CGCTGCTGCA CGCTGCTGCAA	TTGCTCATTT CGCACACACA GCGGGCGTG GACGCCGGC AGCTGCTGCACACACA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGGA ACACGGTAAT CAGTCAGTCAT ATGTCTTAGA ACAGTAATCCA CAACTAAGTA ACACTAAGTT TGAACACGG AATGCTCTT AAGGCACCAC GAATTGTCAT TGGGCCACAC TCGGACAGTC TTGGACAAGC TTGGACAGTC TTGGACAAGC TTGGACAAGC TTGGACAAGC TTGGACAAGC ATGCCACCAC ATGCCACCAC ACTGCCACCA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAGA AGTGAAGACA AGTGAAGACA AGCAACGAC TCTGGGTCAC CCAGCCTG CGAAGGAGA AGTGAAGAA ACCACCTCT TCTGGGGTCA ACCACCTCT TGTGAGCTC AAAAGTTAAG GAACATTCGG AAGTCAGGAC ACCTCGCAAA CATCGCAAT ACACCCTCT TCTGGGGTCA CACCCCTCT TCTGGAGCTC ACACCCCTCT TCTGGAGCTC ACACCCAAC ACCACCAAC ACACCCAAC CACCACCA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1260 1320 1380 1440 1560 1680 1740
50 55 60	CACTAACGCT TCAAGGCTGA CCACTGACGTGACCTGA GCCGGGTGGG GCGACGATGG GCCGGTGCTGA GCCGGTGCTGA TCGACTCAAA TATCTGCAAG TGTGATCACA TGTGGATCAC CCAGACCACA AGTGCAACCA AGTGCAACCA ACCGATTCAC CCAGACTAGGA CCACATCA GCCCCAATCA GCCCCAATCA ATCATGACA ACCGCACTACA ACCGCACTACA ACCGCACTACA ACCATCACA ACCACACA ACCACACAC ACCACACA ACCACACA ACCACACAC ACCACACA ACCACACAC ACCACACACAC ACCACACAC ACCACACAC ACCACACAC ACCACACAC ACCACACACAC ACCACACACAC ACCACACACAC ACCACACACAC ACCACACACACAC ACCACACACACAC ACCACACACACACACACAC ACCACACACACACACACACACACACACACACACACACACA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCGAGG GATGTGCAG GATGTGCAG CAGGGGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAG ATGGACATTAT ACAGATACAA ATGACAACAC CAAGAAGGCA TAGAGATTGC TAGAGATTGC TAGAGATTGC TAGAGATTGC TAGAGATTGC TAGAGATTGC TAGAGATTGC TAGAGCATGGA GCCTCCATGA ATGCCAGCT TGAGCATGGG CCACCAGGA ATGCCAGGC CAGCACAGG CTCCACGG CCACGAGAA CTGGACAGG CCAGCAGGA TCGGGGGCCA AGCCAGGGACTCG GCAGGGACTCG GCAGGGACTCG GCAGGGACTCG	3036 21 CCCGGGCCAA AACGGGGCCAA AACGGGGGCCAA AACGGGGGCCCGGGCTGCCGGG CTGCCGGGGCTGCCGGG AGAAGTGCTG AGAAGTGCTG AAATGAAGGATT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCCA TAAAAGAGAG TAATCACGTT AGTGTGGAAT ATTTCTGGAC CGTGACCCTG GGGCTGTAGGC GGGCTGTAGGC GGGCTGTAGGAT ATTTCTGGAC CGTGACCCTG GGGCTGTAGGC CACGGCAGAC CGTGACCCTG GAAAGGATT GAAAGGATT GAAAGGATT GAAAGGATT CACATTGGCCTG CACGCAGAC CGTGACCCTG CACATGGCCTG	31 CTCGGACAGT GCGCGACGCA CAGCGCGCGCCC CGGGCCCGCC CGGGCCGAGA AGTGGGGGGAA AGTGGGGACC AATATTCAC AATGAAAGCT TCTGATTCAG AATGAAAGCG GCTGCAAAGA ACCCTCAAGG AGGCAAGAAG AGCAAGTTT GACATGGACA TGTGAGTAATGG CCAGTCTGGG GCACATGAGC AGGAGAAGA TGTCAAATGG CCAGTCTGGG CCAGTCTGGG CCCAGTGTGCC AACAGTTTG CGCTGCTGAA TGCGTGCTGCA TGCGTGCTGCA TGTGAACCC TGTGTGAAG TGTGAACCC	TTGCTCATTT TGGCTCATTT TGGCACACA GCGGCCTGG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAT TCAGATCCT ATGTCTTAGA ACACGTAAT ATGTCTTAGA ACAGACCACT TGAACACGC TGAACAGCCACT TGAACTCT TGAACCACT TGAACTCT TGAACCACT TGAACTCT TGAACTCTCT TGAACTCTCT TGAACTCTCT TGAACTCTCT TGGAACACAC TTGGCACACA CGGTTTAACA TCAGCACTC TGGAAGAAGG ATGCCACCAC ACTGCCACCT CAGAGTTCTC CAGAGTTCTC CAGAGTTCTC CAGAGTTCTC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGCTCGGC CTGAAGGCCG GCAAGGAAGA AGTGAAGACG AGTGAAGACC ACCACCTCT ACCACCCTCT TOTGGAGTCA AAACATTCAA ACCACCCTCT AAAAGTTAAG GAACATTCAG AACTTCGGATTAA CCTCGCAAA CATCGCATC ACCACCTCT TTTGGGACTC AAAACTTCAG AAGTTAAG GAACATTCGG AAGTATCAA CTTCGGCATG AGGAGGCTGC ACCAGGAGCT CTTTCGGGATC ACCAGGAGC CACCAGGAGC CACCAGGAGC CACCAGGAGC ACCTCGCAAA CATCGCATG AGGAGGCTGC CACAGGAGC CCGCAGGAGT CTTTACCCTC GAAGCCTGCA CACAGGGGCC	120 180 240 300 360 420 540 600 780 900 960 1020 1140 1200 1320 1440 1560 1620 1680 1680 1840
50 55 60 65 70	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGACCTGG GCGACGATGG GCGCGGTGGT GCGCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA TGTGATCAC TCTGGTCTCA AGTGCAACA CAGACATGAG GCACATGAA ATCGTGTTGG CAGCGATTAA ATCGTGTGG CCAATCAC ACCCCAATCAC ACCCCAATCAC GCCCAATCAC GCCCAATCAC GCCCAATCAC GCCCAATCAC GCCCCATTCACC ATCATGACGG GCACTTGACA ATCATGACGG GACATTGACGG GACATTGACGG GACACGGGAACAGCGG AAGCCGCACAC ATCATGACGG GACACGCGG AAGCCCCCACT	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG ATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCCC TTGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGGACATGT ACAGAACAC CAAGAAGCA TAGAGATACAA ATCACAACAC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGCATGC TGGCCAGC ATGTGGACAC CTTCCACCG CCACTGGACAC CTTCCACCGG CCACTGGACAC CTTCCACCGG CCACTGGACC AGCCAGACGA CTTGTTGCCC GCCAGGCACC GCAGGGACTC GCCAGGCCCAA	3036 21 CCCGGGCCAA AACGGCGGC CTAGAAGAGCT CAGGAAATCC CGCTCGCGG GCTGCCGTG CTGCAGGCC CTCTGTTCGG AAAATGACTG TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA TATTCAGT AGTGTGGAAT TGTCTTCGAC TGTGTGGAAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA TGTCTTCGGA TGTCTTCGGA TGTCAGTGGG CACGGCAGAC CGTGACCCT GGGCTGTAGC GGAGTGTGGA ATGTAGGG GAAGTGTGGA ATGTAGGG ATGTAGCAC CGTGCACCCC CGGGCACCC CGGGCACCC CGAGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGCCACCC CGGGCACCC CGGCCACC CGCGCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGCGCACC CGGCCACC CGCGCACC CGCGCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGCGCACC CGCCACC CGCGCACC CGCCACC CGCCACC CCCC CGCGCACC CCCC CGCCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	31 CTCGGACAGT GCGCGACGCA GCAGCCCGAGCCCGAGCCCAGCC CGAGGGGCCCGAG AGTGGGGACC AATATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGA ACCCTCAAGG ACCATCGAGG AGCAAGAAGA GCTGAAGAAG GCTGCAAGG TGTCAAGG GCACATGGACA GCCATGGAGA GCCATGGAGA CCCATGGTGT GGGGTGTGCA GGCTGCAAGG TGTCAAATGG CCCATGGTGT GGGGTGTGCA CGCTGCTGCA CGCTGCTGCAC CACGATTGACCC CACGATTGACCC CACGATTGACCC CACGATTGACCC CACGATTGACCCC CACGATGGAGCA CGCTGCTGCAC CACGATTGACCCC CACGATGGGGC CGCAGGTGTGCAC CGCTGCTGCAC CGCGCTGCAC CACGATGGGGC CACGATGGGGC CACGATGGGGC CACGATGGGGC CACGATGGGGC CGCGCTGCAC CACGATGGGGC CGCGCTGCAC CACGATGGGCC CACGATGGGGC CGCGCTGCAC CACGATGGGCC CACGATGGGGC CGCACGATGGGCC CACGATGGGCC CACGATGGCC CACGATGCC CACGATGGCC CACGATGGCC CACGATGCC CACCATC CACCATC CACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGAA CACCGTATT CAGTCATTTACA ACACGTAAT TGAAAAGCGT ATGTCTTAGA ACACTAAGTA AAGATCTGCACTCT AATGCTCTGA ACAGACCACT AATGCTCTGT TGAAGCTACT CAACTAGAA CGATTGCACACCACT TGGAACAACGACACT TGGAACAACGACACT TGGAACAACGACACT TGGAACAACGACACT TGGAACTACGACACCACC TGGAACAACGACACCACCACACCA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGCTCGGC CTGAAGGCCG CTGAAGGCCG CGAAGGAAGA AGTGAAGACA AGCAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACCTCT TGTGGGTCAC ACCACCCTCT TGTGGGCTCA AAAGTTAAG GAACATTCAG GAACATTCGGCATG CACCCCTCT AAAAGTTAAG GAACATTCGCAAA CATCGGCATG CACCACGCATC ACCACGCATC AGCAGGATC AGCAGGATC AGCAGGATC AGCAGGATC CACCAGGAAA CATCGGCATG CACCAGGAAG CCTCTC CAGCAGGATC CACCAGGAAG CCTCTC CAGCAGGAAG CCTCTC CAGCAGGAAG CCTCTC CAGCAGGAAG CCACGGAAG CCCGGAAGT CAGAGGAGTC CACAGGGCC CACAGGGCC CACAGGGCC CGATGTGGAC	120 180 240 360 420 540 660 660 780 960 1020 1140 1200 1140 1560 1560 1680 1740 1800
50 55 60 65 70	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGACCTGG GCGACGATGG GCGCGGTGGT GCGCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA TGTGATCAC TCTGGTCTCA AGTGCAACA CAGACATGAG GCACATGAA ATCGTGTTGG CAGCGATTAA ATCGTGTGG CCAATCAC ACCCCAATCAC ACCCCAATCAC GCCCAATCAC GCCCAATCAC GCCCAATCAC GCCCAATCAC GCCCCATTCACC ATCATGACGG GCACTTGACA ATCATGACGG GACATTGACGG GACATTGACGG GACACGGGAACAGCGG AAGCCGCACAC ATCATGACGG GACACGCGG AAGCCCCCACT	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG ATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCCC TTGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGTCAGTC ATGGACATGT ACAGAACAC CAAGAAGCA TAGAGATACAA ATCACAACAC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGCATGC TGGCCAGC ATGTGGACAC CTTCCACCG CCACTGGACAC CTTCCACCGG CCACTGGACAC CTTCCACCGG CCACTGGACC AGCCAGACGA CTTGTTGCCC GCCAGGCACC GCAGGGACTC GCCAGGCCCAA	3036 21 CCCGGGCCAA AACGGCGGC CTAGAAGAGCT CAGGAAATCC CGCTCGCGG GCTGCCGTG CTGCAGGCC CTCTGTTCGG AAAATGACTG TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA TATTCAGT AGTGTGGAAT TGTCTTCGAC TGTGTGGAAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA TGTCTTCGGA TGTCTTCGGA TGTCAGTGGG CACGGCAGAC CGTGACCCT GGGCTGTAGC GGAGTGTGGA ATGTAGGG GAAGTGTGGA ATGTAGGG ATGTAGCAC CGTGCACCCC CGGGCACCC CGGGCACCC CGAGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGCCACCC CGGGCACCC CGGCCACC CGCGCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGCGCACC CGGCCACC CGCGCACC CGCGCACC CGGCCACC CGGCCACC CGGCCACC CGGCCACC CGCGCACC CGCCACC CGCGCACC CGCCACC CGCCACC CCCC CGCGCACC CCCC CGCCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	31 CTCGGACAGT GCGCGACGCA GCAGCCCGAGCCCGAGCCCAGCC CGAGGGGCCCGAG AGTGGGGACC AATATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGA ACCCTCAAGG ACCATCGAGG AGCAAGAAGA GCTGAAGAAG GCTGCAAGG TGTCAAGG GCACATGGACA GCCATGGAGA GCCATGGAGA CCCATGGTGT GGGGTGTGCA GGCTGCAAGG TGTCAAATGG CCCATGGTGT GGGGTGTGCA CGCTGCTGCA CGCTGCTGCAC CACGATTGACCC CACGATTGACCC CACGATTGACCC CACGATTGACCC CACGATTGACCCC CACGATGGAGCA CGCTGCTGCAC CACGATTGACCCC CACGATGGGGC CGCAGGTGTGCAC CGCTGCTGCAC CGCGCTGCAC CACGATGGGGC CACGATGGGGC CACGATGGGGC CACGATGGGGC CACGATGGGGC CGCGCTGCAC CACGATGGGGC CGCGCTGCAC CACGATGGGCC CACGATGGGGC CGCGCTGCAC CACGATGGGCC CACGATGGGGC CGCACGATGGGCC CACGATGGGCC CACGATGGCC CACGATGCC CACGATGGCC CACGATGGCC CACGATGCC CACCATC CACCATC CACCAC CACCAC CACCAC CACCAC CACCAC CACCAC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGAA GCAGTTTCAC ACACGGTAAT CAGTCATTTAGA TGAAAAGGGT ATGTCTTAGA ACACACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTGT TGAAGCTCT TAGACACCACT AGGGACCAC GAATTGTCAT CGGACTAGAA TCAGCAGTAGA TCAGCAGTAGA TGGCACACA CGATTGAGAA TCAGCAGTCT TGGAAGAAGG ATTGCACACAC ACTGCCACAC ACTGCCACCAC ACTGCCACCAC CCAGGTTCCACCACC CCACGTTCCACCACC CCACGTTCCACCACCACC CCACGTTCCACCACCACC CCACGTTCCACCACCACCACC CCACGTTCCACCACCACC CCACGTTCCACCACCACCACCACCACCACCACCACCACCACCACC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGCTCGGC CTGAAGGCCG GCAAGGAAGA AGTGAAGACG AGTGAAGACC ACCACCTCT ACCACCCTCT TOTGGAGTCA AAACATTCAA ACCACCCTCT AAAAGTTAAG GAACATTCAG AACTTCGGATTAA CCTCGCAAA CATCGCATC ACCACCTCT TTTGGGACTC AAAACTTCAG AAGTTAAG GAACATTCGG AAGTATCAA CTTCGGCATG AGGAGGCTGC ACCAGGAGCT CTTTCGGGATC ACCAGGAGC CACCAGGAGC CACCAGGAGC CACCAGGAGC ACCTCGCAAA CATCGCATG AGGAGGCTGC CACAGGAGC CCGCAGGAGT CTTTACCCTC GAAGCCTGCA CACAGGGGCC	120 180 240 360 420 540 660 660 780 960 1020 1140 1200 1140 1560 1560 1680 1740 1800
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTACGCTGGCCGAGCTGG GCCGCGTGGGGCACCATGG GCCGGTGCTCCACCACCACCACCACCACCACCACCACCACCACCACC	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCCCC TTGTCAGTC TTGTCAGTC ATGTAATACAC ACGCGCCC ATCTGGAAAG ATGACATGT ACAGATACTAC CAACAACAC CAACAACAC TAGGCAGTT TGGTCAGGC TAGGCATGT TGGTCAGGC CCACCGACCAG CTCCACGG CCACCGACCAG CTGCACGG CCACCCAGCAA ACGCACCAACAA ACAATGCCAA	3036 21 CCCGGGCCAA AACGGGGCCAA AACGGGGGCCAC TAGAAGAGCT CAGGAAATCC GGTTGCCGGG GTTGCCGTG CTGTTTCGG AAAATGATGTT AAAAGAGAG TAGTTTTTCAA ACCAAACTC TAAAAGAGAG TAATCACGTT AGTGTTGGAA TGTGTTGGAA TGTGTTGGAA TGTGTTGGAA TGTGTTGGAA TGTGTTGGAA TATTCTGGGG CACGGCAGAC CGTGACCCTG GAAAGGAATG GAAAGGAATG GAAAGGAATG GAAAGGAATG GAAAGGAATG GAAAGGAATG CAGCAAACTCC CAGCAAACTCC CGTGTACCCG CAGCAACTCC CGTGTACCG CGTGACCTGC CGTGTACCG CGTGTACCTG CCGTGTACCG CGTGTACCTG CCGTGTACCG CGTGTACCTG CCGTGTACCTG CTGCCAGACT CCGTGTACCTG CTGCCAGACT CTGCCAGACT CTGCCAGACT CTGCCAGACT CTGCCAGACT CTGCCAGACT CTGCCAGACT CTGCCAGACCTC CTGCCAGACTC CTGCCAGACCTC CTGCCAGACCTC CTGCCAGACCTC CTGCCAGACCTC CTGCCAGACTC CTGCCAGACCTC CTGCCAGACCTC CTGCCAGACT CTGCC	31 CTCGGACAGT GCGCGACGCA CAGCAGCA CAGCGCGCGCCCCC CGAGGGGCGAA AGTGGGGACCA AGTATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAG ACCCTCAAGG AGCAAGAAG AGCAAGAAG AGCAAGAAG AGCAAGAAG GTTAATTCG CAGTCTGGGG GCACATGAGA GCTAAAATG CCATGGGG CACATGAGG TGTCAAAG TGTGGGGAGA TGTGACTCG CACGAGCAG CGCCCCCCC CACGAGCAG CACGAGCAG CACGAGCAG CACGAGCAG CACGAGCAG CACGAGCAG CACGAGCAG CACGAGCAGC CACGAGCAGC	TTGCTCATTT CGCACACACA GCGGCCGGG GACGCCGGC AGCTGCTGC GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCAGTCAT ATGTCTTAGA TGAAAAGGGT ATGTGTTTCAC CAACTAAGTA ACAGTAAGTA ACAGTACT AATGCTCTGT TGAAGCTCTGT TGAAGCTCTGT TGAAGCTCTGT TGAAGCTCTGT TGAAGCTCTGT TGAAGCTCTGT TGAAGCTCTGT TGAAGCTCTGT TGAAGCTCTCT TGAAGCTCTCT AGGCCACAC CAGATTTCAT TGGCACACAC ACTGCCACCAC ACTGCCACCAC ACTGCCACCAC ACTGCCACCAC ACTGCCACCAC ACTGCCACCAC CACTACTCAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCT CGAAGGAGA AGTGAAGACA AGTGAAGACA TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTC AAAGTAAA CCACCCTCT TGTGGAGCTG AAAGTTAAG GAACATTCGG AAGTCAGGAC TTTCGGAGTC ACCTCGCAAA CATCGGCATG GGACCATTCA TTTCGGAGTC CACCAGGGCTC AGAGGACTGC CACAGGGCTGC CACAGGGGCTGC CACAGGGGCTGC CACAGGGGCTGC CACAGGGGCTGC CACAGGGGCTGC CACAGGGGCTGC CACAGGGGCTGC CACAGGGGCTGCA CACAGGGGCTGCA CACTCGGGATGCAC CACTGGGACGCAC CACTGGGGAC ACTCTGGGGA	120 180 240 300 360 420 540 660 720 780 960 1020 1320 1320 1320 1560 1560 1680 1740 1880 1740 1860 1920
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGGG GCGACCATGG GCGACCATGG GCGACCATGG TTCGACTCAA TATCTGCAAG TGTGCAACA TGTGGATCAC CAGACATGG GCGACTAGA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATGACG GACTTGCAGA AGGGACTCA GACTGCGACG AGCCCGACG AGCCCGACG GGAACACCGT CCCCATGCC CACTTGCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA AGGGACTCTTGCACA AGCCCCACTC CGCTACTCC CGCTACTCC CCAGGTCCT CCAGGTCCT CCAGGTCCT CCAGGTCCTAC CCAGCTCTAC CCAGGTCCTAC CCAGCTCCTAC CCAGGTCCTAC CCAGCTAC CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTAC	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCAGGGGCCC TGCTCGCGCCAG GATGTGCAG GATGTGCAG AATGAAAG AATGAAAGC AATGAAAGC AATGAAAAG ACGATACTAA ACAGAACACC CAAGAAGCA CAAGAAGCA TCAGAAAG CAAGAACACC TAGGCAGGC TTGGCAGGC TAGGCATGAA ATGACAACAC CAAGAAGCA CCAGCATGAA ATGACATGCA CACTGGAAG CCACTGGAAG CCACCCAGGC CCAGCCCAAA ACAATGCAC GCCAGCCAAA ACAATGCAC AACTGGCACC GCCCAGCCCA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTTGCCGGG GCTGCCGGG GCTGCCGGG AGAAGTGCT AAATGAAGGT TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA ACTCTTCCCA ACGAGGCC GTACCCTG GGGCTGTAGGG CAGGGCAGAC CGTGACCTG GAAAGGTTTCGA ATGTAGAGT ATGTAGAGT GAAAGGAAT CGTACCTG GAAAGGTTTCGCA CGTGACCCTG GGACCTGGCAGAC CGTGACCCTG GAAAGGAAT CGTACCATTT GAAAGGAATG CAGGCAGAC CGTGTACCTG CAGCAACTCC CGTGTACCTG CTGCCAGACT TGGGAACTCGC CTGCCAGACT TGGGAACTCGC	TCTCGGACAGT GCGCGACGCA CAGCAGCA AGTGGGGCCGAGG AGTGGGGCCGAGG AGTATTCGAC CTCATTGCA AGTGGAGAAGA ACTGAAAGAT TCTGATTCAG AATGAAAGCT TCTGATTCAG AATGAAAGCT GCGAAGAGA ACCTCAAGGA ACCATCAAGGA AGCAAGGAA ACCATCAAGGA CGAGCAAGGAA GCAAGTTTT GACATGGACAAGA TGTCAAAGG TGTGAAGG TGTGAAGG TGTGAAGG TGTGAAGG TGTGAAGG TGTGAAGGAGC TTTGAAGAGAGAG	TTGCTCATTT CGCACACAC GCGGCCGGC GACGCCCGGC AGCTGCTGCACACACAC GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT TAGTCTTAGA ATGTCTTAGA ACAGTCAGTC ATGTCTTAGA ACAGTCAGTC TGAAAGGGT TGAAGACCACT AATGCTCTT AATGCTCTG TGAAGCTCT TGAAGCTCT TGAAGCTCT TGGACGACAC CGGTTGAGAA TCAGCACTC TGGACGAGT TGTTTACCT TGGACGAGT CGATTTACCT TGGACGAGT CGATTCCACCAC ACTGCCACC ACTGCCACC ACTGCCACC ACTCCACCT ACTGCACTC ACTGCACTC ACTGCACTC ACTGCACCAC ACTGCCACC ACTGCACTC ACTCATTCAC ACTGCACTC ACTGCACT ACTGCACTC ACTGCACT ACTGCACTC ACTGCACT	ATTGCAACGG CGGGGGGAAA CGCGGGGGGAAA CGCGGGCCTG CCAGAGGCCT CGAGGCCTG CGAAGGAAGA AGTGAAGACC CTCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACTCT TCTGGAGCTG AAAAGTTAAG GAACATTCAG AAGTTAAGAC ACCCCCTCT TTTGGGACTC AAAAGTTAAG CACACCTCTCT TTTCGGAGCTG AAAAGTTAAG CACCCACTCTCACCACACCA	120 180 240 360 420 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1740 1860 1860 1980
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGGTGGG GCGACGATGG GCCGGTGCTCA GCCGGTGCTCA TATCTGCAAG TGTTACTACA TGTGTTCTCA AGTGCAACCA TGTGGATCAC TCTGGTCTCA AGTGCAACCA AGCATTCACCA TCCCATCACCA CCCCAATCA GCCCCAATCA GCCCCAATCA GACAGTGGG GACTTGGGGA ATCATGACA ATCATGACC AATCATGACC AATCATGACC GACTTGGGGGA AGCCGACTCA CCAGGGCTTCACCA AGCAGTCACCA CCCAGGGCTCACT CCAGGGCTACTCA CCAGGGCTACTCACT CCAGGGCCTCACT CCAGGGCCTCACT CCAGGGCCTCACT CCAGGGCCTCACT CCAGGGCCTCACT TATGGCAACT	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG ATGAAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGACA ATCACACAC CAAGAAGGCA CAGACAACAC TAGAGATTCC TAGAGATTCC TAGAGATTCC TAGAGATTCC TAGACATCC CTTCCACCGG CCAGCCAGC CCACTCGACC CCACCCAGC ACCATCGCACC GCACGGACCC GCACGCCAA ACAATGCCAT AACCTCCCCC GTGCCAAAGT	3036 21 CCCGGGCCAA AACGCGCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCGGG GTTGCCGTG CTGCTGTTGGG AAAATGACTG AAATGATGT TGTCTTCCCA ACCAAACTTC TAAAAGAGA AGTTTTCAGA AGTTTTCAGA ACTCTTCCCA ACCAAACTTC TAAAAGAGA TAATCAGGT TATTTCTGGAC TGTCAGTGGG CACGACAGC GGGCTGTAGC GGGCTGTAGC GTAACCATC GGACCCT GAAGGATT GAATGAGGT TATTTCTGGAC TGTCAGTTGAA ACTCTTCCCA CCTGCACACT CCTGCCAGACTC CCTGCACAGCT TGGGATCTCC CTTGCACAGCT TGGGATCTCC CTTGCACAGGT TGGGATCTCC CTTGCACAGTT TGGGATCTCC CTTGCACAGGT TGGGATCTCC CTCGAAGAGT CTCGAACAGTT TGGGATCTCC CTCGAACAGTT TGGGATCTCC CTCGAACAGTT TGGGAACTCC	CTCGGACAGT GCGCGACGCA CAGCAGCA AGCGGGCCCGAG GCGCCCGAGGGCCCGAGGCA AGTGGGGACC CTCATTGCA GCTCGAAATT TCTGATTCAG GCTGCAAGAA ACCCTCAAGG ACCATGAAGAAG GCAAGATTT GACATGGCA GCTGCAAGG ACCATGAGGA GCCATGAGGA GCCATGAGGA GCCATGAGG TGTCAAATG CCCATGTGT CGGGTGTCCA TGTCAATGG CCATGTGT CGGGTGTCCA TGCTGCAGC CACGAGTGCGC CACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CTTTCAGAGAGC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT TCAGCACACACACACACACACACACACACACACACACACA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTGAGGAGAAA AGTGAAGAGA AGTGAAGAGC CAGCACGTC CAGCACGTCAAGCACA CAGCACGTT TOTIGGAGCTG AAAAGTTAAG GAACATTCAG AACTTCAGCACA ACTCGCATA ACCACCTCT AAAAGTTAAG GAACATTCAG AACTTCGGAAA CATCGGCATG AGGAGGCTGC CAGCAGGAGTC CAGCAGGAGTC CAGCAGGAGT CAGCAGGAGT CAGCAGGAGT AGGAGGCTGC CAGCAGGAGT CAGCAGGAGT CAGCAGGAGT CAGCAGGAGT CAGCAGGAGT CACAGGGGCC GAGTGTGAC ACTCTGCGCA ACGTGTACCCT GAGAGGTCC GGATGTGGAC ACTCTGCGCA ACTCTGCGCA ACGTGATCCT GAGAGATCCT GGAGATCCT	120 180 240 360 420 540 660 780 960 1020 1140 1200 1140 1560 1620 1680 1740 1860 1920 1860 1920
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGGTGGG GCGACGATGG GCCGGTGCTCA GCCGGTGCTCA TATCTGCAAG TGTTACTACA TGTGTTCTCA AGTGCAACCA TGTGGATCAC TCTGGTCTCA AGTGCAACCA AGCATTCACCA TCCCATCACCA CCCCAATCA GCCCCAATCA GCCCCAATCA GACAGTGGG GACTTGGGGA ATCATGACA ATCATGACC AATCATGACC AATCATGACC GACTTGGGGGA AGCCGACTCA CCAGGGCTTCACCA AGCAGTCACCA CCCAGGGCTCACT CCAGGGCTACTCA CCAGGGCTACTCACT CCAGGGCCTCACT CCAGGGCCTCACT CCAGGGCCTCACT CCAGGGCCTCACT CCAGGGCCTCACT TATGGCAACT	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG ATGAAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGTCC ATGTCAGACA ATCACACAC CAAGAAGGCA CAGACAACAC TAGAGATTCC TAGAGATTCC TAGAGATTCC TAGAGATTCC TAGACATCC CTTCCACCGG CCAGCCAGC CCACTCGACC CCACCCAGC ACCATCGCACC GCACGGACCC GCACGCCAA ACAATGCCAT AACCTCCCCC GTGCCAAAGT	3036 21 CCCGGGCCAA AACGCGCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCGGG GTTGCCGTG CTGCTGTTGGG AAAATGACTG AAATGATGT TGTCTTCCCA ACCAAACTTC TAAAAGAGA AGTTTTCAGA AGTTTTCAGA ACTCTTCCCA ACCAAACTTC TAAAAGAGA TAATCAGGT TATTTCTGGAC TGTCAGTGGG CACGACAGC GGGCTGTAGC GGGCTGTAGC GTAACCATC GGACCCT GAAGGATT GAATGAGGT TATTTCTGGAC TGTCAGTTGAA ACTCTTCCCA CCTGCACACT CCTGCCAGACTC CCTGCACAGCT TGGGATCTCC CTTGCACAGCT TGGGATCTCC CTTGCACAGGT TGGGATCTCC CTTGCACAGTT TGGGATCTCC CTTGCACAGGT TGGGATCTCC CTCGAAGAGT CTCGAACAGTT TGGGATCTCC CTCGAACAGTT TGGGATCTCC CTCGAACAGTT TGGGAACTCC	CTCGGACAGT GCGCGACGCA CAGCAGCA AGCGGGCCCGAG GCGCCCGAGGGCCCGAGGCA AGTGGGGACC CTCATTGCA GCTCGAAATT TCTGATTCAG GCTGCAAGAA ACCCTCAAGG ACCATGAAGAAG GCAAGATTT GACATGGCA GCTGCAAGG ACCATGAGGA GCCATGAGGA GCCATGAGGA GCCATGAGG TGTCAAATG CCCATGTGT CGGGTGTCCA TGTCAATGG CCATGTGT CGGGTGTCCA TGCTGCAGC CACGAGTGCGC CACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CCACGAGCAGC CTTTCAGAGAGC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT TCAGCACACACACACACACACACACACACACACACACACA	ATTGCAACGG CGGGGGGAAA CGCGGGGGGAAA CGCGGGCCTG CCAGAGGCCT CGAGGCCTG CGAAGGAAGA AGTGAAGACC CTCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACTCT TCTGGAGCTG AAAAGTTAAG GAACATTCAG AAGTTAAGAC ACCCCCTCT TTTGGGACTC AAAAGTTAAG CACACCTCTCT TTTCGGAGCTG AAAAGTTAAG CACCCACTCTCACCACACCA	120 180 240 360 420 540 660 780 960 1020 1140 1200 1140 1560 1620 1680 1740 1860 1920 1860 1920
50 55 60 65 70	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCGACGATGG GCGCGGTGGT GCGACGATGA GCCCGGTGGT GTGATGAAG TTCGACTCCA TGTCATCAAC TGTGATCACA AGTGCAACCA TGTGGATCAC AGTGCAACCA TGTGGATCAC ATCATGACACA ATCATGACACA ATCATGACACA GCCCCAATCA ATCATGACA AGGACATTCA AGCACATCACA ATCATGACA ATCATGACA ATCATGACA AGCACACT CACTGGGG AAGCCGCACT CACTGCTCACT AGCCCTCACT AGCCCTCACT AAATGTGGAACT AAATGTGGAACA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCCC TTGTCAGTC TTGTCAGTC TTGTCAGTC ATGTGAAAG ATGACATCA ATGACATACTA ATCACAACAC CAAGAAGAGCA ATGACATACTA ATCACAACAC TAGAGATTGC TAGAGATTGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TGGTCCATGA ATCACACG CTCCATGA ATCACACG CTTCCACCG CCACTCGAAC CTTCCACCG CCACTCGAAC CTTGTGTCACC GCCAGCCCAA ACATGCCAC CGCCCCAAC AACATGCCAC CTTGCCACC GTGGCAAACT AAACTGCCAT AAATCCAGTGC AAACTGCCAC TAGACAACT TAGACAACGC TAGAGGAAACT AAATCCAGTGC TAGACAACGC TAGACAACGC TAGACAACGC TAGACAACGC CCGTGGCAAACT AAATCCAGTGC TAGACAACGC TTGCCACC TTGCACAGC TAGACAACGC TAGACAACACC TAGACAACCACAACC TAGACAACCACAACC TAGACAACCACAACC TAGACAACCACC TAGACAACCACAACC TAGACAACCACAACC TAGACAACCACAACC TAGACAACCACAACC TAGACAACCACACC TAGACAACCACACC TAGACAACCACACC TAGACAACCACACC TAGACAACCACC TAGACAACCACACC TAGACAACCACC TAGACAACCACC TAGACAACCACACCAC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGC TAGAAGAGC TAGAAGAGC CGCTCGCGG GCTGCCGTG CTGCCGTG TGCCAGGCC CTCTGTTCGG AAATGCTG AAATGCTG AAATGCTG AAATGCTG AAATGCTT TGTCTCCCA ACCAAACCTC TAAAAGAGAG TAATCAGGT AGTGTGGAAG TATCAGGTAACTC GGAAGAGT ATTCTGGAC GTACCCATTT GAAAGGAAG GTACCCATTT GAAAGGAAG CGTGACCTC CAGCAACCTC TAGAAGGATG CAGCAACCC CTTGCAGACT CGTGCAGACT CGTGCAGACT CTGCCAGACT CTGCCAGACT TGGGATCTGC CTTGCAAGAGT TCCAAGAGGT TCCAAGGAGGT TCCAAGAGGT TCCAAGAGAGT TCCAAGAGAT TCCAAGA	CTCGGACAGT GCGCGACGGC GCGGCGCGCGC GCGGCCCGAGGGCCCGAGGGCCCGAGGGCCCGAGGGGCCCGAGGGGCCCGAGGGGCCCGAGGGGCCCGAGGGGCCCGAGGGAGAGAGAGCCCCCAGGGGCCCGAGGGGAGGA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCAC ACACGGTAAT CAGTCATTTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTGT AAGGCACAC CGAATTCACA CGGTAATT TGAAAAGCT TTGAAGATCATA ACATAAGT TGAAGCCACT AATGCTCTGT TGAAGCTATT TGGAAAAGCA TCAGCACTA TCAGCACTT TGGAAGAGG ATGCCACCAC ACTGCCAGCT CAGAGTTCTCA AGGGTTCAC ACTGCAGCT CAGAGTTCTCA ACTGCAGCT CAGAGTTCTCA ACTGCAGCT AATGCAGCACA AATGCAGCACA CAATGCAGCACA AATGCAGAGT AATGCAGAGT CAATTCTGC AATGCAGGAGT CAGTCATTCACA AATGCAGGAGT CAGTCATTCACA AATGCAGGAGT CAGTCATTCACA AATGCAGGAGT CAGTCATTCACACACAC AATGCAGGAGT CAGTCATTCACACACAC AATGCAGGAGT CAGTCATTCACACACACACACACACACACACACACACACA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CGAAGGCAG AGTGAAGACA AGTGAAGACA AGCAACGAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC ACCACCTCT TGTGGAGCTC AACCACCTCT TGTGGAGCTG AAAAGTTAAG GAACATTCAG CATCGGCAAA CATCGGCATG ACTCTGGCAAA CATCGGCATG AGGACCATTCC CAGCAGGGTCC CACCAGGGCTC CACCAGGGAAG CCCGGAAGTC CACAGGGGCTC CACAGGGGCTGC CACAGGGGCC GAATGTGGAC ACTCTGCAAA CATCGCAGAGAG CCCGAAGTC CACAGGGGCC GAATGTGGAC ACTCTGGGAA CATCGGCAGAG CCCGAAGTC CACAGGGGCC GAATGTGGAC ACTCTGGGGA AGGTGATCC GAGAGATGCT GAGAGATGCT GAGAGATGCT GAGAGATGCT GAGAGATGCT GAGAGATGCC GGAAGTGCC GGAAGTGCT TACCAATGCC	120 180 240 360 420 660 660 6720 780 840 900 1020 1140 1200 1140 1560 1560 1620 1680 1740 1860 1920 1980 2100
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCGACCATGG GCGACCATGA TATCTGCAAG TGTGATCAAA TATCTGCAAG TGTGATCACA CTGGTCTCA AGTGCAACA CAGACATGG CAGCATTAA ATCGTCTGG CAGCATTAA ACCGTGTTGG CACTCATGACA GCCCCAATCA ACCATGACA GCCCCAATCA ACCATGACA GACATGGAGA AGGGAGTCTA CACCATGACA GACATGCAGCA GACATGCAGCA GACATGCAGCA CCCCATCACT CACCATGCACA GACATCCCC CACTGCAGCA AGGCACCACT CACCATGCACA CACCATCACA CA	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTGC ATGTAGTAG ATGAAAGA ATGACATGT ACAGATACAA ATCACACAC CAAGAAGCA CAAGAAGCA TAGGCAGTGA TAGGCAGTGA ATGGCAGTGA ATGCCAGCAG TAGGCAGTGA ATGCCAGCAG TAGGCAGTGA ATGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC GGTCCCGTG CTGCTGTTCGG AGAAGTTCTCCA AACTCTCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGA ACTCTTCCCA ACGAACCTC TAAAAGAGAG TAATCAGGTTAGG CAGGCAGAC GGGCTGTAGC GTACCCTG GAAGGATTCGG AGGGTTTCGCA ACTGTAGCCTC CGGCAGACTCC GGAACTCCC CTGCAGACT CGTGACCTG CTGCAGACT CCCCCTGCACC CCCCCCCCCC	S11 CTCGGACAGT GCGCGACGCA CAGCAGCA ACAGCGGCGCAGGA AGTCGCGCGCCCAGG CTCCGGTCGA AGTGGGGACCA AGTGGGGACCA AGTGGAGAAT TCTGATTCAG GCTCGAAAT TCTGATTCAG AATGAAAGCT GCGAAGAAGA ACCCTCAAGG AGCAAGAAGA ACCTTCAAGG AGCAAGAAGA CCTCAAGGA AGCAAGATTTT GACATGGACA TGGAGGAAGA GTTAATTTCC CAGTCTGGGG GCACATTGGCC TGTCAAAT TGGAGGAGAG TTTCAAATGG CCATGGTGT AACAGATTTG CGCTGCTGCAG TGTGACTCC CACGATGGGC CACGAGCAGC TTTTGAGAGAG TTTTGAGAGAG TTTTTGCCAG CCACGAGCAGC CCAAGGAGCAGC CCAAGGAGGAGC CCAAGGAGGAGC CCAAGGAGGAGC CCAAGGAGGACC CCAAGGAGAGC CCAAGGAGGACC CCAAGGAGGACC CCAAGGAGAGC CCAAGGAGGACC CCAAGGAGAGC CCAAGGAGAGC CCAAGGAGGACC CCAAGGAGAGC CCAAGAGAGACC CCAAGGAGACC CCAAGGAGACC CCAAGGAGAGC CCAAGGAGAGC CCAAGGAGACC CCAAGCAGC CCAAGCA	TTGCTCATTT CGCACACACA GCGGGCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGTAAT CAGTCAGTCAT ATGTCTTAGA ACAGGTAAT ATGTCTTAGA ACAGTACCC CAACTAGTCT TGAGACACG GAATTCTCAT TGGGCCACAC GAATTGTCAT TGGGCCACAC TGGAGAGAGT TGGAGAGAGT TGGAGAGAGC ACTGCACCAC ACTGCCACC CAGAGTTCTCACC ACTGCCACC ACTGCCACC CAGAGTTCTCC CAGAGTTCTCC CAGAGTTCTCC CAGAGTTCTCC CAGAGTTCTCC CAGAGTTCTCC CAGAGTTCTCC CAGTCATTCCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTCC CACCTC CACCTCC CACCTC CACCT CACCTC CACCT CACC CACCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAGA AGTGAAGACG AAGCAAGAA AGTGAAGACC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG AACTTCAGAAT CACCCCTCT TGTGGAGCT ACCACCCTCT TGTGGAGCT ACCACCCTCT TGTGGAGTCA ACCACCCTCT TCTGGAGCTG AAAGTTAAG GAACATTCGGAAT CATCGGCATG GAACCATTCA TTTCGGGATG CAGCAGGAGTC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACTTGGAA ACTCTGGGAA CTCTTGGGAC CACTGGGAA AGGTGTGTC CACTGGGAC AGCTTGGAC AGCTTGCAC CACAGGGGCC CACTTGGGGA AGTTTGGGCA CACTTGGGGA AGTTTTGGCC TGAAGAGTTCT TACCCTTG GAAGAGTTCT TACCAATGCC CCCGGGGAC TTCCGAGGAC TTCCGAGGAC TTCCGAGGAC TTCCGAGGAC CCCGGGGGCC TACCAATGCC TCCCGAGGGCC TCCCAATGCC TCCCCAGGGCCC TCCCAATGCC TCCCCAGGGCCC TCCCCAGGGCC TCCCCAGGGCC TCCCCAGGGCC TCCCCAGGGCC TCCCCAGGGAC TCCCCAGGGCC TCCCCAGGGCC TCCCCAGGGAC TCCCCGGGGAC TCCCCAGGGGCC TCCCCAGGGGCC TCCCCAGGGCC TCCCCAGGGCC TCCCCAGGGAC TCCCCAGGGCC TCCCCAGGGAC TCCCCAGGGAC TCCCGGGGAC TCCCGGGAC TCCCGGGGAC TCCCGGGAC TCCCGGCAC TCCCGGCAC TCCCGGCAC TCCCGGCAC TCCCCGGAC TCCCCCCGGAC TCCCCCCGGAC TCCCCCCGGAC TCCCCCCCCCC	120 180 240 360 420 540 660 720 780 960 1020 1140 1200 1320 1560 1560 1620 1580 1590 1980 2040 2040 2160
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCTT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGGG GCGACCATGG GCCACTACTAA TATCTGCAAG TTTGGATCAAC TCTGGTCTAA AGTGCAACAC CAGACATGGG GCACTACAC AGTGCAACAC ACTGTGTCAAC ACTGTGTCAAC ACTGTGTCAC AATCATCAC AATCATCAC AATCATCAC AATCATCAC AATCATCACA ATCATGACC AATCATCACA ACTGTGGGAC AAGCGGACTAC CGCTACTAC AATCATCACC CAGGGACTACTC CCAGGGACAC AGCCCTCACT CCCAGGGACAC AGCCCTCACT CCCAGGGACAC AGCCCTCACT CCCAGGGTGTACT CCAGGGTCTAC CCAGGGTGTACT CCAGGGTACTC CAGGGTGTACTC CCAGGTGTACTC CCAGGTGTACT CCAGGTACT CCAGGTGTACT CCAGGTGTACT CCAGGTGTACT CCAGGTGTACT CCAGGTGTACT C	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCAGGGGCCC TGCTCGGCCC ATGTCAGTC ATGAAAG ACAGTACTAG ATGAAAG ACAGTACTAG ACAGTACTAG ACAGAACAC CAAGAAGGCA CAAGAACAC CAAGAAGGCA TTGGCAGCC TTGGCCCTCATGA ATGCCACGGC TAGGCATGCA ATGCCACGGC CCACCCAGC CCAGCCTAGA TCGGGGGCCA AGCCAGAGC CCAGCCCAGA ACCAGCGCCAA ACAATGCCA CTGGCACCCC GCCCAGCCCA	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGC TAGAAGAGC TAGAAGAGC CAGCAGAACC CGCTCGCCGC GCTGCCCGTG AGAAGTGCT AAATGAAGGT TGTCTCCCT ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGAG ACTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACTCTTCCAA ACGGGATAT AGTGTGGAAT ATTTCTGGAC CGTGACCCTG GAAAGGTTTCAG GAAGTTTCAG GAAGTTTCAG CATGGCAGAC CGTGACCCTG CAGCAACCCC CGTGTACCTG CAGCAACTCC CGGGATCTGCC CGTGCAAGAGT TGCAAGAGT TCAAGGGGT CCCCTGCAC CTGCAAGAGT CCCCTGCAC CCTGCACCC CCTGCACCCCCCCCCC	31 CTCGGACAGT GCGCGACGCA GCACGCGCCCCCCCCCC	TTGCTCATTT TGGCTCATTT TGGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC ACACGGGA GCAGTTTCAC ACACGGTAAT TGAAAAGGGT ATGTCTTAGA AGATCTGGA ACAGACCACT AATGCTCTT AATGCTCTT AATGCTCTGT TGAAGACCACT TGAAGTCAGA CGGATTGTAGA CGGATTGTAGA TGGAAGACCACT TGGAAGACACT TGGAAGACGC TGTTTAACCT TGGAAGACGC ACTGCCAGCT CAGAGTTCTGC ACTGCCAGCT CAGAGTTCTGC ACTGCAGCT CTCATTTGCG GGATTCTGCC GGGTTTGCAGCG GGATTCTGCC GGGTTTGCAGCT TCATTTGCG GGATTCTGCC GGGTTTGCAGCG TGCTTTGCAGCT TGCTTGCAGCT TGCTTTGCAGCT TGCTTTGCAGCT TGCTTTGCAGCT TGCTTTGCAGCT TGCTTGCAGCT TGCTTTGCAGCT TGCTTTTCAGCT TGCTTTCAGCT TGCTTTTTTTTTT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTGACGCCTG CGAAGGAAGA AGTGAAGACC ACTGGGTCAC ACCACCTCT TCTGGGTCAC AAAACTTAAG GAACATTCAG AAACTTCAG AACTTCAGAAA CCTCGCAAA CCACCCTCT TCTGGAGCTG AAAACTTCAG AACTTCAGCATG AACTTCAGCATG AAGCATTCA TTTCGGGATC CGACAGGAGC CACCAGGAGC CACCAGGAGC ACCTCGCAAA CATCGCCATG AGGAGGCTGC CACAGGAGC CACCAGGAGC CACCAGGAGC CCGGATGTGAC CTCTACCCTG GAAGCTTCA CACAGGGCC CGATGTGGAC ACTCTGCGAA ACTCTGCGAA CTTCACCTG CACAGGAGC CCGGGAGTCC CACAGGAGC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGGCC CCCGGGGGCC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCACAAAGTGT	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560 1620 1680 1860 1980 2040 2160 2160 2220
50 55 60 65 70	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCGACGATGG GCGCGGTGGT GCGCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA TGTGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC AGTGCAACA TGTGGATCAC AGTGCATCAC ATCATGACA TGCCCAATTAA ATGGGAGATTAA ATGGGAGATCTT GACTGTGGGG AAGCCGCTCACT GCCTACTCC CCAGGTGCTT TATGGCAACT AAATGTGAAC GCTACTCATACA CCAGTTGCTACT CCAGGTGCTACT AAATGTGAAC GCAGTGCTACT AAATGTGAAC GCAGTGCTACT CCAGGTGCTACT CCAGGTCTACT CCAGGTGCTACT CCAGG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCCC TTGTCAGTC TTGTCAGTC TTGTCAGTC ATGTAAAGGC AGAGACATGT ACAGAACAC TAGGACATAT ACAGATACAA ATCACAACAC TAGGCGTGGA ATGGCATGT TGGGCATGT TGGGCATGT TGGCCAGC TGGTCAGC CACTGGACAG CTTCCACCG CCACCTGGA ACATGCCAG ACCAGCCAG ACCAGCCAG ACCAGCCAG ACACTGCC CGCCCCAGC AACCTGCCCAG AAACATCCAGTG AAACTGCCAG AAACAACCG TGGGCAAACG AAACAACCG AAACAACCG AAACCTGCCCAG AAACAACCG AAACCAGCCAAC AAACAACCAG AAACCAGCCAAACCAG AAACAACCAG AAACAACCAG AAACAACCAG AAACAACACACAC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGG GCTGCCGTG CTGCAGGCC CTCTGTTCGG AAAATGCT AAATGATGTT TGTCTCCCC ACGGGGTAT TGTCTTCCCA ACCAAACCTC TAAAAGAGT TATCTTCCCA ACCAAACCTC TAAAAGAGT TGTCTTCGGA TGTGTTGGAAT ATTCTGGAC TGTCAGTGGGC CAGGCAGCC CGTGACCCT GGACTGTAGC GAAAGGTTAGC TAAAGGAGT TGTCAGTGGG CACGCCAGC CGTGCCCC CCTGGAGCT CCCCCTGCAGCT CCCCCTGCAG CATGCCGGAC CATGCCGCAC CATGCCCCCCTCCCCCCCCCC	CTCGGACAGT GCGCGACGGA CAGCGGGGCCCGAG GCGGGCCCGAG GCGCGCCCCGCCCG	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGG AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATTTAGA TGAAAAGCGT ATGTCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTT TGAAGCTACT TGAAGCTCC TGAAGCACAC ACTGCCACAC ACTGCCACC ACTGCCACC ACTGCCACC TCAATTCTGC AATGCGACAT CAGTCTTCTGC ACTCATTCTGC TCATGTCTCAC TCATGCTCACC TTAGTGTCACC TTAGTGTCACC TTAGTGTCTCT TTAGTGTCTTCTCT TTAGTGTCTCT TTAGTGTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTCT TTAGTGTCTCT TTAGTGTCTTCTCT TTAGTGTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTCT TTAGTGTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCTCT TTAGTGTCTTCTCTCTCT TTAGTGTCTTCTCTCTCTCTCTCT TTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGTCGGC CTGAAGGCCG CGAAGGAGA AGTGAAGAGA AGTGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTCT TGTGGGTCAC ACCACCCTCT TGTGGGTCAA ACCACCCTCT TGTGGAGCTG AAAGTAAAA CAGCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG CACCACCCTCT TGTGGGGTCA ACCACCCTCT TGTGGGGTCA ACCACCCTCT CGGGGATCA ACCACCCTCT CGGGAAG CATCGGCATG GGACCATTCG GAAGCTTCC GAAGGCTGC ACTCTGGGAA ACTCTGGGAA CATCTGGGAC CCGGAAGTC CACAGGGGCC CGATGTGGAC ACTCTGGGGA AGGTGATCCT GAAGGTGCT CGGGGGACC CCCGGGGGACC CCCCGGGGGACC CCCCGGGGGACC CCCCGGGGGACC CCCCAAAGTGCT CCCCGGGGGACC CCCCAAAAGTGT TGGGGTTCAC CCCGGGGGACC CCCAAAAGTGT TGGGGTTCAC	120 180 240 360 420 540 660 720 780 960 1020 1140 1200 1320 1560 1560 1620 1580 1590 1980 2040 2040 2160
50 55 60 65 70 75	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCGACGATGG GCGCGGTGGT GCGCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA TGTGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC AGTGCAACA TGTGGATCAC AGTGCATCAC ATCATGACA TGCCCAATTAA ATGGGAGATTAA ATGGGAGATCTT GACTGTGGGG AAGCCGCTCACT GCCTACTCC CCAGGTGCTT TATGGCAACT AAATGTGAAC GCTACTCATACA CCAGTTGCTACT CCAGGTGCTACT AAATGTGAAC GCAGTGCTACT AAATGTGAAC GCAGTGCTACT CCAGGTGCTACT CCAGGTCTACT CCAGGTGCTACT CCAGG	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG CAGCGCGCCC TTGTCAGTC TTGTCAGTC TTGTCAGTC ATGTAAAGGC AGAGACATGT ACAGAACAC TAGGACATAT ACAGATACAA ATCACAACAC TAGGCGTGGA ATGGCATGT TGGGCATGT TGGGCATGT TGGCCAGC TGGTCAGC CACTGGACAG CTTCCACCG CCACCTGGA ACATGCCAG ACCAGCCAG ACCAGCCAG ACCAGCCAG ACACTGCC CGCCCCAGC AACCTGCCCAG AAACATCCAGTG AAACTGCCAG AAACAACCG TGGGCAAACG AAACAACCG AAACAACCG AAACCTGCCCAG AAACAACCG AAACCAGCCAAC AAACAACCAG AAACCAGCCAAACCAG AAACAACCAG AAACAACCAG AAACAACCAG AAACAACACACAC	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT CAGGAAATCC CGCTCGCGG GCTGCCGTG CTGCAGGCC CTCTGTTCGG AAAATGCT AAATGATGTT TGTCTCCCC ACGGGGTAT TGTCTTCCCA ACCAAACCTC TAAAAGAGT TATCTTCCCA ACCAAACCTC TAAAAGAGT TGTCTTCGGA TGTGTTGGAAT ATTCTGGAC TGTCAGTGGGC CAGGCAGCC CGTGACCCT GGACTGTAGC GAAAGGTTAGC TAAAGGAGT TGTCAGTGGG CACGCCAGC CGTGCCCC CCTGGAGCT CCCCCTGCAGCT CCCCCTGCAG CATGCCGGAC CATGCCGCAC CATGCCCCCCTCCCCCCCCCC	CTCGGACAGT GCGCGACGGA CAGCGGGGCCCGAG GCGGGCCCGAG GCGCGCCCCGCCCG	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGG AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATTTAGA TGAAAAGCGT ATGTCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTT TGAAGCTACT TGAAGCTCC TGAAGCACAC ACTGCCACAC ACTGCCACC ACTGCCACC ACTGCCACC TCAATTCTGC AATGCGACAT CAGTCTTCTGC ACTCATTCTGC TCATGTCTCAC TCATGCTCACC TTAGTGTCACC TTAGTGTCACC TTAGTGTCTCT TTAGTGTCTTCTCT TTAGTGTCTCT TTAGTGTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTCT TTAGTGTCTCT TTAGTGTCTTCTCT TTAGTGTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTCT TTAGTGTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTTCTCT TTAGTGTCTTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCT TTAGTGTCTTCTCTCTCT TTAGTGTCTTCTCTCTCT TTAGTGTCTTCTCTCTCTCTCTCT TTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCGGTCGGC CTGAAGGCCG CGAAGGAGA AGTGAAGAGA AGTGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTCT TGTGGGTCAC ACCACCCTCT TGTGGGTCAA ACCACCCTCT TGTGGAGCTG AAAGTAAAA CAGCACCTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG CACCACCCTCT TGTGGGGTCA ACCACCCTCT TGTGGGGTCA ACCACCCTCT CGGGGATCA ACCACCCTCT CGGGAAG CATCGGCATG GGACCATTCG GAAGCTTCC GAAGGCTGC ACTCTGGGAA ACTCTGGGAA CATCTGGGAC CCGGAAGTC CACAGGGGCC CGATGTGGAC ACTCTGGGGA AGGTGATCCT GAAGGTGCT CGGGGGACC CCCGGGGGACC CCCCGGGGGACC CCCCGGGGGACC CCCCGGGGGACC CCCCAAAGTGCT CCCCGGGGGACC CCCCAAAAGTGT TGGGGTTCAC CCCGGGGGACC CCCAAAAGTGT TGGGGTTCAC	120 180 240 300 360 420 600 780 960 1020 1140 1200 1320 1380 1440 1560 1680 1860 1980 2040 2100 2100 2220
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCTT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGGG GCGACCATGG GCGACCATGG GCGACCATGA TTCGACTCCA TCGATCATAA TATCTGCAAG TGTTACTACC TCTGGTTCA AGTGCAACCA CAGACATGGG CAGCGATTAA ATCGTGTTGG CACTCATCA ACTCATCACA ACTCATCACA GCCCCAATCA GCCCTACTC GACATGGGGA AGCCGGACG GGAACAGCGT CCAGGTGCT CCAGGTGCT CAGGTGCT CAGGTGTACT CACTGGACA GCCCTACT CACTGGACA GCCCTACT CACTGGACA GCACTACT CACTGTGGGG AAGCCGTACT CACTGTACT CACTTACT CACTGTACT CACTGTACT CACTGTACT CACTGTACT CACTGTACT CACTGTACT CACTGTACT CACTGTACT CACTTACT CACTGTACT CACTGTACT CACTGTACT CACT	Lence: 37 11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTC TTGTCAGTGC ATCTGGAAAG ACGGTACTGA ATGAAAGAC ATCACAACAC CAACAACAC CAACAACAC TAGGAATACAA ATCACAACAC TAGGACTGAT TGGGCCAGACACC CTGGCCAGC TGGGCCAGACACC CTGGCCAGCC CTGGCAGGAC CTGCCAGGC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC CTGGCAGCAC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC CTGGCAGGAC ACATGGCAT AAACACAC TGGGCACAC ACATGGCAT AAACACAC TGGGCAGCAC AAACACAC TGGGCAGCAC AAACACAC TGGGCAGCAC AAACACAC TGGGCAGCAC AAACACAC TGGGCAGCAC AAACACAC TGGGCATGAA AAATCCACT TGGGCATGAC TTGGGCATGAC TTGGGCATGAC TTGGGCATGAC TTGGGCATGAC TTGGGCATGAC TTGGGCATGAC TTGGGCATGAC TTGGGCATGAC TTGCAGTGCCC TTGCAGTGCC TTGCAGTGC TTGCAG	3036 21 CCCGGGCCAA AACGGGGGC TAGAAGAGCT TAGAAGAGCT CAGGAAATCC GCTCGCGGG GTTGCCGTG AAATGAAGGC CTCTGTTCGG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTCTTCCCA ACCAAACCTC TAAAAGAGAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAGAAA CCTGTAATCAGTT AGTGTGGAAT ATTCTCGAA ACTCTTCAGAGGC CAGGAACCCC CTGTACCCTG CAGCAGCCTG CTGCCAGACT CTGCAGAGCT CTGCAGACT CTGCAGACT CTGCAGACT CTGCAGACT CTGCAGACT CTGCAGACT CTGCAGACT CTGCAGACT CTGAAGGAGT TCAAGGAGT TCAAGGAGT TCAAGGAGT TCAAGGAGT CCCCTGCAC CATGCCGGA CGAATCGTCAG CGAGACTCCC CTGCAGAGGG CGAATCGTCAG CGGCAGAGGG CGAATCGTCAG CGGCAGAGGGC CGCAGAGGGC CGCCAGAGGGC CGCAGAGGGC CGCCAGAGGGC CGCCAGAGGCC CGCCAGAGGGC CGCCAGAGGGC CGCCAGAGGGC CGCCAGAGGGC CGCCAGAGGCC CGCCCAGAGGCC CGCCCCCCC CGCCCCCCCC	CTCGGACAGT GCGCGACGCA CAGCGCGCGCCCGACGCA AGTGGGGGCCCGAC AGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGC GCTCAAAGA ACCCTCAAGG AGCAAGAAGA ACCCTCAAGG AGCAAGAAGA CGCTGAAATT GACATGGACA GGTGAAAGA ACCTTCAAGG AGCAAGGAC GCACATGGTGT GACATGGACA CGCTGCAGAGA GTTTAATTCCC CAGTCTGGGG CCACATGGTGT CGCAAGAGAG CCCATGGTGT CGCAGAGGAG CCCAGGGCTT CCAGGGCTGC CACAGGCAGC CCACAGGCGC CCACAGGCGC CCACAGGCCT CTCCACACAC CCACAGGCCT CCACAGGCT CTCACACAC CTCACACAC CCACAGGCT CTCACACAC CCACAGGCT CTCACACAC CTCACACAC CTCACACAC CCACAGGCT CTCACACAC CTCACAC CTCACACAC CTCACAC CTCACAC CTCACAC CTCACAC CCACACAC CTCACAC CT	TTGCTCATTT CGCACACACA GCGGCCGGC GACGCCGGC AGCTGCTGC GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCAGTCAT ATGTCTTAGA ACACGGTAAT TGAAAAGCGT ATGTGTTTCC CAACTAAGT ACAGGACTACT AAGGCTCTGGA ACAGACTCTGGA ACAGACTCTGGA ACAGACTCTGGA ACAGACTCTGT TGAAGACTACT CGGTTGAGAA TCAGCACTC AATGCTCTGT TGAAGACTCTGT TGAAGACTACT CGGTTGAGAA CGGTTGAGAA TCAGCACTC AATGCTCAT TGGAAGAAGC ACTGCCACCAC ACTGCCACCAC ACTGCCACCAC CACTGCCACCAC CACTGCCACC CACTGCCACCAC CACTACACCAC CACTACAC CACTACACCAC CACTACACCAC CACTACACCAC CACTACACCAC CACTACAC CACTAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTGACGCCTG CGAAGGAAGA AGTGAAGACC ACTGGGTCAC ACCACCTCT TCTGGGTCAC AAAACTTAAG GAACATTCAG AAACTTCAG AACTTCAGAAA CCTCGCAAA CCACCCTCT TCTGGAGCTG AAAACTTCAG AACTTCAGCATG AACTTCAGCATG AAGCATTCA TTTCGGGATC CGACAGGAGC CACCAGGAGC CACCAGGAGC ACCTCGCAAA CATCGCCATG AGGAGGCTGC CACAGGAGC CACCAGGAGC CACCAGGAGC CCGGATGTGAC CTCTACCCTG GAAGCTTCA CACAGGGCC CGATGTGGAC ACTCTGCGAA ACTCTGCGAA CTTCACCTG CACAGGAGC CCGGGAGTCC CACAGGAGC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGGCC CCCGGGGGCC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGGCC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCACAAAGTGT	120 180 240 360 420 540 660 780 900 960 1020 1140 1200 1140 1500 1620 1680 1740 1860 1920 1920 1920 1940 2160 2280

		GGCAAGCAGA					2460
	TGTCTTCTTG	CTGCCGGATT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
		AGAAGACCAC					2580
5		AACCCTGTCA					2640 2700
	CACATCACCA	CCTACCCACC GACCCCTCAA	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAATGTT	2760
		TCCACCGGGC					2820
		TTAGGCAGGC					2880
		CTCTGGCCAG					2940
10		CTGGGCTCCG					3000
		CCACCCACAC					3060
		AGTTTGCACT					3120
		TAATGTTTAA					3180
15		GCTATGGTGC					3240 3300
13		GATTACAGTG AAGGCTTGTT					3360
		GGACAGGATG					3420
		CCAGCTGTGC					3480
		TTTCTGGATT					3540
20		TTTCAGGGAG					3600
	ACACCTGGGA	GAAATCTGGC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
		AGGTGTAGCC					3720
		CTGACCAGCC					3780
25		AGAAATGCCA					3840
25		ATTTAGCTTG					3900
		CCACCTCCCT					3960 4020
		ACCAGATCTA					4080
		ACTCTTTATG					4140
30		GTCTGCTATC					4200
•		TTCCAACTTG					4260
	ACCTATTTCT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
	CAACTTGCTT	ATCAACTTCC	TARATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCCTTGAA	4380
25		TTCAAATGCC					4440
35		GAAATACAAA					4500
		TTTCACATTA					4560
		AGCCTTCTTT ATCTTGGTTT					4620 4680
		ATCTAGGCAA					4740
40		AAAAGGGAAC					4800
. •		GTTATTAAGT					4860
		AGAATTACTG					4920
	TATATACTAT	TAAAAAGGTT	TACAGAATTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
45	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT				4980 5040
45	AGATGCCCAA		CTGGCATGTT				
45	AGATGCCCAA ACCAAAAAAA	ATCCTTAGAT AAAAAAAAAA	CTGGCATGTT AA				
45	AGATGCCCAA ACCAAAAAAA Seq ID NO:	ATCCTTAGAT AAAAAAAAA 78 Protein	CTGGCATGTT AA sequence				
45	AGATGCCCAA ACCAAAAAA Seq ID NO: Protein Acc	ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: 1	CTGGCATGTT AA sequence NP_003465	AGCCCTTCCT	CCAATTATAA	GAGGATATGA	
	AGATGCCCAA ACCAAAAAAA Seq ID NO:	ATCCTTAGAT AAAAAAAAA 78 Protein	CTGGCATGTT AA sequence	AGCCCTTCCT			
45 50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11	CTGGCATGTT AA sequence NP_003465 21	AGCCCTTCCT	CCAATTATAA 41	GAGGATATGA 51	5040
	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG	AGCCCTTCCT 31 VSLWNEGRAD	CCAATTATAA 41 EVVSASVRSG	GAGGATATGA 51 DLWIPVKSFD	5040
	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI	AGCCCTTCCT 31 VSLWNEGRAD ASSPTETHYL	CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR	GAGGATATGA 51 DLWIPVKSPD NYTVILGHCY	5040
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE	31 VSLWNEGRAD ASSPIETHYL SYVLEPMKSA	CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK	GAGGATATGA 51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG	5040 60 120
	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL WARRHKRETL LVGVEVWNDM	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH	60 120 180 240 300
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPSQT FYRPLNIRIV FQGTTIGMAP	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS	31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRA VSLHEFLDWR PLGAAVTLAH	GAGGATATGA 51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKGG KMKLLPRKSH ELGHNFGMNH	60 120 180 240 300 360
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LEGGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSCSRKOL	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV	GAGGATATGA 51	60 120 180 240 300 360 420
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHENTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGCIM FVEBGECCDC	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPPPM GEPEECMNRC	31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGTVMDHSDN VFSSCSRKDL CNATTCTLKP	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKOR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT	60 120 180 240 300 360 420 480
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVEEGECCDC LPEFCTGASP	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM NASTGYPFPM GEPEECMNRC HCPANVYLHD	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSQDVDGY	41	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVFR EDCQLKPAGT QQCVTLWGPG	60 120 180 240 300 420 480 540
50	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTFNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGM ACRDSSNSCD AKPAPGICFE	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVEBGEECDC LPEFCTGASP RVMSAGDPYG	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPPPM GEPEECMNC HCPANVYLHD NCGKVSKSSF	31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKOL CNATTCTLKP GHSQDVDGY AKCEMRDAKC	41	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS	60 120 180 240 300 360 420 540 600
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQQG	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 1 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM PVESGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGUEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG	31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSQDVDGY AKCEMRDAKC LVLAGTKCAD	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAR ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQQGGAS GKICLNRQCQ	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMH CLFNLPEVRE EDCQLKPAGT QCVTLWGPG RPVIGTNAVS NISVFGVHEC	60 120 240 300 360 420 480 540 660
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ DTLDRGCSCQ ACCDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVESGECDC LPEFCTGASP RVMSAGDPYG GRILCRGTHV NNRKNCHCEA	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPPPM GEPECMNRC HCPANVYLHD NCGKVSKSSF TYLGDDMPDPG HWAPPPCDKF	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAL GFGGSTDSGP	41	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS INSVFGVHEC IGILVTILCL	60 120 180 240 300 360 420 540 600
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQGC AMQCHGRGVC LAAGFVVYLK	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM MAVEKGGCIM MAVEKGGCIL LPEFCTGASP RVNSAGDPYG GRILCRGTHV NRRKNCHCAA RKTLIRLLFT	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEEGMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDBG HWAPPFCDKF NKKTTIEKLR	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCILKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG	41	S1 DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVFR EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC LGILVTILCL LGKGLMRKPP	5040 60 120 180 240 300 360 420 540 600 600 720 780
50 55	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVLK DSYPFKDNPR	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVERGECCDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGL LAGGLVFENE WARRHKRETL LVGYEVWNDM IMSMCTADQS NASTGYPFPM GEPRECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP	31 VSLWNEGRAD ASSFTETHYL EXYLEPHKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSCSRKOL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	41	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS INSVFGVHEC IGILVTILCL	60 120 180 240 300 360 420 480 660 720 840
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVLK DSYPFKDNPR	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVERGECCDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGL LAGGLVFENE WARRHKRETL LVGYEVWNDM IMSMCTADQS NASTGYPFPM GEPRECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP	31 VSLWNEGRAD ASSFTETHYL EXYLEPHKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSCSRKOL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	41	51 DLWIPVKSFD NYTVILGHCY KKKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNPGMMH CLFNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 360 420 480 660 720 840
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVULAAGFVVJLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTIGMAP MAVEKGGCIM FVERGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LKGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDK SRPLNGLNVP DPLARTTRLT	31 VSLWNEGRAD ASSFTETHYL EXYLEPHKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSCSRKOL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	41	51 DLWIPVKSFD NYTVILGHCY KKKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNPGMMH CLFNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 360 420 480 660 720 840
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKMHPEVLNI YHGHVRGYSD SHHNTFNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO:	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM PVEDGECDC LPEFCTGASP GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LUGLIVFENE WARRHKRETL LVGYEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT	31 VSLWNEGRAD ASSPTETHYL EXYLEPHMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKOL CNATTCTLKP GHSQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW	41	51 DLWIPVKSFD NYTVILGHCY KKKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNPGMMH CLFNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 360 420 480 660 720 840
50556065	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHINTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQCTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WASTENEMENT LVGVEVWNDM IMSMCTADQS NASTGYPPM GEFECMNRC HCPANVYLHD NCGKVSKSSP YLGDDMPDPG HWAPPPCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003	31 VSLWNEGRAD ASSPTETHYL EXYLEPHMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKOL CNATTCTLKP GHSQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW	41	51 DLWIPVKSFD NYTVILGHCY KKKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNPGMMH CLFNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	60 120 180 240 300 360 420 480 660 720 840
50 55 60	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSI SHINTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSI GNUYPPPSQT FYRPLNIRIV PQCTTIGMAP MAVEKGGCIM FVERGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPPPM GEPECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPPDG HWAPPPCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT UNENCE n #: NM_003 .1043	31 VSLWNEGRAD ASSFTETHYLA SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDIN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTFGQW	41	S1 DLWIPVKSPD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	5040 60 120 180 240 300 360 420 480 660 720 780 840
50556065	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHINTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WASTENEMENT LVGVEVWNDM IMSMCTADQS NASTGYPPM GEFECMINC HCPANVYLHD NCGKVSKSSP YLGDDMPDPG HWAPPPCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003	31 VSLWNEGRAD ASSPTETHYL EXYLEPHMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKOL CNATTCTLKP GHSQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW	41	51 DLWIPVKSFD NYTVILGHCY KKKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNPGMMH CLFNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP	5040 60 120 180 240 300 360 420 480 660 720 780 840
50556065	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTILDRGCSCQ SFGGQKCGNR ACRDSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP PVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11	SEQUENCE SEQ	31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDI VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW 714 31	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQQQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR	GAGGATATGA 51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMH CLIFNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	5040 60 120 180 240 300 360 420 480 660 720 780 840
50 55 60 65 70	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSO SHINTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1 GAGGAGGAGGAGG	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG GNVPPPSQT FYRPLNIRIV PQCTTIGMAP MAVEKGGCIM FVERGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11 GAAAAAGGCGA	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPPPM GEPECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPPCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21	31 VSLWNEGRAD ASSFTETHYLA SYVLEPMKSA KATKYVELVI DKCSVSQDPP GGIVMDHSDIN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG	41	GAGGATATGA 51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMH CLIFNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	5040 60 120 180 300 360 480 540 660 720 780 900
50556065	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVERGECIDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA ARKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11 GAAAAAGGCGA AGGAGGAGGAGAA	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LEGGLIVFENE WARRHKRETL LVGVEYWNDM IMSMCTADQS NASTGYPFPM GEPRECMNCC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGAGC	31 VSLWNEGRAD ASSFTETHYL EXYLEPHKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSCSRKOL CNATTCTLKP GHSCQDVDF AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPGSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC	41 EVVSASVRSG QDGTDVSLAR VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA GAGGAGGGGA CAGGTCTCCC	S1 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS IISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	5040 60 120 240 300 420 480 540 600 720 900
50 55 60 65 70	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 1 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVEGGECDC LPEFCTGASP GRILCRGTHV NNRKNCHCEA RKTLIRLLFA TP DNA seq id Accessio uence: 135. 11 GAAAAGGCGA AGGAGGAGGA AACCATGTGT	SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE ALLAPCEARG INLERNEGLI LAGLIVFENE WARRHKRETL LVGYEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANVYLHD NCGKVSKSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKF NKKTTIEKF SEPLINGLNVP DPLARTTRLT USENCE SEQUENCE SEQ	31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKOL CNATTCTLKP GHSQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGTT	41 EVVSASVRSG QDGTDVSLAR VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQQQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTG	GAGGATATGA 51	5040 60 120 300 360 420 480 540 660 720 780 900
50 55 60 65 70	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVYLK DSYPPKDNPR ALRQAGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1 GAGGAGGAGG GAGGAAGAGG GAGGAAGAGG GAGGAAGAGG TAATACCAAG TGCCCACTT ACAGGAGCTC	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTIIGMAP MAVEKGGCIM FVERGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA ARTILLIFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio ueance: 135. 11 GAAAAGGCGA AGGAGGAGGA AACCATGTGT TGACCCGGGG CCCAGCAGAAA	CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LEGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPRECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGAGCG GCCGAGGGGCG GCCGAGGGGCG GGCCGAGCGGCG GGCCGCCTGT	31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP QVPSSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACTA ACGCCACCAA	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIÇCQGGAS GKICLNRQCQ IRQADNGGLI FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTAG TACAGCGGAG TACAGCGGAG	51 UNIPVKSPD NYTVILGHCY KKKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMMH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCI LGKGLMRKPP VPARPLPAKP FAPQYPHQVP 51 AGCGGCGAAG GACGGCGAAG GACGGGAGGT GGTCCCAAG ATCCAGCACT	60 120 180 240 300 360 420 540 600 600 720 780 840 900
50 55 60 65 70	AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc	ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 1 ARALLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV PQGTTIGMAP MAVEKGGCIM FVEGGECDC LPEFCTGASP GRILCRGTHV NNRKNCHCEA RKTLIRLLFA TRLLQCONVDI PNPPQKPLPA . 79 DNA seq id Accessio uence: 135. 11 GAAAAGGCGA AGGAGGAGGA AGCATGTT TGACCCGGCG CCAGCAGAAA CGCTGGCGATA	SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE ALLAPCEARG INLERNEGLI LAGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPECMNRC HCPANVYLHD NCGKVSKSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKF NKKTTIEKF SEPLINGLNVP DPLARTTRLT USENCE SEQUENCE SEQ	31 VSLWNEGRAD ASSPTETHYL SYNLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKOL CNATTCTLKP GHSQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPG CVRPSRPPG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGTT ACGCCACCAA CCCTGCAGAA	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQQQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH FUHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTG CCCACCCGAG TACAGCGGAG ATGTTTCGAG	GAGGATATGA 51 DLWIPVKSFD NYTVILGRCY KKKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHIPFGMNH CLFNLPEVRE EDCQLKPAGT QCVTLWGPG RPVIGTINAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP 51 AGCGGCGAAG GACGGGAGGT GCTTTGGTGT GGTCCCCAAG ATCCAGCACT AACAACTCTT	60 120 300 360 420 480 540 660 720 780 900
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50	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA	CAGGAAGAAG TCAACTGATA GGGCACAGCC AAGAAGACCT	AGCAGTGCAG TCAAATTCCA TTAGCCACTC	ACTCTTCATT GAGACCTTGC AGTGTTATCA	TTGCTTTGTT CTTCAGGATT AAAGCAATCA	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT	360° 420 480
50	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT	CAGGAAGAAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCC	ACTOTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG	360° 420 480 540
50	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT	CAGGAAGAAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCC AACAGCAGTG	ACTOTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG	360° 420 480 540 600
	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGAA	CAGGAAGAAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG	360° 420 480 540 600
50 55	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT	CAGGAAGAAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT GCCCAAAAAC	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT	360° 420 480 540 600 660 720
	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATGT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG	CAGGAAGAAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TCTGTAAACAT TATTGGCTTC TGGCATCTGC	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT GCCCAAAAAC AGTAGAGGTG	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA	360° 420 480 540 600 660 720 780
	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGCAGAA CCTTAAACTT AGGAATCCTG TGGGTGCAGT	CAGGAAGAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA	360° 420 480 540 600 660 720
	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGCAGAA CCTTAAACTT AGGAATCCTG TGGGTGCAGT	CAGGAAGAAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TCTGTAAACAT TATTGGCTTC TGGCATCTGC	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA	360° 420 480 540 600 660 720 780
55	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGGTGCAGT TGACCCCTGG	CAGGAAGAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT	AGCAGTGCAG TCAAATTCCA TTAGCCACTT TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA	360° 420 480 540 600 660 720 780
	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGGA CCTTAAACTT AGGAATCCTG TGGGTGCAGT TGACCCCTGG Seq ID NO:	CAGGAAGAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC TCACCCTGTG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA	360° 420 480 540 600 660 720 780
55	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTT AGGATCCTGG TGGCTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT ATTGTAAACAT TATTGGCTTC TGGCATCTGG ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accessio	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TTGGGACGTCC AACAGCAGTG TTCCTCCTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LLENCE LLENCE H#: XM_061	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC TCACCCTGTG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA	360° 420 480 540 600 660 720 780
55	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTT AGGATCCTGG TGGCTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT ATTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accessiouence: 12	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TTGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG Lience n #: XM_061 481	ACTOTTCATT GAGACCTIGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAGTATTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC TCACCCTGTG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA	360° 420 480 540 600 660 720 780
55 60 ·	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGGTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT ATTGTAAACAT TATTGGCTTC TGGCATCTGG ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accessio	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TTGGGACGTCC AACAGCAGTG TTCCTCCTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LLENCE LLENCE H#: XM_061	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC TCACCCTGTG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG CCG	GGTGCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC	360° 420 480 540 600 660 720 780
55 60 ·	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT ACAGGAATCTT AGGAATCCTT AGGAATCCTG TGGCTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq 1	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GACATTGTGT ACACCTTGTT ATTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accession uence: 12	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TTGGGACGTCC AACAGCAGTG TTCCTCCTCT TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG uence n #: XM_061 481	ACTOTTCATT GAGACCTIGG ASTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGC TCGAAGAAAA TTCCAGCTGG TCACCCTGTG 091.1 31	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG CCG	GGTGCCTTGG TGAGGTGGGC CCAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC	360° 420 480 540 600 720 780 840
55	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTGA TTTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGGTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TAGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA seguid Accession uence: 12 11	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TTAGGCACTCC AACAGCAGTG TTCCTCCTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LLENCE n #: XM_061 481 21 AACCAGGATT	ACTCTTCATT GAGACCTTGC AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC TCACCCTGTG 091.1 31 GAAATTTGGC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT GCCCAAAAC AGTAGAGGTG GATTTCAGAG CCG	GGTGCCTTGG TGAGGTGGGC CCAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC	360° 420 480 540 660 720 780 840
55 60 ·	GCATCCTGGA GAGTGTTGGG AAGGATGTGA ATTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA ATGCCAAATA ATGCCAAATA	CAGGAAGAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TATTGAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA sequid Accession uence: 12 11	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TAATGGTGAT TTACGAAATG CCTATTTCAG LEENCE ##: XM_061 481 21 AACCAGGATT TCTCCTTCCG	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC 091.1 31 GAAATTTGGC GAAATTTGGC GTGATTCCCCA	TTGCTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG ACAGTATCTA GAATCCCCCC	360° 420 480 540 600 720 780 840
55 60 ·	GCATCCTGGA GAGTGTTGGG AGGCATGTGA AAAGATGTTA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA ATGCCAAATA CACCGAGCGC CCCGGGTACC	CAGGAAGAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC TGGTTGCCGC CGCCAGTGCC	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG Lence n #: XM_061 481 21 AACCAGGATT TCTCCTCCGG GGCTGCCGAT	ACTOTTCATT GAGACCTIGG ASTGTIATCA ATCAGCAGTA TACACCCGGT ACCAAATTIG CCACTGCGGG TGGAAGAAG TTCACCCTGTG 091.1 31 GAAATTTGGC GTGACCCCACTGCGACCCACTGCGACCCACTGCGACCCACTGCGACCCACTGCGACCCACTGCACCCACTGCACCCACTGCACCCACC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT AGTTAGAGTG GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT CGCTCCCCGAT	GGTGCCTTGG TGAGGTGGGC CCCAAAGAGT TCTTTACTGG TATCTAATGG AAACATGTAG TATCCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT	360° 420 480 540 600 660 720 780 840
55 60 ·	GCATCCTGGA GAGTGTTGGG GAGCATGTGA AAAGATGTGA ATTTTGCATCT ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGATCCTG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA ATGCCAAATA CACCGAGGGC CCCGGGTACC CAGATGCATG	CAGGAAGAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TATTAAACAT TATTGGCTTC TGGCATCTGC 82 DNA sequid Accession uence: 12 11 CTTCAGGAAC TGGTCGCGC GGCCAGTGCC GTCAGAAGGGT	AGCAGTGCAG TCAAATTCCA TTAGCACTC TTAGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LLENCE LLEN	ACTOTTCATT GAGACCTTGC ATCAGCAGTA TACACCCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGG 091.1 31 GAAATTTGGC GTGAGTCCCA AGCCTGTGTGAAAATTTGGC AAAATTTGGC AAAATTTGGC AACGATTCCA AGCCTTGGTGAAACTCCCA AGCCTTGGTGAACTCCCA	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT GCCCAAAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTGCTA	GGTGCCTTGG TGAGGTGGGC CCAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTTAG TATCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCCGGG GGCTCTGGGG GATTGGAGGT TGAATTTTTA	420 480 540 600 660 720 840 60 120 180 240
55 60 ·	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAGGATGTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCACGAT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA ATGCCAAATA CACCGAGCGC CCCGGTACCC CAGATGCACG GTTGGGAAGAGC	CAGGAAGAAG TCAACTGATA GGGCACAGACC AAGAAGACCT GGCATTGTGT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC TGGTCGCCGC CGCCAGTGCC GTGAGAAGGT CTCCTTTTGA	AGCAGTGCAG TCAAATTCCA TTAGGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TAATGGTGAT TTACGAAATG CCTATTTCAG LENCE #: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAA AGATCTCTGG	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGC 091.1 31 GAAATTTGGC GTGAGTCCCA GACGATTCA AGCCTTGGTG AGCCTTGGTG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGCCAAAAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTTGCTA	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAAATTTTA CATCGGAAAG CATCGGAAAG	420 480 540 600 660 720 840 60 120 180 240 300
55 60 ·	GCATCCTGGA GAGTGTTGGG GAGTGTTGA AAAGATGTTA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq I ATGCCAAATA CCCCAGGGC CCCGGGTACC CAGATCCATG ATTCAGCTG ATTCAGCTG AATTCAGCTG AATTCAGCTG AATTCAGCTG AATTCAGCTG AAATTCAGCTG AATTCAGCTG AATTCAGCTG AATTCAGCTG AATTCAGCTG AATTCAGCTG AATTCAGCTG AAAGCATTCAGCTG AATTCAGCTG AAAGCATCATG ATTTCAGCTG AATTCAGCTG AAGCGTACCTG AAAATAA AATTCAGCTG AATTTCAGCTG AAATTCAGCTG AATTCAGCTG AATTTCAGCTG AAAATAA AATTCAGCTG AATTTCAGCTG AAAATAA AATTCAGCTG AAAATAAATAA AAAATAAATAAAATA	CAGGAAGAAG CAACTIGTT GGCATTGTGT TATTAGACTT TATTAGACTT TATTAGACTT TATTAGCTTC GCATCTGC ACCAGAACTA 2 DNA sequid Accession uence: 12 11 CTTCAGGAAC TGGTCGCCGC CGCCAGTGCC GTCAGAAGGGT CTCCTCTTGA	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LEENCE ##: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAT AGATCTCTGG GGCAAACGAA GATTTGGTGG	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCGGT ACCAAATTTG CCACTGCGGG TGGAAGAAAG TTCCAGCTGG 091.1 31 GAAATTTGGC GTGAATTTGGC GTGAGTCCCA GACCGATTCA AGCCTTGGTA TCGGCTGGTA TCGGCTGGTA	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAA AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTGCTA GCAAAGAAAC	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG ACAGTATCTA GAATCCCCCC 51 GCCGCCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTTTTA CATCGGAGG GTTTCTGTTA	420 480 540 600 600 720 780 840
55 60 ·	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTGA AAAGATGTTA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA CACCGAGGGC CCCGGGTACC CCCGGGTACC CAGATGCATG GTTGGGAAGCG ATTTCAGCTG ATTTCAGCTG GATGGGTCTA	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC GCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC TGGTCGCGC GCCAGTGCC GTGAGAAGGT CCTCTTTTGA CCAGCAAAAT ACAGCGTCGG	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG Lence n #: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAT AGATCTCTGG GGCAAACGAA GATGTGGTGC GAAAGGGAGG	ACTOTTCATT GAGACCTIGG ASTGTTATCA ATCAGCAGTA TACACCCGGT ACCAAATTIG CTCACCCTGTG 091.1 31 GAAATTTGGC GTGACCCCCGTG GTGACCCCCCCCCCC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTGCTA GCAAAGAAAC TTGGACATCAT CCCAAGCACTT	GGTGCCTTGG TGAGGTGGGC CCAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TATCCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGGG GATTGGAGGT TGAATTTTA CATCGGAAG GTTTCTGTTA TGCCATCACA	420 420 540 600 660 720 780 840 60 120 120 120 240 300 420
55 60 ·	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTGA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCAGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA CACCGAGCGC CCCGGGTACC CCAGATGCATG GTTGGGAAGG ATTTCAGCTG GATGGGTCTA GTCTGTGACG	CAGGAAGAG TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA 82 DNA seguid Accession concern 12 11 CTTCAGGAAC TGGTCGCGC CGCCAGTGCGC GTGAGAAGGT CTCCTTTTGA CCAGCACAAAAT ACAGCGTCGG GTCTGGACA	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCT ACAGCAGTG TTCCCTCTT TTACGAAATG CCTATTTCAG LENCE . #: XM_061 481 21 . AACCAGGATT TCTCCTTCCG GGCTGCCGAT TCTCCTTCCG GGCTGCCGAG GAAAGGGAG CAGCCCCGAG	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAGTGCCAGCTGC O91.1 31 GAAATTTGGC GTGAGTCCCAGCTGCCGGTGCCCCGTGGAATTTGCCTGGTGCTGCTGCTGGTGCTGCTGCTGCTGCTGCT	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCCGAGTT CCGCTCCCGAT TTCTTTGTA GCAAAGAAAC TTGGACATCAT TCAAGAACACATT TCAAGACACTT TCAAGACACTT TCAAGAACATT TCAAAGAAACT TCAAAGAAACT TCAAAGAAACT TCAAAGAAACT TCAAAGAACATT TCAAAGAACATT TCAAAGAACATT TCAAAGAACATT	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTTTTA CATCGGAAG GTTTCTGTTA TGCCATCACA CCAGTTCACGT	420 480 540 660 720 780 840 60 120 180 360 420 420
55 60 ·	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTTG ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGATCCTG TGGCTGCAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA CACCGAGCGC CCCGGTACC CAGATGCAT GTTGGGAAGG ATTCAGCTG GATGGGTCTAA GTCTGTGACG TCCACTCCTC	CAGGAAGAAG CCAACTGATE GGGCACAGCC AGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC GGCATCTGC ACCAGAACTA 82 DNA seq id Accessio uence: 12 11 CTTCAGGAAC TGGTCGCCGC CGCCAGTGCC GTGAGAAGGT CTCCTTTTGA CCAGCACATA ACAGGTCGC GTCAGCACAT ACAGGTCGC	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TAATGGTGAT TTACGAAATG CCTATTTCAG LLENCE LL	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCGGT ACCAATTTG CCACTGCGGG TGGAAGAAG TTCCAGCTGG 091.1 31 GAAATTTGGC GTGAATTCGA GCCTTGGTG TCCACCTGTG TCCACCTGTG TCCACCTGTG TCACCTTGTG TCTGAAGTTCA AGCCTTGGTG TTCGAAGGT TTGGAAGGT TTGGAAGGT TTGGAAGGT TTGTAAAGGT TATGGAAGGT TATGGAAGGT TATGGAAGGT TATGGAAGGT TATGGAAGGT TATGAAGGT TATGATTCAA	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCGAGTT CGCTCCGAT TTCTTTTGTA GCAAACAAC TTGACATCAT TCGAACAGAA CCAAGCACTT TGGACATCAT CCCAACAGGA	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCCGG GCCTCTGGCG GATTGGAGGT TGAATTTTA CATCGGAAG GTTTCTGTTA TGCCATCACA ACCAGTTCACA ACCAGTTCACA ACCAGTTCACA	420 480 540 600 600 720 780 840 60 120 180 240 420 420 440 540
55 60 · 65 70	GCATCCTGGA GAGTGTTGGG AAAGATGTGA AAAGATGTGA AAAGATGTGA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCAAATA CACCAGGGC CCCGGGTACC CCCGGGTACC CAGATGCATG GTTGGGAAGC TTGGGAAGC TTGGGAAGC TTGGGAAGC TTGGGAAGC TTCGCTGTACG TCCATCCTC TCACTCCTC AGAATCAAGA	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA sequid Accession uence: 12 11 CTTCAGGAAC TGGTCGCCC GTGAGAAGGT CCCCCTTTTGA ACACGGTCGCC GTGAGAAGGT ACACGGCAGAAT ACACGGTCGCAC TGTCTGCAGAAT ACACGTCGCAC TGGTTCGCAGA TATCTGGAATT GGATGGTTTTT GGATGGTTTTT GGATGGTTTTT GGATGGTTTT GGATGGTTTT TGGATGTTTT TGGATGTTTT TGGATGGTTTT TGGATGGTTT TGGATGGTTTT TGGATGTTT TGGATGTTT TGGATGGTTTT TGGATGGTTTT TGGATGGTTTT TGGATGGTTTT TGGATGGTTTT TGGATGGTTTT TGGATGTTT TGGATGTTT TGGATGTTT TGGATGTTT TGGATGTTT TGGATGTTT TGGATGTTT TGGATGTTT TGGATGTT TGGATGTTT TGGATGTTT TGGATGTT TGGATGTT TGGATGTT TGGATGTT TGGATGT TGGAT	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LEENCE ##: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCGGAT AGATCTTCGG GGCAAACGAA GATGTGGTGG GAAAGGAGG CAGCCCCGAG CCCCTTGGAT CAAAGGAGGG	ACTOTTCATT GAGACCTIGG ACTCATC ACCACATTT TACACCCGGT TACACCCGGT TACACCCGGT TACACCCTGTG 091.1 31 GAAATTTGC GACGATCCA GACGATCCA GACGATCCA GACGATCCA AGCCTTGGTG TTGAAAGGT TAGAAGGT TAGAAGGT TAGAAGGT TAGAAGGT TAGAAGGT CACACAGAACC CACAGGACCA TAGAAGGT CACACAGACC CACAGGACC CACACAGCACC CACACACC CACACACC CACACACC CACACCC CACACC CACACCC CACACC CACACCC CACACC CACACC CACACC CACACC CACACCC CACACC CACA	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAA AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTGCTA TGGACATCAT TGGAGCATCAT CCAAGGACT TGGAGCATTAC	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTTTTA CATCGGAAG GTTTCTGTTA TGCCATCACA CCAGTTCAGT AGTGAAGGCA TCTGAAATAC	420 480 540 600 660 780 840 60 120 180 240 306 420 480 540
55 60 ·	GCATCCTGGA GAGTGTTGGG GAGCATGTGA AAAGATGTGA AAAGATGTTA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCTGCAGT Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA CACCGAGGC CCCGGGTACC CAGATGCATG GTTGGGAAGG ATTTCAGCTG GATGGATCAA GCTCTGTGACG TCCACTCCTC AGAATCAGAC ACTTCTGACA	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA 82 DNA seggid Accession concern 12 11 CTTCAGGAAC TGGTGCGC CGCCAGTGCC GTGAGAAGGT CTCCTTTTGA ACAGCGTCGC GTGAGAAGGT ACAGCATCGG GTCTGGACAT ACTGGAATT GGAGTGTTGGACTT GGAGTGTTGGACTT GGAGTGTTGGACTT GGAGTGTTGGACTT GGAGTGTTGACGTTTT GAGGGTTGCC GGCATGTCT GGAGTGTTGT	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCT ACAGCAGTG TTCCCTCTT TATACGAAATG CCTATTTCAG LENCE . #: XM_061 481 21 . AACCAGGATT TCTCCTTCCG GGCTGCCGAG GGCTGCCGAG GAAAGGGAG CCAGCCCCAGG CCAGCCCCAGG CCAGCCCGAG CCAGCCAG	ACTOTICATE GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAGTGCCAGCTGC O91.1 31 GAAATTTGC GAGATCCCAGCTGC GACGATCCCAGCTGCAGCCCATCCA GCCTCGTGG GTCCATCTGAAGGT TTTGAAGGT AGGGTGCAG CACTTTCAAAGGT AGGGTGCAGA CACTTTTCAAAGGT AAGGCTTCAAAAGACT AAGGCTTCAAAAGACT AAGGCTAGAAAGACT AAGGCTAGAAAGACT AAGGCTAGAAAGACT AAGGCTAGAAAGACT AAGGCTAGAAAGACT AAGGCTAGAAAGACT AAGGCTTCAAAAGACT AAAAGACTTCAAAAGACT AAAAGACTTCAAAAGACT AAAAGACTTCAAAAGACT AAAAGACTTCAAAAGACT AAAAGACTTCAAAAAGACT AAAAAAAAAA	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGTAGAGGTG GATTTCAGAG CCG 41 TTCTTCCAAGA GCCCCGAGTT CCGCCCCGAT TTCTTTGCTA GCAAAGAAAC TTGGACATCT TCCTAGGACATCT CCCAACACTT CCCAACAGCACTT TCGGAGCACTTGCCGACT TGCGCACATGGACTTGCCGACTTGCCCGACT TGGGAGCACTTGCCGACTTGCCGACTTGCCGACTTGCCGACTTGCCCGACTTGCCCGACTTGCCGACCTGCT TGGGAGCACTTGCCCCAGGACTTGCCCCAGCTTGCCCCAGCTTGCCCCAGCTTGCCCCAGCTTCCCAGCTTCCCCAGCTTCCCCAGCTTCCCCAGCTTCCCCAGCTTCCCCACCTCCCAGCTTCCCCACCAGCTTCCCCACCTCCCACCCA	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTTTA CATCGGAAG GTTTCTGTTA TGCCATCACT ACTGAAATA CCTCAACAT CCTCAACAT CCTCAACAT	420 420 540 600 660 720 780 840 60 120 180 240 300 360 420 540 600
55 60 · 65 70	GCATCCTGGA GAGTGTTGGG GAGGCATGTGA AAAGATGTGA AAAGATGTTG ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCTGCAGT TGACCCCTGG Nucleic Ac Coding seq 1 ATGCCAAATA CACCGAGCGC CCCGGGTACC CAGATGCATC GATGGGAATC GTTGGGAAG TCCACTCCTC AGAATCAGA CTTCTGCAA GTCACTCATG	CAGGAAGAAG CAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA 82 DNA seq id Accession Usence: 12 11 CTTCAGGAAC TGGTCGCCGC CGCCAGTGCCG CTCAGAACGT CTCCTTTTGA ACAGCGTCGG CTCCTTTTGA ACAGCGTCGG GTCTGGAAT ACAGCGTCGG GTCTGGAAT TTCTGGAAT ACAGCGTCGG GTCTGGAAT GGATGTTTT GAGGGTTTCC GGGAAGTCCCA	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCT ACAGCAGTG TTACTCCTCTT TATAGGTGAT TTACGAAATG CCTATTTCAG LENCE #: XM_061 481 21 } AACCAGGATT TCTCCTTCCG GGCTGCCGAG GGCTGCCGAG CCAGCCCCGAG CCAGCCCCGAG CCAGCCCGAG CCAGCGCAGAG GGGGAGTGTG	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCGGT ACCAATTTG CCACTGCGGG TGGAAGAAAG 091.1 31 GAAATTTGC GTGAGTCCCA GACCGATCCCA GACCATTGGA GCATTGGA GTCCATGTAA TCGGCTGCAG TCTCATGTAAAGGT TCATTTTCAA GCACGAGGAGA AGCCTTGCAG AGCGTGCAGA TCTTTTCAAAGGT AGGGTCAGAG TCATTTTCAA GCCCACGGAGA AATGCTCCCA GCCATGCCAT	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGCCAAAAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT TCCTTTGCTA GCAAACAACA TTGGACATCAT CCCAACACTT TCGGAGACTTT CCCAACACGT TGGGACTTTGCCAGAC CCGGACTTTCCCAGCACT CCCAACACGCA CCGGACTTGC CCCAACACGCA CCGGACTTGC TGCCCCAGGT CCCAAGCACTTGC CCCAAGCACT CCCCAAGCACT CCCCCAAGCACT CCCCCAAGCACT CCCCAAGCACT CCCCCAAGCACT CCCCCAACCACT CCCCCAAGCACT CCCCCAAGCACT CCCCCAAGCACT CCCCCAAGCACT CCCCCAACCACT CCCCCAACCACT CCCCCCAACCACT CCCCCCAACCACT CCCCCAACCACT CCCCCCAACCACT CCCCCCAACCACT CCCCCCAACCACT CCCCCCAACCACT CCCCCCAACCACT CCCCCCCACT CCCCCCACT CCCCCCACT CCCCCCACT CCCCCCACT CCCCCCACT	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGT TGAATTGTTA TGAATTGTTA TGCATCACA CCAGTTCAGGT AGTGAAGGCA TCTGAAATAC CCTCATCATC GAAGGAAAGGC	420 480 540 600 660 720 780 840 120 180 240 360 420 540 600 660 600 600 720
55 60 · 65 70	GCATCCTGGA GAGTGTTGG GAGGCATGTGA AAAGATGTGA AAAGATGTGA ACAGGAATCTT ACAAGTATTT AGGAATCTT AGGAATCTT AGGAATCTG Seq ID NO: Nucleic Ac. Coding seq 1 ATGCCAAATA ACACCGAGGCC CCCGGGTACC CCCGGGTACC CAGATGCATG GTTGGGAAGC TTGGGAAGC GTTGGGAAGC CTCTGTAACG GTTGGAAGA CTTCTGCACAC GTCACTCCTC AGAATCAAGA CTTCTGCACAC GTCACTCTTG	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TTGTAAACAT TATTGGCTTC TGGCATCTGC 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC TGGTTGCCCGC CGCCAGTGCC GTGAGAAGGT ACAGCGTCGC GTGAGAAGT ACAGCGTCGC GTTCGCAAAT ACAGCGTCGG GTTTGGAACT TGGTTGGAACT CGGAAGT ATCTGGAATT GGATGGTTTT GGATGGTTTT GGATGGTTTT GGATGGTTTCC TGGAAGTCCCA TGTTTGCTGTT GGAAGTCCCA	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LIENCE ##: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAT AGATCTTCTGG GGCAAACGAA GATGTGGTGG CAAGCCCCGAG CCCCTTGGAT CAAAGGAGG TGGAGGCAGG TGGAGGCAGG GGGGAATGTGGGGGGAGGC CCGGAGGCCGGAGGCCCGAGG CCCCTTGGAT CAAAGGAGGG TGGAGGCAGGGGGGATGTGGGGGGGATGTGGGGGGGAGGGGGGGG	ACTOTICATE GAGACCTIGG ACTORICA ATCAGCAGTA TACACCCGGT ACCAAATTIG CCACTGCGGG TGGAAGAAG TTCCAGCTGC 091.1 31 GAAATTTGGC GTGACCTCGTG GTCACCTGTGAAGCGATCA AGCCTTGTGAAGGT TTGGAGGGCAGATCA AGCGTTGAAGGT TTGGAAGGT AGGGTCAGAG TTTGAAAGGT AGGGTCAGAG AATGCTCCAG AATGCTCCAG TTTTCCAGGTGAA ATGCTTCCAG	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCA TGGATGGAAA AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTGCTA TGGAGCACTT TCGAACAACA CCGAACATGC CCGAACATGC TGCCCAGGAT CCCAACAGGA CGGAACTTGC TGCCCAGGT TCCAAGCACTT TCGCAACAGAAC CGGAACTTGC TGCCCAGGAT CCAAGCACTT CCAAGCACTT CCCAAGCACTT CCCAAGCACTT CCCAAGCACT TCGCCCAGGAT CCAAGCACT TCCCAAGCACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCCAACACT TCCCCAACACT TCCCAACACT TCCCAACACT TCCCCAACACT TCCCCAACACT TCCCCAACACT TCCCCAACACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCAACACT TCCCCAACACT TCCCAACACT T	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG ACAGTATCTA GAATCCCCCC 51 GCCGCCCCGGG GGCTCTGGGG GATTGGAGTT TGAATTTTA TGCCATCACA CCAGTTCAGT ACTGGTAAGCA TCTGAAATAC CCTCATCACA CCAGTTCAGT GGTGAAGGAAGGAAAGG	420 480 540 600 600 720 780 840 60 120 180 240 420 480 540 660 720 780
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55 60 65 70 75	GCATCCTGGA GAGTGTTGGG GAGCATGTGA AAAGATGTGA AAAGATGTTG ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCTGCAGT Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAATA CACCGAGGC CCCGGGTACC CAGGATGCATG GTTGGGAAGG ATTTCAGCTG GATGGATCA GTCACTGTGACG CTCACTGCACA GTCACTGATG GGCGGTCACTG GGCAGCAGGG GGCCTCTCA	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA 82 DNA sequid Accession concern 1.2 11 CTTCAGGAAC CTTCAGGAAC TGGTGCCGC GTGAGAAGGT CTCCTTTTGA ACAGCGTCGC GTGAGAAGGT ACAGCATCGG GTCTGGACAT TGGGTTGCCGC GTGAGAGGT TGTTTGGAATT GAGGGTTGCC GGAATCCCAG TGTTTGCTGACAT GAGGGTTGCC GGAACTCCCAG GGAACTCCCAG GGCACCCCAGGC GGCACCCCAGGCC GGAACTCCCAGGCACCCCAGGCACCCCCCAGGCACCCCCAGGCACCCCCC	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCT ACAGCAGTG TTACTCCTTT TTACGAAATG CCTATTTCAG LENCE . #: XM_061 481 21 . AACCAGGATT TCTCCTTCOG GGCTGCCGAG GGAAGCGAG CCAGCCCCAGG CCAGCCCCCAGG CCACCTCCAGC CCAGCCCCCAGC CCAGCCCCCAGC CCACCTCCAGC CCACCTCCACC CC	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCCGGT ACCAGTGC CCACTGCGGG TGGAAGAAGA 091.1 31 GAAATTTGGC GTGAGTCCCA GACCGATTCA AGCCTTGGTG TTCACCTGTG TTCACCAGTTCA TTGGAGTGCAG TTTGAAAGGT TTTGAAAGGT AGGGTAGAA TTTGAAAGGT TTTGAAAGGT TTTGAAAGGT TTTGCAGGT AGGGTCCAT TTTCCAGGT TT	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGTCAGAGA AGTAGAGGTG GATTTCAGAG CCG 41 TTCTTCCAAGA GCCCCGAGTT TCCTTTGCTA GCAAAGAAAC TGGACATCAT CCCAACAGGA TTGGACATCAT CCAACAGGA TGGACCAGGT CCAACAGGA TGCCCCAGAT CCAACAGGA TGCCCCAGAT CCAACAGGA TGCCCCAGAT CCAACAGGA TGCCCCAGAT CCAACAGGA TGCCCCAGAT CCAACAGCA TGCCCCAGAT CCAACAGGA TGCCCCAGAT CCAACAGGA TGCCCCAGAT CCAACAGCA TGCCCCAGAT CCAACAGCA TGCCCAGAT CCAACAGCA TGCCCCAGAT CCAACAGCA	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTGTTA CATCGGAAG GTTTCTGTTA TGCATCACA CCAGTACACA CCTCATCACT GAAGGAAAGG GCATGCAACA GGATGCAACA GCATGCACAC AGGGAAAGG AGGAAAAGG GCATGCACAC AGGTGGAGGC AGCTGGGAGGC AGCTGGGAGGC AGCTGGGAGGC	420 420 540 600 660 720 780 840 120 180 240 300 360 420 540 600 720 780 840
55 60 · 65 70	GCATCCTGGA GAGTGTTGGG AAGGATGTGA AAAGATGTTG ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGATCCTG TGGCACAGT TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq I ATGCCAAATA CCCGAGCGC CCCGGTACC CAGATGCATT GATGCAAATA GTCTGTGACG TCCACTCCTC AGAATCAAGA CTTCTGCACG GTCACTCCTC AGAATCAATG GTCACTCCTC AGAATCAATG GTCACTCCTC AGAATCAATG GCCAGCGTCC CCCAGGCTTCC CCCAGGCTTCC CCCAGGCTTCC CCCAGGCTTCC CCCAGGCTTCC CCCAGGCTTCC	CAGGAAGAAG CAACTGATA GAGAAGACCT GAGAAGACCT GAGATGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA ACGTGGTTCT 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC GTGGTCGCCGC GTGAGAGGT CTCCTTTTGA CCAGCAAAAT ACAGCGTGGC GTCAGAAGGT GTCTGGACAT GAGAGGTTTC GAGAAGT GTTTGGACT GAGAGGTTCC GGAAATCCCAG TGTTTGCTGT CTTTTGCTGT CTTTTGCTGT CTTTTGCTGT CTTTTGCTGT CTTTTGCTGT CTTTTGCTGA	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TAATGGTGAT TTACGAAATG CCTATTTCAG LIENCE II #: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAT AGATCTCTGG GGAAACGAA GATGTGGTGC CAGCCCCGGC CAGCCCCGGC CGGGGTGAGG GGGGGATGTG GGGGGATGTG GGGGGTGAGG GCAGTTGAGG GGGGGTTAATG	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCGGT ACCAGTGCGGG TGGAAGAAGA O91.1 31 GAAATTTGGC GAAATTTGG GTGACTCCCA GACCTTGTG TCCACCTGTG TCCACCTGTG TCCACCTGTG TCCACCTGTG TCCACCTGTG TTCCACCTGTG TCCACCTGTG TCCACTTCA AGCCTTGTA TCGGCTGCAG TTATGAAGGT TATGATGCTTCAC GCACTGCAG TTTCCCAGGT TTTCCAGGT TTTC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGCCAAAAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTTGTA TGCAACAGAA CGGACACTT CCCAACAGA CGGACATT CCAACAGGA CGGAGCACTT CGAACAGGA CGGAGCACTT CCAACAGGA CGGAGCACT CGAACAGGA CGGAGCACT CGAACAGGA CGGAGCACT CGAACAGGA CGGAGCACT CGAACAGGA CGGAGCACT CGAACAGGA CGGCACGGC TGATAGGCCC TGATAGGCCC TGATAGGCCC	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GGCTCTGGCG GATTGAATTT TGCCATCACT ACTGAAATAC CCTCATCACT CGAAGGAAGG GCATGCACT GGAGGGAAGG GCATGCACT TGCCACCACAC CAGCTCGCACCC CAGCTCGCACCCCCCCCCC	420 480 540 600 600 720 780 840 120 180 240 420 420 420 420 420 600 600 720 780 840 900
55 60 65 70 75	GCATCCTGGA GAGTGTTGGG GAGCCTGTGA AAAGATGTGA AAAGATGTGA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGATCATT AGGATCATG TGACCCCTGG Seq ID NO: Nucleic Ac Coding seq I ATGCCAAATA ATGCCAAATA CACCGAGGGC CCCGGGTACC CAGATGCATG GTTGGGAAG GTTGGGAAG GTTCACTGTGACG GTTCACTGTGACG GTTCACTGTGACG GCTGACTGGGAGGG GCTCTTCA CCCGAGCTTCA CCCGAGCTGC CCCGGGCTGCC CCGGGCTGCC CCGGGCTGCC CCGGGCTGCC CCGGGCTGCC CCGGGCTGCC CCGGGCTGCC CCGGCCTGCC	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT TATAAACAT TATTGGCTTC TGGCATCTGC 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC CTTCCTTTGGAGAC GGCAGAGAC TGGCGCGC GTGAGAAGGT CCTCTTTGA ACAGGTCGG GTCTGGACAT ACAGGACAT ATCTGGAATT GGAGGTTCCC GGAAGTTCCCGCGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LEENCE ##: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAT AGATCTTCGG GGCAAACGAA GATGTGGTGG CAGCCCCGAG CCCCTTGGAT CAAAGGAGGG GGGGATGTG GGCGGTCAGG GGCGCTCAGC CAGCTCCGCC CACCTGCTCCCC CACCTGCTCCCC CACCTGCTCCCCCCCCCC	ACTOTICATE GAGACCTIGG ACTOGIC ACCAMATTIG CCACTGCGG TGGAAGAAG TTCCAGCTG 091.1 31 GAAATTIGGC GTGACCTGTG GTCACCTGTG GTCACCTGTG TTGAAGGT AGCGTTCA AGCCTTGTG TCACCTGTG TTTGAAGGT TCATTTAA ACCTGTG CCACGAGGA AATGCTTCCG GCACTGCAG ATTTCCAGGT CCACGAGGA AATGCTTCCC CCACGAGGAGGA TTTCCAGGT TTTCCAGGT TTTCCAGGT TTTCCAGGT TTTCCAGGT TTCCCAGGT TTCCCAGGAGGAC ACCTCCTCT CCCAGAAGGAC CCCAGAAGGAC CCCAGAAGGAC CCCAGAAGGAC CCCCAGAAGGAC CCCCCAGAAGGAC CCCCAGAAGGAC CCCCAGAAGGAC CCCCCAGAAGGAC CCCCCCAGAAGGAC CCCCCCCC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAA AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCCGAGTT CGCCCAGATC TTCTTTGCTA TGGAGCATCAT TCGTACAGA CCGAACACT TGGAGCATT TCCTACAGA CCGAACTTGCT TGGAGCATTGCT TGGAGCACTT CCAACAGA CGGAACTTGCC TGCCCAGAT CCAAGGACTTGC TGCCCCAGAT CCAAGGACTTGC TGGAGGAGCT AGGTGGAGGA GCGCCCCCC TGGACCGCT	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTTTTA CATCGGAAG GTTTCTGTTA TGCCATCACA CCAGTTCAGT AGTGAAGGCA TCTGAAATAC CCTCATCATC GAAGGAAAG GCATGCACTG TGCCACCAAC AGCTGGGAG GCTTGGACTG CCAGTTGGCTCG CCTGTGACTCG CCTGTGACTCG CCTGTGACTCG CCTGTGACTCG CCTGTGACTCG CCTGTGACTCG CCAGTGCCTCC	420 420 540 600 660 720 840 120 180 240 300 420 480 540 660 720 780 840 900 900 900 900
55 60 65 70 75	GCATCCTGGA GAGTGTTGGG GAGCATGTGA AAAGATGTGA AAAGATGTGA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGATCCTG Seq ID NO: Nucleic Ac Coding seq I ATGCCAAATA ATGCCAAGAA CCCGGGTACC CCGGGTACC CCGGGTACC GAATCATG GTTGGGAAC GTTGGCAAA GTTCACTGG GTTGCGAAC GTTCTGCACA GTCACTCATC GCCGGGTCC CCCGAGCTCC CCCGAGCTCC CCCGAGCTCC CCGGGTTCC CCCGAGCTCC CCCGAGCTCC CCCGAGCTCC CCCGAGCTCC CCCGAGCTCC CCCGAGCTCC CCCGAGCTCC CCCGCCCCCC CCCCCCCCCC	CAGGAAGAGA CAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC CTTCAGGAAC CTTCAGGAAC CTTCAGGAAC TGGTCGCGC GTCAGAACAT ACAGCTAGGC GTCTGGACAT TATTGGCTTC GGATGCT CTCCTTTTGA CCAGCAAAAT TATTGGAATT GGAGGTTGCC GTGTTTGCTGT GGAGGTTCCC TTGTTTCTGT CTAGGAGC CTCTTTCAGGAC TCTTTCATGGA AGAATGGAGG TCTTTCATGGA AGAATGGAGG CCTTTCAGGAG CCTTTCAGGAG CCTTTCAGGAG CCTTTCATGGA AGAATGGAGG CCTTTTGAGGGCAG CCTTTTTGAGGGCAG CCTTTTGAGGGCAG CCTTTTGAGGGCAG CCTTTTGAGGGCAG CCTTTTGAGGGCAG CCTTTTTGAGGGCAG CCTTTTTGAGGGCAG CCTTTTTGAGGCAG CCTTTTTGAGGCAG CCTTTTTTGAGGCAG CCTTTTTGAGGCAG CCTTTTTGAGGCAG CCTTTTTTTTTT	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCT ACAGCAGTG TTCCCTCTT TTACGAAATG CCTATTTCAG LENCE . #: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAG GCAGCCCGAG CCCCTTGGAT CAAAGGAGGCAG CCCCTTGGAT GGAGGCAGA GGGGGTCACG GGCAGCTCCGAG CCAGCTCCGAG CCAGCTCCGAG CCACTGCAG GCAGCTCGAG GCAGCTCAG GCAGCTCAGAG GCAGCTCAGAG GCAGCTCAGAG GCAGCTCAGAG GCAGCTCAGAG GCAGCTCAGAG GCAGCTCAGAG GCAGCTCAGAG GCAGCTCAGAG GCACTTGAT GGAGGCTAAC GCACTTGAT GGAGGCTAAC	ACTOTICATE GAGACCTIGG AGTGTTATCA ATCAGCAGTA ATCAGCAGTA ACCAGGTG CCACTGCGGG TGGAAGAAAG 091.1 31 GAAATTTGGC GTGAGTCCCA GACCGATTCCA GACCGATTCA GACCAGTTCA AGCCTTGGTG AGCGTGCAG TTTGCAGGTGCAG TTTGCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TCATTTTCCA GCATTCCCAG TTTCCCAGGTGCAG TTTTCCAGGTGCAG TTTTCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCCAGGTGCAG TTTTCAGGTGCAG TTTTCAGGTGC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAT GCCCAAAAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCAAGA GCCCCGAGTT TCGTTAGTA GCAAAGAAAC TTGGACACTT TCGAAGCACTT TCGAAGCACTT CCAAGCACTT CCAAGCACTT CCAAGCACTT CCAAGCACTT AGGAGGAGCT AGGTGGAGGAC TGATAGGCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC TGATAGACCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC TGATAGGCCCC	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTTTA CATCGGAAG GTTTCTGTTA ACTGAAATAC CCAGTACACA CCAGTACACA CCAGTACACA CCTCAACAT GAAGGAAAGG GCATGCACG GCATGCACG TGCCACCACAC CGAGTGCCTC GGAATGCACG CCAGTGCCTC GGAATGCACG CCAGTGCCTC GGAATGCACG CCAGTGCCTC	420 480 540 660 720 780 840 60 120 180 360 420 540 660 720 780 840 960 1080
55 60 65 70 75	GCATCCTGGA GAGTGTTGGG GAGTGTGGA AAAGATGTGA AAAGATGTGA ACAAGTATTT CATGGCAGAA CCTTAAACTT AGGAATCCTG TGGCTGCAGT Seq ID NO: Nucleic Ac Coding seq 1 ATGCCAAGTAC ATTCAGCTG GTTGGGAGAC CCCGGGTACC CAGATGCATC GATGGGTTAC GTTGGGAAG CTTCTGCAC GTCACTCTC GGCAGCGC TCCCGGGCTTCC CCGGGCTTCC CCGGGCTTCC CCGGGCTTCC CCGGCCTCC TGCCCCTCC TGCCCCTCCTC TGCCCCTCCTC TGCCCCTCCTC TGCCCCTCCTC TGCCCCTCCC TGCCCTCCC TGCCCTCCC TGCCCTCCC GTCGACCTTCC	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC ACCAGAACTA 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC TGGTGCCGC GTGAGAAGGT CTCCTTTTGA ACAGCGTCGG GTCTGGAACT ACAGCGTCGG GTCTGGAACT TGTTGGAAT ACAGCGTCGG GTCTGGAACT TGTTGGAAT TGTTGGATTT GAGGGTTGC GGAAGTCCCA TGTTTGCTGT CTAGAGGCA TGTTTGCTGT CTTCATGGA TCTTCATGGA CCATTTCGAG TCTTCATGGA CCATTTCGAG CCTTTTGGAG CCATTTCGAG CCTTTTGGAG CCTTTTCGTGCT TCTTCCTGCT CTTCCTGCT CTTCTTCCTGCT CTTCCTGCT CTTCCTGCT CTTCCTGCT CTTCCTGCT CTTCCTGCT CTTCTTCTTCTTCTCTCT CTTCTTCTTCTTCTTCTT	AGCAGTGCAG TCAAATTCCA TTAGCCACTC TGGGACGTCT ACAGCAGTG TTACTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LENCE #: XM_061 481 21 #: XM_061 ARCCAGGATT TCTCCTTCCG GGCTGCCGAG GGAAACGAA GATGTGGTGC CAGCCCCGAG CCCCTTGGAT CAAAGGAGGA GGGGGATGTG GGGGGATGTG GGGGGTCAGG CAGCTCCGGC CAGCTCCGGC CAGCTCAGC CAGC	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACCGGT ACCAGTGCGGG TGGAAGAAAG 091.1 31 GAAATTTGGC GTGACCCTGTG GAAGTATGGC GTGACCCTGTG TCACCCTGTG TCACCTGTG TCACCTGTG TCACCTGTG TCACCTGTG TCACCTGTG TCACCTGTGAAGCT TTGAAGGT TCATTTTCAA CGCACGGAGGA AATGCTTCTG GCACTGCAG TTTCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCAGGT TTTCCCAGGT TTTCCAGGT TTTCCCAGGT TTTCCCCCT TTTCCCCCCT TTTCCCCCCCT TTTCCCCCC	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGCCAAAAAC AGTAGAGGTG GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTGTA GCAAACAAAC CCAAGCACTT CCCAAGCACT CCCAGGT CCGAGCAGT CCGAGCAGCT CCAAGCAGCT CCGACGCC TGGACGGCT AGGTGGAGGAGA AGCTGAGCCC CTGGACGGCT AGGCGCTAA	GGTGCCTTGG TGAGGTGGGC CCCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GGCTCTGGCG GATTGAGAT TGAATTTTA TGCATCAGT AGTGAAGGCA TCTGAAATAC CCTTCATCAG GCATCCACC GAAGGAAAGG GCATGCACC CCTCATCC GAAGGAAAGG GCATGCACC CCTCATCC TGCCACCACC CCAGTGCCTC CGGAATGCACG CCAGTGCCTC CGGAATGCAGG CCTGTGACTCG GGAATGCAGG CCTGTGACTCG GGAATGCAGG	420 480 540 600 660 720 780 840 120 180 240 300 360 420 720 780 840 900 960 1020 1020 1140
55 60 65 70 75	GCATCCTGGA GAGTGTTGG GAGCCTTGGA AAAGATGTGA AAAGATGTGA AAAGATGTGA ACAGTATTT ACAGGAGAA CCTTAAACTT AGGAATCCTG Seq ID NO: Nucleic Ac. Coding seq I ATGCCAAATA CACCGAGCGC CCCGGGTACC CCCGGGTACC CAGATCCTG GATGCGTCAC GTCACTCCTG AGAATCAAGA CTTCTGCACA GTCACTCTGCACA GTCACTCTCTCCACCCTCCC GCGAGCTTCCCCCGAGCTTCCCCCGAGCTTCCCCCGGCTCCCCCGGCCCCCCGGCCCCCCGGCCCCCC	CAGGAAGAGA TCAACTGATA GGGCACAGCC AAGAAGACCT GGCATTGTGT ACACCTTGTT TTGTAAACAT TATTGGCTTC TGGCATCTGC 82 DNA seq id Accession uence: 12 11 CTTCAGGAAC TGGTCGCCG GTGAGAAGGT ACAGCGTGGCC GTGAGAAGT ATCTGCAAC TGGTTCGCCGC GGCAAAT ATCTGGAAT TGGATGGCC GGAAGTTCGCCGC GGAAGTTCCC GGAAGTTCCC GGAAGTTCCC GGAAGTTCCC GGAAGTTCCC GGAAGTTCCC GGAAGTTCCC GGAAGTTCCC TTGGAGGCC TCTTCAGGA TGTTTCAGGA TGTTTCAGG TCTTCATGGA TCTTCATGGC TCTTCCTGCT TCGTGAAGCC TCTTCAGGCC TCTTTCAGCC TCTTCAGAGCC TCTTCAGACC TCTTCAGC TCTTCAGACC TCTTCAGC TCTTCAGACC TCTTCAGC	AGCAGTGCAG TCAAATTCCA TTAGCACTC TGGGACGTCC AACAGCAGTG TTCCTCCTTC TCCGGTCTTG TAATGGTGAT TTACGAAATG CCTATTTCAG LEENCE ##: XM_061 481 21 AACCAGGATT TCTCCTTCCG GGCTGCCGAT AGATCTCGG GGCAGCCCCGAG CCCCTTGGAT CAAAGGAGG CCCCTTGGAT CAAAGGAGG GGCAAACGAA GGGGGTCAGG GCACGTCTGG CAGCTCGGG CAGCTCGGG CAGCTCGGT CACATGTGTT GGGAGCTAATG GGAGCTAATG GGAGCTAATG GGAACGCTCTG GGAACAGCTCTG GGAACAGCTCTCTG GGAACAGCTCTCTCTG GGAACAGCTCTCTCTG GGAACAGCTCTCTCTG GGAACAGCTCTCTCTG GGAACAGCTCTCTCTG GGAACAGCTCTCTCTG GGAACAGCTCTCTCTCTCTCCCCCCTCTCTCTCTCCCCCCTCTCTCT	ACTOTTCATT GAGACCTIGG AGTGTTATCA ATCAGCAGTA TACACAGGT ACCAAATTTG CCACTGGGGG TGGAAGAAG 091.1 31 GAAATTTGGC GTGAATTCGC GTGAATTTGGC GTGAATTCGA GCCTTGGTG TTGAAAGGT TCACCTGGTG TTGAAAGGT TCACCTGGTG TTTGAAAGGT TCATTTCAA CGCACGGATCA AGCCTTGGTG TTTTCACGGTGCAG TTTTCACGGTGCAG TTTTCCAGGT TTTTCCAGGT TTTTCCAGGT TTTCCCAGGT TTTCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCAGGT TTTCCCCGGT CCAGAAGGAC TTTGCCCTGF GCGGGCACCT GCGCGGCACCT GCGCGGCACCT GCGCGGCACCT GCGCGGCACCT GCGCGGCACCT GCGCGGCACCT GCGCGCGCCTGGGGCACCT	TTGCTTTGTT CTTCAGGATT AAAGCAATCA CCGTACGGTC GGAAAACTCC TGGATGGAAT AGTGAGAT AGTTGAGGTC GGATGGAAT AGTTGAGGTC GATTTCAGAG CCG 41 TTCTCCCAAGA GCCCCGAGTT CGCTCCCGAT TTCTTTTGTT TGGAGCACTT CCCAACAGGA CCGAACTTGC GGAGCACTT CCCAAGCAGT CCCAGGAT CCCAGGACT CCCAGGACTTCC TGGACGGACT CCCAGCAGC TGGACGGACT CCCAGGACT CCCAGCAGC TGGACGGACT CCCAGCAGC TGGACGGCC TGGACGGCC TGGACGGCC TGGACGGCC TGGACGGCC CTGGACGGCC CCCGGACCC CCCGGACCC CCCCGGCC CCCCGCC CCCCCCC CCCCCCC CCCCCC	GGTGCCTTGG TGAGGTGGGC CCAAAGAAGT TCTTTACTGG TATCTAATGG AAACATGTAG TTTCAGAAGT ACAGTATCTA GAATCCCCCC 51 GCCGCCCGGG GGCTCTGGCG GATTGGAGGT TGAATTTTA CATCGGAAG GTTTCTGTTA ACTGAAATAC CCAGTACACA CCAGTACACA CCAGTACACA CCTCAACAT GAAGGAAAGG GCATGCACG GCATGCACG TGCCACCACAC CGAGTGCCTC GGAATGCACG CCAGTGCCTC GGAATGCACG CCAGTGCCTC GGAATGCACG CCAGTGCCTC	420 480 540 600 600 720 780 840 600 120 180 240 420 480 660 720 780 840 900 900 900 1020 1080 11200

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				CGTGGCTTCG			1380
	CAGGACCGGC	CACGTAGAGT	GGTGGTTTTG	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	1440
5	GCGGGCCCAG	CGCGTCACGC	AAGGGCGCGA	GAGCTGCTCC	TGCTGGGTGT	AGGCAGTGAG	1500
)	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	1560
	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	GAGCTGCAGG	GGAAGCTGTG	CAGCCGGCAG	1620
				CTCGTCTTCA			1680
				AGCTTTGTGA			1740
10				CTGGTGGTGT			1800
10				GCTGCGATGC			1860
				ACCGCCCTGC			1920
				GTCCCCAAAG			1980
	GGGAGAGGCG	CAGAGGATGC	AGCCGTTCCT	GCCCAGAAGC	TGAGGAACAA	TGGCATCTCT	2040
				AGTGAGGGTC			2100
15	CGGGATTCCC	TGATCCACGT	GGCAGCTTAC	GCCGACCTGC	GGTACCACCA	GGACGTGCTC	2160
	ATTGAGTGGC	TGTGTGGAGA	AGCCAAGCAG	CCAGTCAACC	TCTGCAAACC	CAGCCCGTGC	2220
	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAAT	GGGAGCTACC	GCTGCAAGTG	TCGGGATGGC	2280
	TGGGAGGCC	CCCACTGCGA	GAACCGTGAG	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	2340
	GGATGGATTC	TTGAGACGCC	CCTGAGGCAC	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCCGT	2400
20	ACCCCTCCCA	GCAACTACAG	AGAAGGCCTG	GGCACTGAAA	TGGTGCCTAC	CTTCTGGAAT	2460
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				VHVSKETIGK			120
				RVRVGAFQFS			180
30	RIKRMUFKGG	PTETELALKY	T.T.HRGT.PGGR	NASVPQILII	VTDGKSOGDV	ALPSKOLKER	240
-				LAEQUEDATN			300
				PEGLDGYQCL			360
				AVLSEDSRAR			420
	U.ISMV.ICGAU	CIDEDCCDTI.	TOSALDONAE	RGFGSATRTG	ODR PRRVVVI.	LTESHSEDEV	480
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55				SEVRSCALQE			600
	A POCK TOWNED	DALLEDIOUS	DALCUICENC	TALLHIYDKV	MANDONDO	UDKAVVVI.TG	660
	AFGLUIAPIR	AAMLKA LOQA	UT UTION CONT.	SEGLERLAGP	DOCT THURSAY	ADI.PVHODUI.	720
	GRUADDAAVE	MAIL CARCOC	MIRCOCHION	GSYRCKCRDG	MEGDICEMBE	WSSCSVCVSO	780
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45 50	Nucleic According sequents ATGCCCCCTT TCTCTCCCTC AGCARATGA AGCGTCGGGA	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT	120 180 240
	Nucleic Acc Coding segn 1 ATGCCCCCTT TCTCCCTC AGCAAAATGA AGCGTCGGGA CTGGACATCA	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCCGAGAG	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT	120 180 240 300
	Nucleic Actioning sequence of the control of the co	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTT GCCCCGAGAG CCTTGGATTC	n #: Eos se 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG	TGTTTTCCAG TGGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG	120 180 240 300 360
	Nucleic According sequilibrium	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCCGAGGA CCTTGGATTC AAGGAGGGCG	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGT ATTTTCAACC CACGGAGACG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA	120 180 240 300 360 420
50	Nucleic Act Coding sequil 1 	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGGCAGAAAA	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC TGCTCTGTG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTG GGACATTCC CAACAGGAG GAACTTGCTC CCCCAGATCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG	120 180 240 300 360 420 480
	Nucleic Act Coding sequil ATGCCCCTT TCTCTCCCTC AGCAAAATGA AGCGTCGGA CTGGACATCA CTGGAATTCC ATGGTTTTCA GGGTTGCCTG AAGTCCCAGG	id Accession uence: 12 11	n #: Eos se 424 21	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGTGA	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG	120 180 240 300 360 420 480 540
50	Nucleic Act Coding sequil 1 ATGCCCCTT TCTCTCCTC AGCARANTGA AGCGTCGGA CTGGACATCA ATGGTTTTCA GGGTTGCCTG AAGTCCCAGG TTTGCTGTGG	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGTGCTC AAGGAGCTT GCCCCGAGAG CCCTGGATTC AAGGAGGCGG GAGGCAGAAA AGGATGTGGCC GAGGCAGAAA GGGATGTGGC GGGTCAGGTT	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCG TCCCAGGTGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGC CGACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGA	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCACAGT TGAAGGCAAG TGAAATACCT TCATCATCAT AGGAAAGGGG ATGCACTGGC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT	120 180 240 300 360 420 480 540
50	Nucleic Act Coding sequit ATGCCCCTT TCTCTCCTC AGCANATGA AGCGTCGGA CTGGACATCA CTGGACTTCC ATGGTTTCCA GGGTTCCCTG AAGTCCCAGG TTTGCTGTGG AGAGGCAGC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGGATGTGGC GGGTCAGGTT ACCTGCTGTT ACCTGCTGTT	m #: Bos se 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGGGAGCCT CCTCTTCAGC	120 180 240 300 360 420 480 540 600 660
50	Nucleic According sequilibrium of the control of th	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT AGCAGGAGG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGATCAGGT ACGTGCTGTT ACGTGCTGTT ACGTGCTGTT ACGTGCTGTT ACGTGCTGTT	m #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC TCCCAGGAGCG ACTGCCTCTGTG ACTGCCATCC TCCCAGGTGG CGCTGAGCAG CTGCTCCAGC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGA GAGGAGCTGA GAGGAGCTGA GCACGCCAG	TGTTTTCAB TCGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CGAGGGTCAC	120 180 240 300 360 420 480 540 600 660 720
50 55	Nucleic Act Coding sequit I ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA ACTGGACATCA ATGGTTTTCA GGGTTGCCTG AAGTCCCAGG ATTTGCTGTGGA AGGGCCAGG ACCCTCAGGA ACCCTCAGGA ACCCTCAGGA ACCCTCAGGA	id Accession uence: 12: 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCCGAGAGA AAGGAGGGCGGAGAAA GGGATGTGGC GGGCAGAAA ACGGATGTGGC GGGTCAGGTT ACCTGCTGTT ACAGGACGCT	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGTCAGATG TGAAAGGTCC GGTCAGATG ATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGGTGG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGGTGAGCAG GGGAGATGGTC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG GCCACGCCAG	I TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGCTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CGAGGCTCAC CCCATGCTGG	120 180 240 300 360 420 480 540 600 660 720 780
50	Nucleic Act Coding sequit ATGCCCCTT TCTCTCCTT AGCARATGA AGCGTCGGA AGGTTTTCA ATGGTTTTCA AGGTTGCTG AAGTCCAGG ATTTGCTGTGG AGAGGCAGC ACCTCAGCA CCTGTGAGG AGAGGATCGC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCGAGAGG CCTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGTT ACGTGCTGTT ACGTGCTGTT ACGTGCTGTT ACGGACCCT GGGGACCCCT	m #: Bos se 424 21	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGGGAGTTGG GTGGACGATG GCCACCCAG GCCACGCCAG GCGGAGTTCG GCTGCACACT	TGTTTTCCAG TGGGAAGAT TTCTGTTAGA CCATCACTA AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGG CAGCTGGAG CACTGGTAGG	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTC AGCARATGA AGCGTCGGGA CTGGACATCA CTGGATTTCA GGGTTGCCTG AAGTCCCAGG ATTCCTAGGA ACCCTCAGGA ACCCTCAGCA ACCCTGTGAGCA ACAGGATGCC AGAGGTGTCCCAGCA ACAGGATGCC AGAGGTGTCCAGCA ACAGGATGCC AGAGGTGTTCCAGGAAGATCGC AGAGGTTCCCAGGAAGATCGC AGAGGTTTCCCAGGAAGATCGC AGAGTTTCCCAGGAAGATCGCAAGAGGTTTCCCAGGAACACCAGAGATCGCAAGAGTTTCCCAGGAACACCACAGAGTTTCCCAGGAACACACAC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTT GCCCGAGAG CCTTGGATTC GAGCAGATC GAGCAGATGGCT GAGCAGAAA GGGATGTGGC GGGTCAGGTT GCTCGGCCAT ACAGGACGCT TAACCCACCCC TAACCCACCCC	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAAC CCACGGGACAC TGCTTCTGTG ACTGCCATCC TCCCAGGTGG GGCTGAGCAG CTGCTCCAGC GGAGATGGTC TGCCGGTGCT	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG GCGACGCCAG GCGGAGTTCG TGCACACT TACAGGACCA	TGTTTTCAB TCGGAAGAT TCGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CCTCTTCAGC CGAGGCTCAC CCCATGCTGG CACTGGAAG CACTGGAAG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	Nucleic Activities of the control of	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT AAGGAGGCT AAGGAGGCG AAGGAGGCAGAAAA GGATCAGGTT ACGTGCTGTT ACGTGCTGTT ACGGCCAT ACAGGACCCT TAACCCACCC GCCAGAATGG	m#: Bos se 424 21	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTGC GAACAGGACG CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GAGCAGCTGA GAGCAGCTGA GAGCAGCTGA GCGACGCCAG CCGGGAGTCG GCTGCACACC GTTGCACACC GTTCCAGAACG	TGTTTTCAG TCGGAAGAT TCGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CGAGGCTCAC CCCATGCTGG CCCCTGTGAC CCTACTGTGAC CCCCTGTGAC CTACCAGTGG	120 180 240 360 420 480 540 660 720 780 840 900 960
50 55	Nucleic Act Coding sequit Tortcocort AGCARANATGA AGCGTCGGA AGGTTTTCA CTGGACATCA AGGTTGCTG AAGTCCAGG ATTCCTGCTGA AGGGCAGCA ACCCTCAGCA ACCCTCAGCA AGAGGATCGC AGAGGATCGC AGAGGATCGC AGAGGATCGC TCGCAGCCCT CTCTGCCCGGC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGCTTGGATTC AAGGAGGCTAGATTC AAGGAGGCGGAGAAA AGGATGTGGCTGGCTTAGGTTGGCTGGCATTC GCTCGGCATT ACAGGACGCT TAACCCACCC GCCAGAAGG	m #: Bos se 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGAGGAGTGC GTGGAGGATG GCCCCAGGATCG CCGGAGTTCG GCTGCACACT TACAGGACACT ATCAGGACCA AGTTCCAGAAG AACTGTGCCC	I TGTTTTCAG TGGGAGAGAT TCGGTAGAGA GCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCCATGCTGG CAGCTGGAAG CCCCTGTGAC CTACCAGTGG CTACCAGTGG CCTGGAATGC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55 60	Nucleic Act	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCT AAGGAGGCT GCCCGAGAAG GGGATGGGT ACGTGGTTAC ACGAGGAGCT ACGTGGTTAC ACGAGCCT TACCAGCAG GCCAGAATGG GCCAGAATGG TGGCCTTTGG TGCCCTTTGG TGCCCTTTGG TGCCCTTTGG TGCCCTTTCG	m #: Bos se 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCCAGATCC AAGCAGCTGA GGAGCTGC GTGGAGGATG GCACGCCAG TCACGCAGT TACAGGACCA GTTCCAGAAG GATCCACCC TTCCAGAAG TTCCAGAGC TTCCAGAGC TCTCCCGGGCACC	TGTTTTCAG TGGGAAGAT TTCGTTAGA CCATCACTA AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGT CCTCTTCAGC CAGGGGTCAC CCCATGCTGG CAGCTGGAAG CCCCTGGAAG CCCTGGAAG CCCTGGAAG CCCTGGAAGC CCCAGATGC CCTGGAATGC CCTGGAATGC CCGGCTTCCTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	Nucleic According sequilibrium of the control of th	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGCAGAAAA GGGATGTGGC GGTCAGGTT GCTCGGCCAT ACAGGACGCT TACCTGCTGTT GCTCGGCACCT TAACCCACCC GCCAGAATGG TGGCCTTTGG TCTCTCTCTTCT TCTTCGTGAA	n #: Eos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTCAGAGTG TGAAAGGTCC GGTCAGAGTG ACTTCTGTG ACTGCCATCC TCCCAGGTG GGCTGAGCAG CTGCTCCAGC GGAGATGGTC TGCCAGCTG TGCTCCAGC GGAGATGGTC TGCGGTGCTG AGGCACATGT AGGGAAGGT AGGGAAGGT AGGGAAGGT GCTGGACAGC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GACTTGCTC CCCCAGATCC AAGCAGCTGA GGGGAGCTGA GGGGAGTGA GGGGAGTTCG GGGGAGTTCG GGTGCACACT TACAGGACCA GTTCCAGAAG AACTGTGCCC TCTGCGGGCA CGGGCCGTGC	TGTTTTCAG TGGGAGAT TCGGAGAGAT TCGGTAGAT TCTGATGAT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CGAGGAGCTCAC CCCATGCTGA CACTGTGAC CCCATGCTGG CAGCTGGAC CCCTGTGAC CTCTGGACTGC CGGCTTCCTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	Nucleic Act Coding sequit I ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA ATGCTTTCA ATGCTTTCA AGGTTGCTG AGAGCCAGG ACCCTCAGC ACCCTCAGC AGAGGTTGTC AGAGCCCT CTCTGCCCGC AGGGTCGACC AGGGTCGACC CGGGCCAAG CGAGTTGGT	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TCTGGTGCTC AAGGAGGTT GCCCCGAGAGA AGGATGTGGC GAGGATGTGGC GAGGATGTGGC GAGGATGTGGC GGTCAGGTT ACAGGACGT ACAGGACGCT TAACCCACCC GCCAGAATGG TCGCCTTTGGTTGGCTTTTGGTGATGGCTTTTGGTGATGGCTTTTGGTGATGGCTTTTGGTGATGGCTTTTGGTCAGATGGCTTTTGGTCATTTGGTCATTTGGTCATTTGGTCATTTGGTCATTTGGTCATTAGTTGGCCACTATAGTGGCCACTATAGTGGCCACTATAGTGGCCACTATAGTGGCCACTATAGTGGCCACATA	n #: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGTCAGAGG GGTCAGAGG ATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCAGGTG GGTGAGCAG GGTGAGCAG CTGCTCCAGG GGAGATGGTC TGCGGTGTG AGGCACATGT AGGGGAGGCT AGGCACATGT AGGGGAGGCT GCTGACAGC GCGGTTGAGCAG CTGCACAGC CTGCACAGC CTGCACAGC CTGCACAGC CGCGGTTGACAGC CGCGGTTGACAGC CGCGGTTGACAGC CCACAGGGAGGCT	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGC GAACAGGACG CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GAGCAGCCGCAG GCACCGCAGA CGGGAGTCG GCTGCACACT TACAGGACCT TACAGGACCT AACTGTGCCG CTTGCCGGGCCGTGC CTTGCCGGGCCGTGC CTGCTGGTGCG CTGCTTGCT	I TGTTTTCAG TGGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGCTCTAAC TTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATCGGC CCATGCTCAC CCATGCTCAC CCATGCTCAC CCCATGCTCAC CCCCTGTGAA CCCCTGTGAC CCTGCAATGC CCTCTCGGGC CGGGGGAGTAC	120 180 240 300 360 420 540 600 720 780 840 960 1020 1080 1140 1200
50 55 60	Nucleic Activities of the control of	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTTGGATTC AAGGAGGCTGGATTC AAGGAGGCGG GAGGCAGAAA GGATGTGGTT ACGTGCTGTTAGGTCAGGTT ACGTGCTGTTAGGTCAGGTT ACAGGACGCT GCCAGAAAG GGATGTGGCTTTGGTGAGGTT TCCTCTTCCTTCCTTCCTTCCTTCTTTGTGAAA TGGCCACATAG	m #: Bos se 424 21	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGGACG GGAGCTGA GGCACCCAG GCTGCACACCCAG GCTGCACACC TACAGGACCA TTCCAGAAG AACTGTGCCC TCTGCCGGCA CCGGCCTGG CCGGCCTGC CCGGCCTGC CCGCCTGGC CCGCCTGGC CCGCTCGCGGCACTTCC	I TGTTTTCAB TGGGAAGAT TCGGTAGAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CAGCTGGGAGC CCCATGCTGG CAGCTGGAAG CCCTGTGAC CTACCAGTGC CGGGGAGTAC CTCCTGGGATGC CTCTCGGGC CTGGAATGC CGGGGGAGTAC TGGCCCCACC	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1200 1260
50 55 60	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTC AGCANATGA AGCGTCGGAC CTGGACATCA AGGTTCCTCC AGGTTCCTC AGGTTCCTC AGGTTCCAGG AGTCCCAGG ACCCTCAGCA CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCCTGTCAGCA CCCTGTCAGCA CCCTGTCAGCA CCCTGTCAGCA CCGGCCAAAG CGAGTGTCC CGGGCCAAAG CGAGTGGTGC CAGGATGTGC CAGGATGTGC CAGGATGTGC CAGGATGTGC CAGGATGTGC CTGACGGGCCA	id Accession uence: 12: 11	#: Bos se 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATGC GTGCACGCAG GTTCCAGAAG ACTGCACCAC TACAGGACCA CTTCCAGAAG AACTGTGCC TCTGCGGGCA CGGGCCGTGC CTGTGCGGCAC CGGGCCGTGC CTGTGCACTGC CGGGCGTGC CTGTGCGGGCA CGGGCCGTGC CGGGCTGCC GGAGGTTGCCATTCC GGGCGTGCC GGGCGTGCC GGGCGTGCC	TGTTTTCAB TGGGAAGAT TTCGTTAGA CCATCACTA AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGT CAGCGAGCCT CCCTTTCAGC CAGGGAGCCT CCCATGCTGG CAGCTGGAAG CCCCTGTGAC CCTGGAATGC CCTGGAATGC CCTGGAATGC CTGCAGTGC CTTCGGGCC CGGGGGGAGTAC CTCCAGCCCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140 1200 1260 1320
50556065	Nucleic Activities Act	id Accession uence: 12: 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAGGT ACGGAGGT ACGGAGGAGT ACGGAGGAGT ACGGCAGAAGA ACGAGGGGGGAGAAA ACGACGGT GCCGGCCAT ACCGCCCT TAACCCACCG GCCAGACGG TCGCCTTCGT TCTTCGTGAA TCGCCACAGA TCGCCACAGAG TCCCACAGAG TCCC	#: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGT GGTCAGAGC GGTCAGAGC ACTCCAGC TGCTTCTGTG ACTCCAGC GGAGATGT TCCCAGGTGG GGAGATGT TGCGCTCCAGC GGAGATGT GGTGCACAGC AGGCACATGT CGGGTGGACAGC GGGGTTGTGG CGGGGTTGTGG GCGGTTGTGG CGGGGTTGTGG CGGGGGCGCAGC CGGGGGCGCAGCGGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GCACGCCAG CTGGAGAGT GCTGCACAC GTTCCAGAAG CTTCCAGAAG CTTCCAGAAG CTTCCAGAAG CTTCCAGGAG CTCTCCGGGCA CTGCTGCTGC CTGCTGCGTGC CTGCTGGTGG CTGCTGCTGC	I TGTTTTCAG TGGGAAGAT TTCTTTAGA CCATCACTT TGAGGCAG TGAATACCT TCATCATCT TCATCATCAT TCATCATCAT TCATCATCAT TCATCATCAT TCACACACCACACACA	AGTGCCCCA TTCAGCTGCC TTGGCTCTAAC TTGTGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CAGCGTGAAC CCCATGCTGG CCCATGCTGG CCCTGTGAC CCTGCTGAC CCTGCTGAC CCTGCTGAC CCTGCTGCCC CCTGCAATGC CCTGCAATGC CCCTGCAATGC CCCCTGCAATGC CCCCGCCCCCCCCCC	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1250 1380
50 55 60	Nucleic Act Coding sequil ATGCCCCTT TCTCTCCTC AGCAAAATGA AGCGTCGGAA ATGCCAGGATTCC ATGGTTTTCA AGGTTGCTGG AGGTCCAGG ACCCTCAGCA ACCCTCAGCA ACCCTCAGCA CCCTGTGAGC AGAGGATCGC AGAGGTTTCC TCTCTGCCCGC AGGGTCGACC CGGGCCAAAG CGAGTGGTC CGGGCCAGGGC CGGGCCAGGGC CGGGCCAGGGC CGGGCCAGGGC CGGCCAGGGC CGGCCAGGGC CGGCCAGGGC CGGCCAGGGC CGGCCAGGGC CGGCCAGGGC CGTTGCCGGC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTTGGATTC AAGGAGGCTGGATTC AAGGAGGCGGGACCTTAGGTCAGGTTAGGTCAGGTTAGGTCAGGTTTACCCACCC	n #: Eos se 424 21 21 GGAGGCCGTC CCATGTAAGC GGTCAGAGTG TGAAAGGTCC GGTCAGAGTG ACTGCTACAGC TGCTTCTGTG ACTGCAGCG GGCTGAGCAG GGCTGAGCAG GGAGATGGTC TGCGTCCAGC TGCTCCAGC TGCTCCAGC TGCTCCAGC TGCGTTCCAGC TGCAGCTGC TGCAGCTGC TGCAGCTGC TGCAGCTGC TGCAGCTGC TGCAGCTGC TGCAGCAGCGC TGCAGCAGCGC TGCAGCGCGC TGCAGCGCGC TGCAGGCGCC TGCAGCGCGCC TGCAGGCGCCT TGCAGCCCTC TGCAGGCGCCT TGCAGGGGGCCCT TGCAGGCGCCT TGCAGGCGCCC TGCAGGCGCCC TGCAGGCGCCC TGCAGGCGCCC TGCAGGCGCCC TGCAGGCGCCC TGCAGGCGCCC TGCAGGCGCC TGCAGGCGCC TGCAGGCGCC TGCAGGCGCC TGCAGGCGCC TGCAGGCGCCC TGCAGGCGCC TGCAGGCGCC TGCAGGCGCC TGCAGCCC TGCAGCCCC TGCAGCCCC TGCAGCCCC TGCAGCCCC TGCAGCCC TGCACC TGCAGCCC TGCAGCCC TGCAGCC TGCAGCCC TGCAGCCC TGCAGCC TGCAGCCC TGCAGCCC TGCAGCCC TGCAGCC TGCAGC TGCAGC TGCAGCC TGCAGCC TGCAGCC TGCAGCC TGCAGCC TGCAGCC TGCAGCC T	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCAGATCC AAGCAGCTGA GGCACCCAG GTGCACCACG GTGCACACC TACAGGACCA TTCCAGAAG AACTGTGCCC TCTGCGGCA CCGGCCTGC CTGCTGCTGGC GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGTGG	I TGTTTTCAG TGGGAAGAT TCTGTTAGA CCATCAGTT AGATCAGTT TGAAGGCAAG TGAAATACCT TCATCATCT TCATCAGTC TCATCAGTC CACCAACGG ACTGCAGCG GACTGAGGGAT GCACTGAGGG TGAACTGGC CCACCACGG TGAGCTGGACGG TGAGCTGGACGG TGAGCTGGACGG TGAGCTGGACGG TGAGCTGGACGG TGAGCGAGGG TGAGCGAGGACGC TGAGCAGGGACGC TGAGCAGGAGGA TGAGCAGGAG CCATCTCGGAG TGAGCAGGAGCA TCTCCGTGG TGGGAGCGC TCTCCGTGG	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCAGCCT CCTCTTCAGC CAGCTGGAGCT CCCATGCTGG CAGCTGGAAG CCCTGTGAC CTACCAGTGC CTTCCTGGGC CTGCACC CTACCAGGAGCT CTCCGGGGAGTAC CTCCTGGGATGC CTCCTGGGATGC CTCCTGGAATGC CGCGGGAGTAC TGGCCCCACC CACCAGGACA CGAGGACTAC TGGCCCCACC CACCAGGACA CGAGGATAGG	120 180 240 300 360 420 600 660 720 780 840 900 1020 1140 1200 1260 1320 1380
50556065	Nucleic According sequilibrium of the control of th	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGGGGGGGCAGAAA GGGATGGGC GAGGCAGAAA GGGACCT ACCGGCAGT ACCGCCCT TACCCACCC GCCAGAATGG TGGCCTTTGG TCCTCTCCT TCTCGTGAA TGGCCACTAG CTGCCTTTGG TCCTCTCCT TCTCGTGAA TGGCCACTAG CTGCCCTGGC GGGCACCTGG CGGCACCTGG CGGCACCTGG CGGCACCTGGC GGCACCTGGC GGCACCTGGC GGCACCTGGC GGCACCTGGC GGCACCTAGC GGCACCTAGC GGCACCTAGC GGCACCTAGC GCCACGAGAGC CAGCACGTCAC CGGCCACGAGAGC CAGCGCGCCTCACCGGCCACACACCACCACCACCACCACCACCACCACCA	m#: Bos se 424 21 21 GGAGGCCGTC CCATGTAGG GGTCGAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCTCTGTG ACTGCTCTGTG ACTGCTCAGCG GGAGATGGT TGCAGCAGC TGCTCCAGC GGAGATGGT TGCGGTGCTC TGCGGTGCTG CGGAGAGGGT CGCGGTGGTGG CGGAGAGGGT GCGGAGAGGGT CGCGGAGAGGGT CGCAGGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCCAGATCC AAGCAGCTGA GAGCAGCGC GTGGAGGAGT GCCACGCCAG TTCCAGAAG TACAGGACCA TTCCAGAGC TCTGCTGGGC TCTGCTGGGC CTGCTGGTGC GAGGCTTCC GAGGCTTCC TTTGCTCACTG GAGGCTTCC TTGCTCACTG GAGGCTTCC AACGGCACTCC ACAGGCAGCCC ACAGGCAGCCC ACAGGCAGCCC ACAGGCAGCCC ACAGGCAGCCC ACAGGCAGCCC ACAGGCAGCCC ACAGGCAGCCC	TGTTTTCAB TGGGAAGAT TTCGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTACTGTG CAGGGAGCCT CCCTTTCAGC CAGGTCAC CCCATGCTGGA CCCTGGAAG CCCTGGAATGC CCTTCCGGCC CTGGGATGC CTGGGATGC CTGGGATGC CTGGGATGC CGGGGGATAC CGGGGGATAC CGGGGATAC CGAGGATGC CACCAGGACA CGAGGATGAC CTACCAGTGC CTGCAGCAC CGAGGATGC CACCAGGACA CGAGGATGAC CGAGATGAC CGAGGATGAC CGAGGATGAC CGAGGATCAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATAC CGAGGATCAC CGAGGATAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGATAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGAC CGAGC	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1260 1320 1320 1440 1500
50556065	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTC AGCARATGA AGCGTCGGAC CTGGACATCA CTGGACTTC AGGATTTCA GGGTTCCTGG AGTCCCAGG ACCCTCAGCA CCCTGTGAGA CCCTCAGCA CCCTGTGAGAC CCCTGTGAGC CCCTGTGAGC CCCTGTGAGC CCGGCCAAAG CGAGTGTTCC CTGCCGCG CGGCCAAAG CGAGTGGTG CAGGATCGC CTGACGGCCA CCTGACGGCC CTGACGGCCA CCTGACGGCC CTGACGGCC CTGCCGCC CTGACGGCC CTGACGCC CTGACGGCC CTGACGGCC CTGACGGCC CTGACGGCC CTGACGGCC CTCGGATCCT CCGGATCCT CCGGCCAT CCGGATCCT CCGGATCCT CCGGATCCT CCGGATCCT CCGGATCCT CCGGATCT CCGGATCCT CCGGATCT CCGCATCT CCGCATCT CCGCATCT CCGCATCT CCGCATCT CCGCATCT CCGCATCT CCGCATCT CCGCATCT CCCCCT CCCCCT CCCCT CCCCT CCCCC CCCCT CCCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCGAGAG CCTTGGATT GCCCGAGAG GGATGGGTC GAGGAGCT AAGGAGGCG GGGTCAGGTT ACTGCTGTT GCTCGGCCAT ACAGGACGCT TAACCCACCC GCCAGAATGG TCCTCTTCGT TCTTCGTGAA TGGCCACATA CGGCCACATA CGGCCACATA CGGCCACCATA CGGCCACCTCGC GGCAGACTCG CGGCCACGTAG CGGCACGTAG CGGCCACGTAG CGGCCACGTAG CGGCCACGTAG CGGCCACGTAG CGGCCACGTAG CGGCACGTTAG CGCCTCC CGCACGTCC CGCCACGTCC CGCCACGTCC CGCCACGTCC CGCCACGTCC CGCCACGTCC CGCCACGTCC CGCCACGTCC CGCCACGTCC CGCCACGTCC CGCCCCC CGCCACGTCC CGCCC CGCCACGTCC CGCCCC CGCCC CGCCCC CGCCC CGCCCC CGCCC CGCCC CGCCC CGCCC CGCC CGCCC CGCC CGCCC CGCC CGCCC CGCC CGCCC CGCC CCC	#: Bos se 424 21 21 GGAGGCCGTC CCATGTAAGC GGTCAGAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGGTGA CTGCTCCAGC GGAGATGGTC TGCGGTCCAGC GGAGATGGTC TGCGGTCCTGC GGAGATGGTC GCTGGACAGC GCAGGGGGC GCAGGGGGC GGAGGGGCT GCGAGGGGCT GCGAGGGGCT GCGAGGGGGCT GCGAGGGGGCT GCGAGGGGGCT GCGAGGGGGCT GCGAGGGGCC GGAAGGGCCC GGAAGGGCCC GGAAGGGCT CGGAAGGGCCC GGAAGGGCT CGGAAGGGCT CGGAAGGGCCC GGAAGGGCT CGGAAGGGCT CGGAAGGGCT CGGAAGGGCT CGGAAGGGCT CGAACCAAATC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GACTTGGTC CCCCAGATCC AAGCAGCTGA GGAGCATGC GTGGAGGATG GCTGCCAGATCC TACAGGACGC CGGGAGTTCG TTGCAGAAG AACTGTGCC TCTGCGGGCA CGGGCCGTGC CTGTGCGGGCA CGGGCGTGC TTGCTGGTGG CGAGGCTGC CGAGAGGTGCC CGAGAGGTGCC CACAGGCAGCC CCCGAGCTGCC CCCGAGCTGCC CCCGAGCTGCC CCCGAGCTGCC	TGTTTTCAG TGGGAAGAT TCGGTAGA AGTTCAGTTC TGAAGGCAAG TGAAATACCT TCATCATCOT TCATCATCOT AGGAAAGGGC CCACCAACGG ACTGCACGGT CTGCACGGT CTGCCAGG GACTGAC GACTGAC CCACTCTGC CCACTCTCA CCTGCCAGG TGAAGCTGAC CCACTCTGC CCACTCTGC CCACTCTGC CCACTCTGC CCACTCTGC CCACTCTGC TGAGCGAGGC CGATCCTTT TCCTTCGT TCGGGAGGC AGTCACACT TCCTTCTGCAGG CCACTCTCTTCCATCGG CCACTCTCTTCGT TCGGGAGGCC AGTCACACT TCCTTCTGCGGC CCAACACCT AGGGAAGCATGT AGGGAAGCATGT AGGGAAGCATGT AGGGAAGCATGT AGGGAAGCATGT AGGGAAAGCATGT AGGGAAAGCATGT AGGGAAAGCATGT AGGGAAAGCATGT	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGT CAGGGAGCCT CCTCTTCAGC CAGGGAGCCT CCCATGCTGG CAGCTGGAAG CCCTGTGAC CCCTGTGAC CTCTCGGGCC GGGGGAGTAC CTCTCGGGCC CGCGGAAGC CTGCACC CTGCCCCC CTGCACC CTGCACC CTGCACC CTGCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCCC CTGCCCCC CTGCCCCCC CTGCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCCC	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500
50556065	Nucleic Act Coding sequit I ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA AGGTTGCTG AGGTTGCTG AGGTCCTGG AGGTCCAGG AGGGCCAGC ACCTCAGC AGGGTTGTGG AGAGGTTGTG AGAGGTTGTTC TCTGCCCGC AGGGTCGACC CGGGCCAAG CGAGGTGGTG CAGGCTGCGGC GGGCAGCA GGCCAGGAC GGCAGGAC GGCAGGAC GGCAGGAC GGCGGCCAGG	id Accession uence: 12: 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGTGTGCTC AAGGAGGCTG GCCCCGAGAG AGGAGGGCG GAGGATGTGGC GAGGATGTGGC GGCTCAGGTT ACAGGACGT ACAGGACGCT TAACCCACCC GCCAGAATGG TCGCCTTCGT TCTTCGTTGAT TCTTCGTTGAT CTGCCTCTTCCT TCTTCGTTGGC CGCCAGATGGC CGCCACATA CGGCCACATA CTGACCTGGT CAGCCTTGGGC CAGCCGTCA CAGCCGCTCA CAGCCGCTCA CAGCCGCTCA CAGCCGCTCA CAGCCGCTCA CAGCCGCTCA CAGCCGCACA CAGCCGCTCA CAGCCGCTCA CAGCCGCACA CAGCCGCCCACA CAGCCCGCACA CAGCCCGCACA CAGCCCGCACA CAGCCCGCACA CAGCCCGCACA CAGCCCGCACA CAGCCCCCACA CAGCCCCCACA CAGCCCCCCACA CAGCCCCCCCACA CAGCCCCCCCACA CAGCCCCCCCACA CAGCCCCCCCC	n #: Bos se 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GAGCATTCC CAACAGGAAG GACTTGCTC CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GCACGCCAG CGGGAGTTCG GCTGCACACT TTCCCGGGA CTCCCGGGAG CTGCTGCTGCC CTGCTGCGGCA CTGCTGCTGCG CTGCTGCTGC CTGCTGCGGCA CTGCTGCTGC CTGCTGCGGCA CTGCTGCTGC CTGCTGCGGCA CTGCTGCTGC CTGCTGCGGCA CTGCTGCTGC CTGCTGCGGCA CTGCTGCGGCA CCGGCCTGCC CTGCTGCTGC CGACGCTGCC CTGCTCTCTGCGGCA CGGCCTGCC CTGCTCTCTCTGCGGCA CGGCCTGCC CTCTGCTGCGCA CGGCCTGCC CTCTGCTCTCTCTGCGCACC CCTGAGCTGCC CCTGAGCTGCC GACCTCCTCTCT	I TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGCCTAAC TTGTGACGTT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATCGG CAGCGAGCCT CCTCTTCAGC CCATGCTCAC CCCATGCTCG CAGCTGCAC CCCTGTGAC CCCTGTGAC CCTGCAGC CCCTGTGAC CCCTGGAATGC CCTGCGGCC CGGGGAGTAC CCCCACGCCACC CGCGGAGTAC CTGCCACC CGGGGAGTAC CGAGGATGAC CGAGGATGAC CGAGGATCAC CGAGGATCAC CGAGGACAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGACCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGACCAC CGAGGACCAC CGAGGACCAC CGAGGATCAC CGAGGACCAC CGACCACCC CGCCCCCC CGCCCCCC CCCCCCCC	120 180 240 300 360 420 540 660 720 780 840 960 1020 1140 1200 1250 1380 1440 1560 1620
5055606570	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTT AGCANATGA AGCGTCGGA AGCGTTCCAGGA AGGGTTCCAGGA AGAGGCAGCA ACCCTCAGCA AGAGGATCCC AGAGGATCCC AGAGGATCCC AGAGGATCCC AGAGGATCCC CTGTCAGCA CCTGTAGCA CCTGTGAGC AGAGGATCGC AGAGGTCGACC CGGCCCAAG CGGCCAAG CGGGCCAAG CGGGCCAAG CGGGCCAAG CGGGCCAGCC CTGACGGCC CAGGGTCGCC CAGGGTCGCC CAGGGTCGCC CAGGGTCGCC CAGGGTCGCC CAGGGTCGCC CAGGGCCCACC CGAGGCCCCC CAGGGCCCACC CAGGGCCCACC CAGGGCCCACC CAGGGCCCACC CAGGGCCCACC CAGGCCCCCC CAGGGCCCACC CAGGGCCCTCC CAGGGCCCTCC CAGGGCCCTCC CAGGGCCCCC CAGGGCCCTCC CAGGCGCCCCAC CCAGTAGGGCCCTCC CAGGGCCCTCC CAGGGCCCTCC CAGGGCCCTCC CAGGAGCCCTCC CAGGGCCCTCC CAGGGCCCTCC CAGGGCCCTCC CAGGGCCCTCC CAGGAGCACC CCAGTAGGGCCCTCC CAGGAGCCCTCC CAGGAGCCCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCCCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCTCC CAGGAGCCCCCC CAGGAGCCCTCCC CAGGAGCCCTCC CAGGAGCCCCCC CAGGAGCCCCCC CAGGAG	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTTGGATTC AAGGAGGCT GCCCGAGAAG GCGTGGATTC AAGGAGGCGG GAGCAGAAA ACGGCTGGTT ACGTGCTGT ACGGCACCCT TACCCACCC GCCAGAATGG TGGCTTTGG TCCTCTTCCT TCTTCGTGAA TGGCCACATA CTGACCTGGT GGCGACCCT CGCCAGAATGG CGGGCACAGATG GGGCACAGATGG CGGGCACAGATGG CGGGCACAGACT GGCCAGAATGG CGGGCACAGACT GGGCACAGACT GGGCACAGACT GGGCACAGACT GGGCACAGACT GGGCACAGACT GGGCACAGACT GGGCACAGACT CGGGCACAGACT CGGGCACAGACT CGGGCACAGACT CGGGCACAGACT CCGGGAGAATTT	#: Eos se 424 21 21 GGAGGCCGTC CCATGTAAGC GGTCGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC GGTCAGAGTG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGAGATGTC TGCGGTCCAG CTGCTCCAGC GGAGATGTC GGAGCAGCAG CTGCACCTGC GCAGCAGCAGC CCGCAGCAGCAGC CCGCAGCAGCAGC CCGCAGGAGCAGC CCGGAGGAGCAC CCGGAGGAGCCT CGCAGGGGCC CGGAGGAGATC CCAACCAAATC CCAACCAAATC CCAACCACAATC CCAACAACCCTC CCACCACACCCCTC CCACCCCCTC CCACCCCCCCC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCCAGATCC AAGCAGCTGA GGAGCTGC GTGGAGGATG GCCACGCAG GTTCCAGAAG ACTGTGCCC TCTGCGGGCA CGGGCCGTGC GATGCCCC TTTGCTCACTG GATGGCACCT TTGCTCACTG CGAGGAGTTC ACAGGAGCTGC CCTGAGGCGC CCTGAGGCGC CCTGAGGCGC CCTGAGCTGC CCTGAGGCGCC CCTGAGCTGC CCTGAGCTGC CGGCCTGCC CCTGAGCTGC CGGCCTGCC CCTGAGCTGC CGGCCTGCC CCTGAGCTGC CGACCCCCTTGC CGACCCCCTTGC CGACCCCCTTGC CGACCCCCTTGC CGACCCCCTTGC CGACCCCCTTGC CGACCCCCTTCC CCACAGCCTCCCT CCACAGCCTCCTC CCACAGCCCCCTCCCCCCCCCC	I TGTTTTCAB TGGGAAGAT TCGGTAGAAGAT CATCACTGT GAAGGCAAG TGAAATACCT TCATCATCGT TCATCATCGT AGGAAGGGA ATGCACTGGC CCACCAACGG ACTGCACAGG GACTCGACGG TGAAGGGA CTGCCCAGG GACTCGACGG TGAAGCTGAC CCACTCTGC CCACCAGG GACTCTGGA CCGGTCCTGT TCAGCGAGGA TGAAGCTGAG CCGTCCTGGA TGAAGCTGAG TCAGCGAGGA TCATCTGGA AGGAAGCA AGGAAGCT TCATGTTGGA AGGGAAGCT TCATGTTGGG TGAGGAGGA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATGGG CAGTGAGGCTAC CCCATGCTGG CAGCTGGAAG CCCTGTGAC CCTCTCGGCC CTCTCGGGCC CGGGGGAGTAC TGGCCCACC CGAGGATAC TGGCCCACC CACCAGGACA CGAGGATAC TGGCCCACC CACCAGGACA CGAGGATAC TGGCCCACC CACCAGGACA CGAGGATAC TGGCCCCACC CACCAGGACA CGAGGATAC TGGCCCCACC CACCAGGACA CGAGGATAC TGGCCCCACC CACCAGGACA CGAGGATAC TGGCCCCACC CACCAGGACA CGAGGATAC TGTAGCCAG TGTAGCCCG CACCTCTCCC CACCTCTCCC	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500
50556065	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTCT AGGARATCA AGGGTCGGA CTGGACATCA AGGGTTGCCTG AGGTTCCAGG AGAGGCCAGC ACCCTCAGCA CCCTGTAGGC AGAGGTCCCT TCGCAGCCCT TCGCAGCCCT CCTGCCAGC CGGGCCAAAG CGAGTGGTGC CGGGCCAAAG CGAGTGGTGC CGGGCCAAAG CGAGTGGTGC CTGACGGCCAC CGGGCCAAAG CGAGTGGCTCAGCAGC CTGACGGCCAC CTGCAGGCCT CAGGGTCACC CTGACGGCCAC CTAGCAGGCCT CAGGGCCAGACC CTAGCAGGCCT CAGGGCCTGC CAGGATCCT CAGCAGCCCT CAGCAGCACC CTCAGCAGCCCT CAGCAGCACC CTCAGCAGCCC CTCAGCAGCCCT CAGCAGCACC CTCAGCAGCACC CTCAGCACC CTCACC CTCAGCACC CTCACC CTCAC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCT AAGGAGGCT GCCCGAGAAG GGGTCAGGTT ACCGGCAGT ACCGGCCAT ACCGCCCT TACCCACCC GCCAGAATGG TGGCCTTTGGT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCACTTGG TCCTTCCT TCTTCGTGAA TGGCCACTTGG CGGCACCTTGG CGGCACCTTGG CGGCACCTTGG CGGCACCTTGG CGGCACCTTGG CGGCACGTGG CGGCAGAGGC AGGATCTGG CGGCAGAGC CGGGAGGC CCGAGAATG	#: Bos se 424 21 21 GGAGGCCGTC CCATGTAAGG GGTCAGAGG GGTCAGAGG ATTTTCAAC CACGGAGACG TGCTCTGTG ACTGCTCAGC GGTTCAGTG GGTGAGCAG GGTGAGCAG GGAGATGGT TGCACCTGC TGCGGTGG GGAGATGGT GGAGAGGGT GCGGGTGAGCAG GGAGATGGT GGAGAGGGT GGGGAGAGG GGGGAGAGGT GGCGGGGGGGG GGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GACATTGCTC CCCAGATCC AAGCAGCTGA GAGCAGCGCAG GCGACGCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG AACTGCCCC TCTGCGGGCA CGGGCCGTGC CTGTGCACAT GTTCCAGAAG CAGGCCGTGC CTGTGCGGCACT CTGCTGGGCACT CTGCTGTGG CGAGAGCTGC CTGGCACTCC CACAGGCAGCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTTGC CACAGGCTTGC CACAGGCTTGC CACAGGCTTGC CACAGCCTTTG CAGAGCTTTGC CAGAGCTTTGC CAGAGCTTGC CAGAGCTTTGC CAGAGCTTGC CAGAGCTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTCC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTCC CAGAGCTTGC CAGAGCTCC CAGAGCTC	I TGTTTTCAG TGGGAGAGAT TCGGTAGAGAGAT TCTGTTAGA CCATCACAGT AGATCAGTT TGAAGGCAAG TGAAATACCT TCATCATCAT TCATCATCAT TCATCATCAT CATCACAGG ACTGCAGGGT CTGCCAGGG GACTGACCAGG GACTGACGGAGGA TGAAGCTGAG TGAAGCTGAG TGAGCGAGGA TCATCATCAT TCTTCGTGG TCGGAGGGC TCTGCTGGG AGTCACACT TCCTGCTGGG AGTCACACT TCCTGCTGGG TCGAAGCATGT AGGGAAGCT TCATGTTGGG TGAAGCATGT TGAAGCATGT TGAAAGCTGAG TGAAAGCATGT TGAAAGCATGAAAGCATGT TGAAAGCATGT TGAAAGCATGT TGAAAGCATGT TGAAAGCATGAAAGAAACATGT TGAAAGCATGAAAGAAACATGAAAACATGAAAACATGAAAACATGAAAACATGAAAACAAAAAAAA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATCGG CAGCGAGCCT CCTCTTCAGC CAGCGGAAGC CCCATGCTGG CCCTGTGAC CCTCTCGGCC CCTGGAATGC CCTCTCGGCC CCGGGAATGC CCACGAGCT CTCCTGGGCC GGGGGAGTCAC CACCAGGACA CACCAGGACA CGACGATGAC CTGCCCCAC CGCGCCCCC CGCGCCCCC CACCAGGACA CCACCTCTGCC CTGCAGCCGG CGCCCCCCGGACGACA CCACCTCTGCC CTGCAGCCGG CACCTCTGCC CTGCAGCCGG CCACCTCCCAGCCGGCCCGCCCCCCCCCC	120 180 240 300 360 420 540 660 720 780 840 960 1020 1140 1200 1250 1380 1440 1560 1620
5055606570	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTCT AGGARATCA AGGGTCGGA CTGGACATCA AGGGTTGCCTG AGGTTCCAGG AGAGGCCAGC ACCCTCAGCA CCCTGTAGGC AGAGGTCCCT TCGCAGCCCT TCGCAGCCCT CCTGCCAGC CGGGCCAAAG CGAGTGGTGC CGGGCCAAAG CGAGTGGTGC CGGGCCAAAG CGAGTGGTGC CTGACGGCCAC CGGGCCAAAG CGAGTGGCTCAGCAGC CTGACGGCCAC CTGCAGGCCT CAGGGTCACC CTGACGGCCAC CTAGCAGGCCT CAGGGCCAGACC CTAGCAGGCCT CAGGGCCTGC CAGGATCCT CAGCAGCCCT CAGCAGCACC CTCAGCAGCCCT CAGCAGCACC CTCAGCAGCCC CTCAGCAGCCCT CAGCAGCACC CTCAGCAGCACC CTCAGCACC CTCACC CTCAGCACC CTCACC CTCAC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCT AAGGAGGCT GCCCGAGAAG GGGTCAGGTT ACCGGCAGT ACCGGCCAT ACCGCCCT TACCCACCC GCCAGAATGG TGGCCTTTGGT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCCACT TCTTCGTGAA TGGCACTTGG TCCTTCCT TCTTCGTGAA TGGCCACTTGG CGGCACCTTGG CGGCACCTTGG CGGCACCTTGG CGGCACCTTGG CGGCACCTTGG CGGCACGTGG CGGCAGAGGC AGGATCTGG CGGCAGAGC CGGGAGGC CCGAGAATG	#: Bos se 424 21 21 GGAGGCCGTC CCATGTAAGG GGTCAGAGG GGTCAGAGG ATTTTCAAC CACGGAGACG TGCTCTGTG ACTGCTCAGC GGTTCAGTG GGTGAGCAG GGTGAGCAG GGAGATGGT TGCACCTGC TGCGGTGG GGAGATGGT GGAGAGGGT GCGGGTGAGCAG GGAGATGGT GGAGAGGGT GGGGAGAGG GGGGAGAGGT GGCGGGGGGGG GGGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GACATTGCTC CCCAGATCC AAGCAGCTGA GAGCAGCGCAG GCGACGCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG AACTGCCCC TCTGCGGGCA CGGGCCGTGC CTGTGCACAT GTTCCAGAAG CAGGCCGTGC CTGTGCGGCACT CTGCTGGGCACT CTGCTGTGG CGAGAGCTGC CTGGCACTCC CACAGGCAGCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTTGC CACAGGCTTGC CACAGGCTTGC CACAGGCTTGC CACAGCCTTTG CAGAGCTTTGC CAGAGCTTTGC CAGAGCTTGC CAGAGCTTTGC CAGAGCTTGC CAGAGCTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTCC CAGAGCTTGC CAGAGCTTGC CAGAGCTTGC CAGAGCTTCC CAGAGCTTGC CAGAGCTCC CAGAGCTC	I TGTTTTCAG TGGGAGAGAT TCGGTAGAGAGAT TCTGTTAGA CCATCACAGT AGATCAGTT TGAAGGCAAG TGAAATACCT TCATCATCAT TCATCATCAT TCATCATCAT CATCACAGG ACTGCAGGGT CTGCCAGGG GACTGACCAGG GACTGACGGAGGA TGAAGCTGAG TGAAGCTGAG TGAGCGAGGA TCATCATCAT TCTTCGTGG TCGGAGGGC TCTGCTGGG AGTCACACT TCCTGCTGGG AGTCACACT TCCTGCTGGG TCGAAGCATGT AGGGAAGCT TCATGTTGGG TGAAGCATGT TGAAGCATGT TGAAAGCTGAG TGAAAGCATGT TGAAAGCATGAAAGCATGT TGAAAGCATGT TGAAAGCATGT TGAAAGCATGT TGAAAGCATGAAAGAAACATGT TGAAAGCATGAAAGAAACATGAAAACATGAAAACATGAAAACATGAAAACATGAAAACAAAAAAAA	AGTGCCCCA TTCAGCTGCC TTGGCCTAAC TTGTGACGTT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATCGG CAGCGAGCCT CCTCTTCAGC CCATGCTCAC CCCATGCTCG CAGCTGCAC CCCTGTGAC CCCTGTGAC CCTGCAGC CCCTGTGAC CCCTGGAATGC CCTGCGGCC CGGGGAGTAC CCCCACGCCACC CGCGGAGTAC CTGCCACC CGGGGAGTAC CGAGGATGAC CGAGGATGAC CGAGGATCAC CGAGGATCAC CGAGGACAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGACCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGACCAC CGAGGACCAC CGAGGACCAC CGAGGATCAC CGAGGACCAC CGACCACCC CGCCCCCC CGCCCCCC CCCCCCCC	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1260 1380 1440 1500 1500 1620 1680
5055606570	Nucleic Act Coding sequit ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA ATGCTTTCA ATGCTTTCA ATGCTTTCA ATGCTTTCA AGGTTGCTGG AGAGGCAGC ACCCTCAGC AGCGTTGCGG AGAGTTTCC AGGGTTGCCTG AGGGTTGCCTG AGGGTTGCCGC AGGGTTGAGC AGGGTTGACGC CTCTGCCGC AGGGTTGACGGCA AGGGTTGACGGC CTGACGGCC CTGACGCCT CTGACGGCC CTCGACGCCC CTCGACGCCC CTCGACGCCC CTCGACGCCC CTCGACGCCC CTCGACGCCC CTCGCTCC CACCGCCCC CTCGCTCC CACCGCCCC CTCGCTCC CTCGCTCC CTCCC CTCC CTCCC CTCC CTC	id Accession uence: 12: 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGTGGTGCTC AAGGAAGTT ACGGAGATT ACGAGAGAGT ACGGAGATGGC GAGGAGAAAA ACGAGGGC GGCAGAATGGC GCCAGAATGGC TCCTCTTCGT TCTTCGTGAAT CGCCACAC CGCAGAATGGC GGCACACTAG CGCACACC GGCAGATGGC GGCACACTAG CGGCACATAG CGGTGCCGAC CGGACATTAG CGGTGCCGAC CGGGAATTT CGGTGCCGAC CGGGAATTT CGGTGCCGAC CGGGAATTT CACCTGACGT CGGCTGGACACT CGGCTGGACACT CGGCTGGACACT CGGCTGGACACT CGGCTGGACACT CGGCTGGACACT CGGCTGGACACT CGGCTGGACACT CGGCTGGACACC CGGGACACT CGGCTGGACACC CGGGACACT CGGCTGGACACC CGGGACACT CGGCTGGACACC CGGGACACT CGGCCGACACT CGGCCGACACT CGGCCGACACT CGGCCGACACT CGGCCGACACT CGGCCGACACT CGGCCGACACC CGGGACACT CGGCCGACACC CGGGACACT CGGCCGACACC CGGGACACT CGGCCGACACC CGGCACACT CGGCCGACACC CGGCACACT CGGCCGACACC CGGCACACT CGGCCGACACC CGGCACACT CGGCCGACC CGGCACACT CGGCCGACACC CGGCACACT CGGCCGACACC CGGCACACT CGGCCGACC CGCGACACT CGGCCGACC CGCGACACT CGGCCGACC CGCGACACT CGGCCGACC CGCGACC CGCCGACC CGCCGACC CGCCGACC CGCCGACC CGCCGACC CGCCGACC CGCCGCC CGCCGACC CGCCC CGCC CGCCC CGCC CG	#: Bos se 424 21 GGAGGCCGTC CCATGTAAGC GGTCGAGTG TGAAAGGTCC GGTCAGAGTG TGAAAGGTCC GGTCAGAGTG TGCTCTGTG ACTGCCATC TCCCAGGTGG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGAGATGTC TGCGCACTC TGCGACTGG GGAGATGTC GGAGGAGGCT GGTGGACAGC GGAGGAGGGCT GGAGGAGGCT CGAGCAGGGCCT CGCAGCGGGCCT CGCAGCGGCCT CGCAGCAGCGCC CGAAGGGCCT CGCAACAGGCCT CCAACAATT CAAACCAATT CCAAACCACC CCAAACAGGCCT CGAACAAGGCCT CCAACAAATC CAAACCACC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GACATGTCC CACAGATCC CACAGATCC AAGCAGCTGA GGAGCATCC GTGGAGGATCC GTGGAGGATTCC TACAGGACT TACAGGACCA GTTCCAGAAG AACTGTGCC CTGCTGCGGGA CGGCCCTTGC GAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTTCC CAGAGCTTCC CAGAGCTTCC CAGAGCTTCC CGGCCCTGCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCGGCCTGCC CCGGGCTGCC CCGGGCTGCC CCGGGCTGCC	I TGTTTTCAB TGGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGCCTTAAC TTGTGACGTT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGG CAGCTGCAG CCCCTGTGAA CCCTGTGAC CCTGCAGCT CCTCTCGGCC CGGGGATAC CCTGCAGCT CCTCTGGGCC CCTGGAATGC CCTGGAATGC CCCAGGACA CTACCAGGTGC CTACCAGGCAC CTACCAGGCGC CTACCAGGCGC CTACCAGGCGCG CCACCAGCCACC CACCAGGACA CGAGGACAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGGACAC CGACGACCACC CGCCCCCCC CGCCGCGCC CGCCGCCCCCCCC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1260 1320 1380 1440 1500 1500 1560 1680 1740
5055606570	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTC AGCARATGA AGCGTCGGA AGCGTCGGA ATGCTTCA AGGTTGCTC AGGTTCCAGCA AGAGTCCAGG AGAGTCCAGGA ACCTCAGCA AGAGGTTCC AGAGCATCA CCTGAGC AGAGTTTCC TCTCTGCCCGC AGGGTCGACC CGGGCCAAAG CGAGTGGTC CTGACGGCCAGC CTGACGCCAGC CAGTAGGGCCAGC CTCAGCAGCCT CAGCAGCCCTTCC CAGCGCCAGC CTCAGCTCCC CCCCTTCCC CCCCTTCCCCCCCTCCC CCCCTTCCCCCC	id Accession uence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAAGT GCCCCGAGAGG CCTTGGATTC AAGGAGGCTG GAGGCAGAAGT ACGTGCTGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGG	#: Bos se 424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCAGATCC AAGCAGCTGA GGCACCCAG GTGCACCACCAG GTTCCAGAAG GCTGCACACC TACAGGACCA TTCCAGAAG TTCCAGAAG TTCCAGAAG TTCCAGAAG TTCCAGAGA CTGCTGCTGGTG GATGGCTGCC CTGCTGGTGG CACACCTGCC CGAGAGCTTCC CAGAGCTTCC CAGAGCTTCC CAGAGCTTCC CAGAGCTTCC CAGAGCTTCC CAGAGCTTCG CACACCCCCC CCGGCCGGCACCCCCCCCCC	I TGTTTTCCAG TGGGAGAGAT TCGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT TCACTCATA AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCAGAGCCT CCTCTTCAGC CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTGGAATGC GGGGGAGTAC TGGCCCACC CACCAGGACA TGTAGGCAGT TGTAGGCAGT TGTAGGCAGT CACCTCTGCC TGCAGTCCAG CACCTCTGCC TGCAGTCCAG CACCTCTGCC CTGCAGTCAG CTACCAGTCAG CACCTCTGCC CTGCCCAGC CACCTCTGCC CACCAGTCCAG CCACTTCAGCAG CCATTAGCCAG CCATTAGCCAG	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1680 1740
50 55 60 65 70 75	Nucleic Act Coding sequit I ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA ATGCTTTCA ATGCTTTCA ATGCTCCTG AGGTTGCTG AGGTCCAGG AGAGGCAGC ACCTCAGCA AGAGGTTGCTGG AGAGGTTGCTGG AGAGGTTGCTGG AGAGGTTGCC CTCTGCCGC AGGGTCGACG CTGCAGGCCTAC CTGCAGGCCAAG CGAGTGGTGC CTGCAGGCCTGC CTGCAGGCCCAG CTGCAGGCCCAG CTGCAGGCCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCCC CGCGGGGAGAG CGCGCCTACC CGCGGGGAGAGAC CGCGGGGGAGAGAC CGCGGGGGAGAGAC CGCGCGGGGAGAGAC CGCGGGGGAGAGAC CGCGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAAC CGCGGGGGGAGAAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGAGAAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGG	id Accession lence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAGGT TGTGTGCTC AAGGAGGTT ACGGCAGAAA AGGATGTGGC GAGGCAGAAA AGGATGTGGC GAGGCAGAAA ACCCACCG GCCAGAATGGC GCCAGAATGGC TCCTCTTCGT TCTTCGTGAA TCGCCACAC CGCAGAATGG CGCAGATGGC GGCAGACCT TCTTCGTGAA TCGCCTTGGT CGCCACTAGGC CGGCAGATGGC CGGCAGATGGC CGGCAGATGGC CGGCAGATGGC CGGCAGATGGC CGGCAGAGCT AGGATCTGT ACCCTGACGG GGCCAGAGGGG GGCAGAGGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGGG GGCAGAGGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGG GGCAGAGGG GGCAGAGGG GGCAGAGG GCC GGCAGAGG GGC GGC	#: Eos se 424 21 GGAGGCCGTC CCATGTAAGC GGTCAGATG TGAAAGGTCC GGTCAGATG TGAAAGGTCC GGTCAGATG TGCTCTGTG ACTGCCATGC GGTGAGCAG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGAGATGTC TGCGCATCC TGCAGCTG GGAGATGTC TGCACCTGC GGAGATGTC GGAGAGCAT GGCAGCGGC AGGCACATGT AGGGAGAGCT CGCAGCGGGC CGGAGAGAGC CTGCAGCGCC CGACAAATC CAACCAAATC CAAAACCCACC CGGGCTCAGCC CCAAACCCACC CGGGCTCAGCC CCAACCACCC CCAACCACCC CCAACCACCC CCAACCACC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GACATGTCC CACAGATCC CACAGATCC AAGCAGCTGA GGAGCATTGC GTGGAGGATGC GTGGAGGATTCG TACAGGACCA GTTCCAGAAG AACTGTGCCCAC CGGGCCGTGC CTGCTGCGGGCA CGGGCCGTGC CTGTGCGGGCA CGGGCTGCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CGGGCTGCGAGC CGGGCTGCCCAGACCTCCC CGGGCTGCCCAG	I TGTTTTCAB TGGGAAGAT TCGGAAGAT TCGGTAGAG CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGTT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGG CAGCTGATGG CCCCTGTGAAC CCCTGTGAAC CCTGGAATGC CCTGGAATGC CCTCTGGGCC CGGGGATAC CTACCAGTGC CACTTCCAG CCACTTCCAG CCACTTCCAG CCACTTCACA CCATTAGCCAG CCATTAGCCAG CTATTAGCCAG CTATTAGCAAA AGGTGCTACA CGATGCCTACACA CGATGGCTACACA CGATGGCTACACA CAATGGCATC	120 180 240 300 360 420 660 720 780 840 900 1020 1140 1200 1380 1440 1560 1560 1620 1680 1740 1800
50 55 60 65 70 75	Nucleic Act Coding sequit I ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGA AGCGTCGGA ATGCTTTCA ATGCTTTCA ATGCTTTCA ATGCTCCTG AGGTTGCTG AGGTCCAGG AGAGGCAGC ACCTCAGCA AGAGGTTGCTGG AGAGGTTGCTGG AGAGGTTGCTGG AGAGGTTGCC CTCTGCCGC AGGGTCGACG CTGCAGGCCTAC CTGCAGGCCAAG CGAGTGGTGC CTGCAGGCCTGC CTGCAGGCCCAG CTGCAGGCCCAG CTGCAGGCCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCAG CTGGCGCCCC CGCGGGGAGAG CGCGCCTACC CGCGGGGAGAGAC CGCGGGGGAGAGAC CGCGGGGGAGAGAC CGCGCGGGGAGAGAC CGCGGGGGAGAGAC CGCGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAGAC CGCGGGGGGAGAAC CGCGGGGGGAGAAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGAGAAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGAGAC CGCGGGGGGGG	id Accession lence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAGGT TGTGTGCTC AAGGAGGTT ACGGCAGAAA AGGATGTGGC GAGGCAGAAA AGGATGTGGC GAGGCAGAAA ACCCACCG GCCAGAATGGC GCCAGAATGGC TCCTCTTCGT TCTTCGTGAA TCGCCACAC CGCAGAATGG CGCAGATGGC GGCAGACCT TCTTCGTGAA TCGCCTTGGT CGCCACTAGGC CGGCAGATGGC CGGCAGATGGC CGGCAGATGGC CGGCAGATGGC CGGCAGATGGC CGGCAGAGCT AGGATCTGT ACCCTGACGG GGCCAGAGGGG GGCAGAGGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGGG GGCAGAGGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGGG GGCAGAGG GGCAGAGGG GGCAGAGGG GGCAGAGG GCC GGCAGAGG GGC GGC	#: Eos se 424 21 GGAGGCCGTC CCATGTAAGC GGTCAGATG TGAAAGGTCC GGTCAGATG TGAAAGGTCC GGTCAGATG TGCTCTGTG ACTGCCATGC GGTGAGCAG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGAGATGTC TGCGCATCC TGCAGCTG GGAGATGTC TGCACCTGC GGAGATGTC GGAGAGCAT GGCAGCGGC AGGCACATGT AGGGAGAGCT CGCAGCGGGC CGGAGAGAGC CTGCAGCGCC CGACAAATC CAACCAAATC CAAAACCCACC CGGGCTCAGCC CCAAACCCACC CGGGCTCAGCC CCAACCACCC CCAACCACCC CCAACCACCC CCAACCACC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GACATGTCC CACAGATCC CACAGATCC AAGCAGCTGA GGAGCATTGC GTGGAGGATGC GTGGAGGATTCG TACAGGACCA GTTCCAGAAG AACTGTGCCCAC CTGTGCGGGCA CGGGCCGTGC CTGTGCGGGCA CGGGCTGCC CTGTGAGTGCCCC CCTGAGCTGC CCTGAGCTGC GACAGCTGCC CCTGAGCTGC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTGCC CCTGAGCTGCC CGGGCTGCCCAGACCTCCC CGGGCTGCCAGACCTCCC CGGGCTGCCAGACCTCCCCCCCCCC	I TGTTTTCAB TGGGAAGAT TCGGAAGAT TCGGTAGAG CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGTT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGG CAGCTGATGG CCCCTGTGAAC CCCTGTGAAC CCTGGAATGC CCTGGAATGC CCTCTGGGCC CGGGGATAC CTACCAGTGC CACTTCCAG CCACTTCCAG CCACTTCCAG CCACTTCACA CCATTAGCCAG CCATTAGCCAG CTATTAGCCAG CTATTAGCAAA AGGTGCTACA CGATGCCTACACA CGATGGCTACACA CGATGGCTACACA CAATGGCATC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1380 1140 1200 1380 1450 1560 1560 1680 1740 1860 1920
5055606570	Nucleic Act Coding sequit Totoccott AGCARANTGA AGCGTCGGA AGGGTTGCTC ATGGTTTCA AGGTTGCTGG AGGTCCAGG TTTGCTGTGG AGAGCAGCA AGAGGTCCAGG AGAGGTTGCT AGGAGCATCA AGAGGTTGCT CTCTGCCGGC AGGGTCGAGC AGGGTCGAGC CGGGCCAAGG CCAGGGTCGACC CGGGCCAAGG CTGCCGGC AGGGTCGACC CGGGCCAAGG CTGCGGCCAGG CTGCGGCCAGG CTGCGGCCAGG CTGCGGCCAGG TCGGTCAGC CGGGCCAGG TCGGTCCTC CGGGCCAGG TCGGTCCTC CGGGCCTACC GCCCCTACC GCGCGGAGC GCCGGGCCAGG TCGGTGCTTCG CCCCCTACC GTGATGACGC CGGGCCAGC TCGGTGCTTCG CCCCCTACC GTGATGACGC CGCGGGCAGG TCTGTCTTCG CTCTTCGCCTCT CTCTCTCTCTCTC	id Accession lence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAGT TGTGTGCTC AAGGAGGCT AAGGAGGCG GAGGCAGAAA AGGATGTGGCT ACGTCAGGTT ACGTCCTGTTGGT ACGTCAGGTT ACGTCCTGTT ACGTCCTGTT TCTTCGTCAGCAGA TGGCCTTTCGT TCTTCGTTGGT TCTTCGTTGGT CGCCACATA CGGCACATA CGGCACATA CGGCACATA CGGCACATA CGGCACATA CGGCACATA CTGACTTGGT CGGCACATA CTGACTTGGT CGGCACATA CTGACTTGGT CGGCACATA CTGACTGGT CGGCACATA CTGACTGGT CGGCACAGAGGC CCGAGAATTT ACCCTGACGGA CTGACTGGGGC TCGGGCACAG TAGGTGGGGC TCAGGGGGG TCCAGAGGGG TCCAGAGGGG TCCAGAGGGG TCCAGAGGGGG TCCAGAGGGGG TCCAGAGGGGG TCCAGAGGGGG TCCAGAGGGGG TCGTGGGGCG TCGTGGGGGGG TCGTGGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGGG TCGTGGGG TCGGGG TCGTGGGG TCGTGGGGG TCGTGGGG	#: Eos se 424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGG TGCTCAGGTG ACTGCAGCG GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGAGATGGT TGCGCACTGG AGGCACATGT AGGGGAGGCT GCAGGGAGGCT GCAGGAGGCGC CTGCAGGGAGC CTGCAGGAGCCT CAGCAGGGAG CTGCAGCAGGCC CGGAGAGGCCT CGAGCAGGCCC CGGAGAGGCCC CGGAGAGGCCC CGGAGAGGCCC CGGACAATC CGAACAATC CGAACAATC CGAACAATC CGAACACGTT CGAACCCCC CGGGCTCAGC CGGGCTCAGCC CGGGCTCAGCC CGGGCTCAGCC CGGGCTCAGCC CGGGCTCAGCC CGACCAACCACT CGAACCACC CGGGCTCAGCC CGGGCTCAGCC CGGGCTCAGCC CGGGCTCAGCC CGGGCTCAGCC CGGGCCTGTC CGAACCACC CGGGCTCAGCC CGGGCCTGTC CGAACCACC CGGGCTCAGCC CGGGCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGCAGCCCTC CGGGCCCTGTC CGGGCCCTGTC CGGGCCCTGTC CGCAGCCCTC CGGGCCTGTC CGGGCCCTGTC CGCGCCCTC CCACCCCCCCCCC	31 TGTGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GACATTGCTC CCCAGATCC CAACAGGAAG GACATTGCTC GGAGCTGA GGCGCACCAC GGTGCACACT TACAGGACAA AACTGTCCAGAAG AACTGTCCAGAAG CTGCTGGTGG CGGGCCTGC CGCTGGTGG GACGCTGC CGAGGCTGC CGAGGCTGC CGAGGCTGC CGCCTGCCCAGA CGGCCTGCC CGGCCTGCC CGGCCTGCC CGGCCTGCC CGGCCTGCC CGGCCTGCC CGGCCTGCC CGGCCTGCCCAGA CGGCCCCCC CGGTGCTCCC CGGCCCCCCC CGGTGCCCCCC CGGCCCCCCC CGGCCCCCCCC	TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA GCATCAGTT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGCCTAAC TTGTGACGTT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATCAGG CCACTGTCAGC CCACTGCTCAC CCACTGCTCAC CCACTGCTCAC CCACTGCTCAC CCACTGCTCAC CCACTGCTCCC CCACTGCAAC CCACTGCTCCTC CCTCTCCGGCC CCACCAGGACAA CCACTGCAGCC TGCAGCCAGCC CACCAGGACAA CGAGGATCAC CTACCAGGCCAC CACCAGGACAA CGAGGATCAC CTCCTCCCC TGCAGCCGG CCACCCCCCCC CCACCAGCCAC CCACCAGGACAA CGAGGCCACC CCACTGCCAC CCACCAGGCCAC CCACTGCCAC CCACTGCCAC CCACTGCCAC CCACTGCCAC CCACTGCCAC CCACTGCCAC CCATTGCCAG CCATTGCCAGC CCATTGCCAG CCATTGCCAGC CTATGCAGCATC CGCTTCCAGG CCTTCCAGG CCTTCTCCAGG CCTTCTCCAGG CCTTCCAGG CCTTCTCCAGG CCTTCTCCAGG CCTTCTCCAGG CCTTCTCCAGG CCTTCTCCAG CCTTCTCCAGC CCTTCTCCAGC CCTTCTCCAGC CCTTCCAGC CCTTCCACC CCTTCCAGC CCTTCCACC CCTTCCAGC CCTTCCACC CCTTCCAGC CCTTCCAGC CCTTCCACC CCTTCCAGC CCTTCCAGC CCTTCCAGC CCTTCCAGC CCTTCCAGC CCTTCCAGC CCTTCCAGC CCTTCCAGC CC	120 180 240 360 420 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1560 1620 1680 1740 1800 1860 1920
50 55 60 65 70 75	Nucleic Act Coding sequil ATGCCCCTT TCTCTCCTT AGCAAAATGA AGCGTCGGAA AGCGTCGGAA ATGCCAGG AGGGTTGCTGG AGAGCATCA AGGGTTGCTGG AGAGCATCA AGAGTCCAGGA ACCCTCAGCA ACCCTCAGCA AGAGGATCGC AGAGGATCGC AGAGGATCGC AGAGTGGTCAGCA CCTGTGAGGC AGAGTGGTCAGCA CCTGTGCCGGC AGGGTCAGCA CGGGCCAAAG CGAGCCTACC GTGATGGGCCAG CTTGGGGCCAG CTTGGGGCCAG CTTGGGGCCAG CTTGGGGCCAG CTTGGGTCAGC CGGGCCAGC CGGGCCAGC CTGGATGGCCCAG CTTGATGGGGCCAG CTCGGTGATGACCTTCG CCCCCTACC GGGGGGAGAG CTCTGTCTTGC CCCCGGGATT	id Accession lence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTTGGATTC AAGGAGGCGG GAGGCAGAAA GGGATGTGGTTAGGTTA	#: Eos se 424 21 21 GGAGGCCGTC CCATGTAAGC GGGTCGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC CACGAGACAG TGCTTCTGTG ACTGCATCC GGTGAGCAG GGAGACAGGT TGCAGCTG GGAGACAGGT TGCAGCTG GGAGACGT TGCAGCTGC GGAGACGT GCAGCAGGAGC GCAGCAGAGC GCAGCAGAGC TGCAGCAGGAGC TGCAGCAGGAGC TGCAGCAGGAGC TGCAGCAGGAGC TGCAGAGGAGC TGCAAAGCCTC TACAAACCCAC TGCTCAGACC TGCTCAGAGC TGCAAACCCAC TGCTCAGAGC TGCACAAACCCAC TGCTCAGACC TGCTCAGACC TGCTCAGACC TGCTCAGACC TGCCTCAGCC TGCTCAGCC TGCCGGCCT TGCTCAGCCT TGCTCAGACC TGCTCAGCC TGCTGCAGCC TGCTCAGCC TGCTGCAGCC TGCTCAGCC TGCTCAGCC TGCTCAGCC TGCTCAGCC TGCTCAGCC TGCTCAGCC TGCTCAGCC TGCCC TGCTCAGCC TGCCC TGCTCAGCC TGCCC TGCTCAGCC TGCCC TGCTCAGCC TGCCC TGCTCAGCC TGCCC TGCC TGCCC TGCC TGCCC TGCC TG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGGTC CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCGCACCCAG GTTCCAGAGAG GCTGCACACT TACAGGACCA TTCCAGAGA CAGGCCGCAG GATTCCAGAGA CAGGCCGCAG CAGGCTGCACACT CTGCCGGGCACACT CTGCCGGGCACACT CTGCCGGGCACACT CTGCCGGGCACACT CTGCCGGGCACACT CCTGAGAGGCACC CCTGAGAGCACC CCTGAGGCACCC CCTGAGCACCC CCTGAGCACCC CCTGAGCACCC CCTGCCCCAGA CGGCCTCCCCACACCC CCTGCCCCACACCC CCTGCCCACACCC CCTGCCCACACCC CCTGCCCCACACCC CCTGCCCACACCC CCTGCCCACACCC CCTGCCCACACCC CCTGCCCACACCC CCTGCCCACACCC CCTACACTAGACCACCC CTACACTAGACCACCC TACGCCGACC TACGCCACAC TACGCCGACC TACGCCGACC TACGCCGACC TACGCCGACC TACGCCACAC TACGCCGACC TACGCCACACC TACGCCACACC TACGCCGACC TACGCCACACC TACGCCACACC TACGCCACACC TACGCCACACC TACGCCGACC TACGCCACACC TACGCCACA	I TGTTTTCCAG TGGGAGAGAT TTCTGTTAGA CCATCAGTT AGATCAGTT TGAAGGCAAG TGAAATACCT TCATCAGTC TCATCAGTC TCATCAGTC TCATCAGTC CCACCAACGG ACTGCAGAGG GACTGAGGGAGGC GACTCTGGA TGAAGCAGG TGAACTGGC GACTCTGGA TGAGCAGGG TGAGCTGAGC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGGTCTAAC TTGTGACGT TCACTCTCATA AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCAGACCT CCTCTTCAGC CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CGGGGAGTAC TTGCCCCAC TGGCCCAC TGGCCCAC TGGCCCAC TGCCCAGGACA TGTCACAGTGC TGTCAGGAGAC TGGCCCACC CACCAGGACA TGTCAGCAG TGCTCCAG TCCAGGACGT TGCCCAGGT TCCAGGACGT TCCAGCACGT TCCAGCAC TCCAGGACGT TCCAGCAC TCCAGGACGT TCCAGCAC TCCAGGACGT TCCAGCAC TCCAGGACGT TCCAGCAC TCCAGGACGAC TCCAGCAC TCCACAC TCCAGCAC TCCACAC T	120 180 240 360 420 480 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1560 1680 1740 1880 1740 1890 1920 1980
50 55 60 65 70 75	Nucleic Act Coding sequitary ATGCCCCTT TCTCTCCTC AGCANATGA AGCGTCGGA CTGGACATCA AGGGTTGCCAG GGGTGCCTG AGGAGGCCAGC ACCCTCAGCA CCCTGTAGCA CCCTGTAGCA CCCTGTAGCA CCCTGTAGCA CCCTGTAGCA CCCTGTAGCA CCTGTAGCA CCCTGTAGCA CCTGCAGCA CCGGGCCAAAG CGAGGTCGCCGC CGGGCCAAAG CGAGTGGTGC CGGGCCAAAG CGAGTGGTGC CTGACGGCAC CGAGGCCTGC CTGACGGCAC CGAGGCCTGC CTGACGGCAC CGAGGCCTGC CTGACGGCAC CGGGCCAAAG CCTGCCGC CTGACGGCAC CGGGCCAAAG CCTGACGGCAC CGGGCCAAAG CTGACTGCGC CTGACGGCAC CGGGCCAAAG CTGACTGCGC CTGACGGCAC CGGGCCAGAC CGGGCCAGAC CTGGATGCC CCCGGGATCC CCCCCTAC CGCGCGAGAC CCCCCTAC CCCCCTCC CCCCTCCC CCCCTCC CCCTCC CCCTCCT	id Accession lence: 12 11 TCCTGTTGCT TCCAGGARGE TGTGGGTGTT AAGGAGGCT AAGGAGGCT AAGGAGGCA GAGCAGAAA GGGATGGCT TACCCACCAG GCCAGAATGG TGCCTTTGGTT TCTTGTGAA TGGCCACTT TCTTCGTGAA TGGCCACTT TCTTCGTGAA TGGCCACTT CGTGCACTT CGAGGAGGC TGCCTTTGG TCCTTCCT TCTTCGTGAA TGGCACCTGT CGAGGAGGC CGAGAATGG CGAGCACTAG CGAGCACTAG CGACCTGGG CGCAGAATGG CGAGGAGGC TACCCGGCCTC CGCCAGAATGG CGGCACATGG CGGCACACT CGGCCAGAGGC CCGAGAATGT CCCGACGC CCGAGAGGC TCCCTGACC CCGACGCGC CCCGACGC CCCGACGCC CCCGACGCC CCCGACGCC CCCCGACCC CCCCGACCC CCCCGACCC CCCCGACCC CCCCGACCC CCCCCCCC	#: Eos se 424 21 21 GGAGGCCGTC CCATGTAAGC GGTTCAGAGTG TGAAAGGTCC GGTTCAGAGTG ATTTTCAACC CACGGAGAGG TGCTTCTGTG ACTGCTCAGC GGTTGCAGCG GGAGAGGGAGAGG TGCTCCAGC GGAGAGGGAGAGG TGCTCCAGC GGAGAGGGAGAGG TGCTCCAGC GGAGAGGGAG TGCCACCTGC AGGCACATGT AGGGAGCGT GCAGGGGGGGAGGG CTGGACAGC GGAGGGGAGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GAGCATTCC CAACAGGAAG GACATGCTGA GACATGGCAC GAGCAGTGC AAGCAGGAGG GGGGAGTGC GTGGAGGATTCC TACAGGACCA GTTCCAGAAG AACTGCCCC TCTGCGGGCAC GGGGCTGC CTGCTGGGCAC GGGCTGCCCCCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CGGGCTGCCCCCCCCCC	TGTTTTCAB TGGGAAGAT TTCGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCATA ATCAAGAG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CAGCTGGAAG CCCCATGGAAG CCCTGGAAG CCCTGGAATGC CGGGGAGCTAC CGGGGAGCTAC CTCTCGGGCC CTCTCGGGCC CACCAGGACA CGAGGATGC GGGGAGTAC GGGGAGTAC GGGGAGTAC CGACCCCCCCC CACCAGGACA CGACCCCCGC CCACCAGGACA CGACCTCTGC CCACCAGGACA CGACCTCTGC CCACCTCTGC CCACCTCGGC CCACCTCTGC CCACCTCGGC CCACCTCTGC CCACGTCCAG CCACTCTGC CCACGTCCAG CCACTCTGC CCACGGCCG CCACTCTGC CCACGGCCC CCACGGCCC CCACCTCTCC CCACGGCCC CCACGGCCC CCACGGCCC CCACGCCC CCACGCCC CCACGCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACCCCCC CCACGCCCC CCACCCCCC CCACCCCCC CCACCCCCCC CCACCCCCC	120 180 240 360 420 540 660 720 780 900 1020 1140 1200 1380 1440 1500 1560 1680 1740 1860 1860 1920 1980 2040 2160
50 55 60 65 70 75	Nucleic Act Coding sequit ATGCCCCTT TCTCCCTC AGCARANTGA AGCGTCGGGA AGCGTCGGGA AGGTTCCTG AGGTTCCTG AGGTTCCTG AGGTCCAGG AGGTCCAGG AGGGCCAGG AGGGTCGCCT CCCGGGCCAAGG CGAGTTGCCT CGAGGCCAGG CGAGTTGCGGCCAGG CGAGTTGCGGCCAGG CTGCGGCCAGG CTGCGGCCAGG CTGCGGCCAGG CTGCGGCCAGG CTGCGGCCAGG CTGGGGCCAGG CCGGGCCAGG CCGGGCCAGGCCA	id Accession lence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGTGTGCTC AAGGAGGCT AAGGAGGCG GAGGATGTGGC GAGGATGTGGC GAGGATGTGGC GAGGAGGAT ACCGACCAT ACCGACCAT TAACCCACCC GCCAGAATGG TCGCCTTTCGT TCTTCGTTACT TCTTCGTTGAT CTGCCTTTCGT CGCCATAGC CGCCAGATGGC CGCCAGATGGC CGCCAGATGGC CGCCAGATGGC CGCCAGATGGC CGCCAGATGGC CGCCACTAGC CGCCACCTAGC CGCCAGATGGC CGCCAGAGGC CCCGAGATGGC CCCGAGATGGC CCCGAGATGGC CCCGAGAGGC CCCGAGGGC CCCGAGAGGC CCCGAGAGGC CCCGAGAGGC CCCGAGAGGC CCCGAGAGGC CCCGAGGGC CCCGGAGGC CCCGGACGC CCCGGACC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGCC CCCGGACGC CCCGGCC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGACGC CCCGGCC CCCGGCC CCCGGACC CCCGGACGC CCCGGACGC CCCGGCC CCCGGCC CCCGACC CCCGGCC CCCGACC CCCGC CCCGACC CCCGC CCCGC CCCGC CCCCGC CCCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC	#: Eos se 424 21 GGAGGCCGTC CCATGTAAGC GGTCAGAGG GGTCAGAGG GGTCAGAGG TGCATCTAGA ACTCTCTAGG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGAGATGGT GGAGCAG GGAGATGGT GGAGCAGG GGAGAGCGT GGTGACAGC GGAGAGCGT GGAGAGCCT GGAGCAGC GGAGAGCCT GGAGCGAG CTGCAAGCCCT GGAGCCT GGAGCCT CCAACACCACC GGGGTCAGGC CTGCAGGGGG CTGCAGGGGGAG CTGCAGGGGGAG CTGCAGGGGGAG CTGCAGGGGGAG CTGCAGGGGGGAG CTGCAGGGGGAG CTGCAGGGGGGAG CTGCAGGGGGAG CTGCAGGGGGAG CTGCAGGGGGAG CTGCAGGGGGAG CTGCAGGGGGAG CTGCAGGGGGGAG CTGCAGGGGGGAG CTGCAGGGGGGAG CGAACCACC CGGGCTCAGGG CGAGCGGGG CGAACCACC CGAGCGCGG CGAGGGGGGG CGAGCGGGGG CGAGGGGGGG CGAGCGGGGG CGAGGGGGGGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTGG GGAGCATTCC CAACAGGAAG GACATGTG GGAGCATCC CACAGATCC AAGCAGCTGA GGAGCATCC GTGGAGGATG GCACCCCAG GCTGCACAC TACAGGACG CGGGCGTGC CTGCGGGCA CGGGCCTGC CAGAGCTGC CAGAGCAGC CAGAGCAGC CAGCAGCAGC CAGCAGCAGC CAGCAGCAGC CAGCAGCAGC CAGCAGCAGC CAGCAGCAGC CAGCAGCAGC CAGCAGCAGC CAGCAGCAGC CAGAGCAGCC CAGAGCAGCC CAGAGCAGCAC	TGTTTTCCAG TGGGAGAGAT TTCTTTTAGA CCATCAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TTGGCCTCAT TCAGCTGCC TTGGCCCAT TCAGCTGCC TTGGACGAT TCTGCACAGA TCTGCACAGA TCTGCACAGA TCTGCACAGA CACTGATGGG CAGCGAGCCT CCTCTTCAGC CAGCTGGACAG CCCCTGTGAC CCCCTGTGAC CCCCTGTGAC CCCCTGTGAC CCCCTGTGAC CCCCTGTGAC CCCCTGGAATGC CCCCTGGAATGC CCCCTGGAC CCCCCACC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGCC CCCCAGGACA CGAGGATCAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGTCCAC CCATTAGCCAG CCATTAGCCAG CCATTAGCCAG CCATTAGCCAG CCATTAGCAAA CGATGCCAC CCAGGACAT CGAGACAT CGCTTCCAGG CCAGGACAC CCAGGACAC CCAGGACAC CCAGGACAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGCACCCC CGTTCCAGGA CCAGCCCCACCCC CGTTCCAGGAC CCAGCACCCC CGTTCCAGGAC CCAGCACCCC CGTTCCAGGAC CCAGCACCCC CGTGTCCAGGAC CCAGCACCCC CGTGTCCAGGAC CCAGCACCCCC CGTGTCCGGGAC CCAGCACCCCC CGTGTCCGGGAC CTCTCCGGGAC CCCCCCCCCC	120 180 240 360 420 480 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1560 1680 1740 1880 1740 1890 1920 1980
50 55 60 65 70 75	Nucleic Act Coding sequit ATGCCCCTT TCTCTCCTC AGCAAAATGA AGCGTCGGA AGGTTGCCAGG ATGCTTCCAGCA AGAGTCCAGG AGAGTCCAGG AGAGTTTCC AGGAGTTCC AGGAGTTCC AGGAGTTCC AGGAGTTCC AGGAGTTCC AGGAGTTCC AGGAGTTCC AGGAGTTCC CTCTGCCCGC AGGGTCGACC CGGGCCAAAG CGAGTGGTC CAGGGCCAGGC CAGGGTCAGC CTGACGGCCAGC CTGACGGCCAGC CTGACGGCCAGC CTGACGGCCAGC CTGACGGCCAGC CTGACGGCCAGC CTGACGGCCAGC CTGACGGCCAGC CTGACGCCAGCCCAGC	id Accession lence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAAGT GCCCGAGAAG GCATTGGATTC AAGGAGGCGG GAGGCAGAAA GGATGTGGT ACGGCACTAGGCT ACGGCACTAGGCT TAACCCACCC GCCAGAAGT TCCTCTTCCT TCTTCGTGAA TGGCCACTAG CGGCACTTGG TGCCTTGGT CGGCACATAG CGGCACTTGGT CTGCCTTGGT CGGCGAGATGC CGGCAGATGC CGGCAGATGC CGGCAGATGC CGGCAGAGGC CGGCAGAGGC CGGCAGAGGC CGGCAGAGC CGGCAGAGC CGGCAGAGC CGGCAGAGC CGGCAGAGC CCGGGAATTT CGGCTGGAC CCGGGAATTT CGGCTGGGG CCCGGAGACC CGGCGAGAGC CCGGGGAGACC CCGGGGGGC CCCGGACC CCGGGGGGG CCCCGATCC CGGCCGGACC CCGGGGGGGG CCCCGATCC CCCGGATCC CCCGGAGGGC CCCCGATCC CCCGGACC CCCGGGCGGGGG CCCCCACTC CCCCGACCC CCCGGCCC CCCCGACCC CCCGGCCC CCCCGACCC CCCCGACCC CCCCGACCC CCCCGACCC CCCCCCCC	#: Eos se 424 21 21 GGAGGCCGTC CCATGTAAGC GGTCAGAGTG TGAAAGGTCC GGTCAGAGTG ACTCTCTGTA ACTGCATCC GGTCAGAGTG GGTGAGCAG GGTGAGCAG GGTGAGCAG GGAGAGCAG TGCTCCAGC GGAGAGCAG GGAGATGGT GGAGCACTGC AGGCACTGC AGGCACTGC GGAGAGCGC GGAGAGCGC GGAGAGCGC GGAGAGCGCC GGAGAGCGCC GGAGAGCGCC GGAGAGCGCC GGACAAAGCCCAC GGACACAAGCCCT CAAACCCAC GGGCTCAGCC GGACCACAGGT CGACACAGGT CGACACAGGT CGACACAGGT CGACCACCAC CGGCCTGAGCCCC GGCCTGAGCCCCC GGCCTGGAGCCCCC GGCCTGGAGCCGCC GGGCCTGGAGCCGCC GGGCCTGGAGCCGCC GGGCCTGGAGCCGCC GGGCCTGGAGCCGCC GGGCCTGGCAGCCCC GGGCCTGGCAGCCCCC GGGCCTGGCAGCCCCC GGGCCTGGCAGCCCCCCCCCC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GACATTGGTC CCCCAGATCC AAGCAGCTGA GAGCAGCTGA GGCGCACGCCAG GCTGCACACT TACAGGACCA TTCCAGAAG AACTGTGCC CTGCTGGTGG GAGGGTGCCT TGCTCATGG CTGCAGATC CTGCTGGTGG CTGCTGTGG CTGAGGCTGC CTGAGGCTGC CTGAGGCTGC CTGAGTGGG CTAGGCCCC CTGCCCAGAC CTGCCCAGAC CTAGGCAGCC CTGCCCAGAC CTAGGCAGCC CTAGGCGAGCC CTAGGCGAGC CTAGGCAGC CTAGGCAG	TGTTTTCCAG TGGGGAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TTGGTCTAAC CTGTGACGGT CACTCCTCATA ATCAAGAG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CAGCTGGAAG CCCCATGGAAG CCCTGGAAG CCCTGGAATGC CGGGGAGCTAC CGGGGAGCTAC CTCTCGGGCC CTCTCGGGCC CACCAGGACA CGAGGATGC GGGGAGTAC GGGGAGTAC GGGGAGTAC CGACCCCCCCC CACCAGGACA CGACCCCCGC CCACCAGGACA CGACCTCTGC CCACCAGGACA CGACCTCTGC CCACCTCTGC CCACCTCGGC CCACCTCTGC CCACCTCGGC CCACCTCTGC CCACGTCCAG CCACTCTGC CCACGTCCAG CCACTCTGC CCACGGCCG CCACTCTGC CCACGGCCC CCACGGCCC CCACCTCTCC CCACGGCCC CCACGGCCC CCACGGCCC CCACGCCC CCACGCCC CCACGCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACGCCCC CCACCCCCC CCACGCCCC CCACCCCCC CCACCCCCC CCACCCCCCC CCACCCCCC	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560 1620 1680 1740 1800 1980 2040 2160 2220

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45	Coding sequents	lence: 140 11 	086 21 	31	1	1	60
45	Coding segn	lence: 140 11 TCAAGCAGAG	086 21 CCCAGCGCGG	31 TGCTATCGGA	 CAGAGCCTGG	 CGAGCGCAAG	60 120
45	Coding segn 1 GAGCTAGCGC CGGCGCGGG	lence: 140 11 TCAAGCAGAG AGCCAGCGGG	086 21 CCCAGCGCGG GCTGAGCGCG	31	 CAGAGCCTGG GAACCCAGAT	CGAGCGCAAG TTCCCAGACT	
	Coding sequence of the code of	111 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC	086 21 CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG	31 TGCTATCGGA GCCAGGGTCT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT	CGAGCGCAAG TTCCCAGACT CAGCGACCAG	120
45 50	Coding segn 1 GAGCTAGCGC CGGCGCGGGG AGCTACCACT ACGTCCGGGG	lence: 140 11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT	086 21 CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCCG	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC	120 180
	Coding segn 1 	lence: 140 11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCTC	21 CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGC ATGGGAGCTG ACTCTGACCT	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGCGAGGCA GCTTCCCTGG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG	120 180 240 300 360
	Coding segn 1 	Ience: 14 11 † TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCCT CACTGCAGCT TGACCAGAGC TGACCAGAGC	21 CCCAGCGCGG GCTGAGCGCG ACGCCCGGG CCTGGCCCGG ATGGGAGCTC ACTCTGACCT CCTGAGTTGC	31 GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGCGAGGCA GCTTCCCTGG AACCCTGGAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC	120 180 240 300 360 420
	Coding segn 1 	Ience: 140 IT TCAAGCAGAG AGCCAGCGGG CCGCTGCCC CCGCTGCCC CACTGCCAGG CAGCTGGCT TGACCAGAGC TATCGGCCAG	21 CCCAGCGCGG GCTGAGCGCG ACGCCCGGG CCTGGCCCGC ACTGGAGCTG ACTCTGACCT CCTGAGTTGC	31 GCCAGGGTCT AGCTCGCGGC GAGGGTGAC CTGGGAGGCA ACCCTGGAA TGCTGCTCAC	CAGAGCCTGG CAACCCAGAT GCCTGGCGGT ACTGTCTCG GGCACATCC CCCTGGCCAT CTCTTCTGCC	CGAGCGCAAG TTCCCAGACT CAGCGACCAC CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT	120 180 240 300 360 420 480
50	Coding sequilibrium sequilibriu	Jence: 149 11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCCC CACTGCCAGG CAGCTGGCT TGACCAGAGC TATCGGCCAG CTCAGAGGGAG CTCAGAGGGA	21 	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGG GAGGGGTGAC CTGCGGAGGCA ACCCTGGA ACCCTGGA TGCTGCTCAC TCATTAAAGA	CAGAGCCTGG CAGAGCCTGGCGT ACTGTCTCGG GGACTTCCTC CGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTTT	120 180 240 300 360 420 480 540
	Coding segn 	Lence: 141 11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCTC TGACCAGAGC TATCGGCCAG CTCAGAGGGA GCACATCCTG	21 CCCAGCGCGG GCTGAGCGCG GCTGAGCCGGG ACGCCCGGG ACGCAGGAGCTG ACTCTGACTTG CCTGAGTTGC GGCAAGACAG ATTGACAACG	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGGC CTCGCAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT	CAGAGCCTGG GAACCCAGAT GCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGGG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC CGACTGATTTT CCGATTGTTT AGTGCCCTCT	120 180 240 300 360 420 480 540 600
50	Coding segn 1 	Lence: 14/ 11	D86 21	31 	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GGATGCTGGG GGATGCTGGG GGCTGATGAA	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTTT AGTGCCCTCT GGTATTCAGC	120 180 240 300 360 420 480 540 600 660
50	Coding segn GAGCTAGCGC CGGCGCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCC ACCATCTGCA CCATCCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTTA	Hence: 141 TCAAGCAGAG AGCCAGCAGG CCCCTTGCCC CCCCTGCGCT CACTGCCAGG CAGCTGGCT TGACCAGAGC TATCGGCCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA	21 CCCAGCGCGG GCTGAGCGCG ACGCCCGGG ACGCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC GCAAGCTGG ATTGACAACG ATCAACATGA	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGA ACCCTGGA TGCTCACC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCAGACGAG GCATGCTGGG GGCTGATGAA AGGAGGCGCT	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGCTG GACCAAGACC ACGGTCTATT CCGATTGTTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC	120 180 240 300 360 420 480 540 600 660 720
50 55	Coding sequilibrium sequilibriu	Hence: 141 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCCGCTGCCCC CACTGCCAGG CAGCTGGCTC TGACCAGAGGC TATCAGCAGAGG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CCTATGGTCTG GAGCAATTCT AAAGCTCTCC	21 CCCAGCGCGG GCTGAGCGCG GCTGAGCGCG GCTGGCCCGC ATGGGAGCTG ACTCTGACTG CCTGAGTTGC GGCAAGACAC GGCAAGACAC ATTGACAACG ATTGACAACG ACCATCATTT TAGGTACATTC	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGG GAGGCGTGAC CTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATCGAAG GGGTTGGTAA TGAACAAGAC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCAGACGAG GCATGCTGGG GGCTGATGAA AGGAGGGGCT CCTTCACCCA	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGCCTA ACAGTGCTCAT CCGATTGTTT AGTGCCCTCT GGTATTCAG GGTGGCTGC GGTGGCATGG	120 180 240 300 360 420 480 540 600 660
50	Coding segn 1 GAGCTAGCGC CGGCGCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCC ACCATCTACACAT TGCGAACCAG GCCCTTTCCA CGGATCCTTA ATGGACAGAA CAGAAGGAG	Lence: 14	21 CCCAGCGCGG GCTGAGCGCG GCTGAGCCGG ACGCCCGGG ACTGGCAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGCTGG ATTGACAACG ACTACATTT AAGTACATTT TGGAACTTTGACAACG GCAAGCAGCTGG	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGA ACCCTGGA TGCTCACC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC CCCTGGCCAT CCCTTCTGCC CCACGACCAGG CCATCAGCCAG GCATCCTGGCGCAT CCTTCTGCC CCACGACGAG GCATGCTGGG CGCTGATGAA AGGAGGGCT CCTTCACCCA TGGAGTTATT	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAAGCCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAGC CTTGAGTTGG GTTCATGC GTTGCATGG GTTCATGC GTTGCATGC	120 180 240 300 360 420 480 540 600 660 720 780
50 55	Coding sequilibrium sequilibriu	Hence: 141 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCCC CACTGCCCC TGACCAGAGC TATCAGCCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTTT ATCAGGCACA ACGTCTCGGTC	21 CCCAGCGCGG GTGAGCGCG GCTGAGCGCG ACGCCCCGGC ATGGGAGCTG ACTCTGACTTG CCTGAGTTGC GGCAAGACAC GGCAAGACAC ACCATCATTT AAGTACATTG TGGACATTTC GAAAGGAGCT GTCATCACTTC CAGTATTTGA	311 TGCTATCGGA GCCAGGGTCT AGCTCGCAGC CTGCGAGCGTGAC GCTTCCCTGG AACCCTGGA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG TGGTTGGTAA TGAACAAGAC GCGGCCACCG CTGACCGGTT ACGCGGTTCACCG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CACGACGAG GCATGCTGGC GCTTCTCTCCC CACGACGAG GCATGCTGGC CTTCACCCA TGGAGTTATA CGATGCCAT CGATGCCAG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGCTG ACCGTCTATT CCGATTGTTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GTTGAGTTGC GTTGAGTTGC ACTGAGTTGC ACTGAGTTGC ACTGAGTTGC ACTGAGTTGC ACTGAGTTGC ACTGAGTTGC ACTCATGTCA	120 180 240 300 420 480 540 600 660 720 780 840 900 960
50 55	Coding sequilibrium control co	Lence: 141 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCTC TGACCAGAGGC TATCGGCCAG GCACATCCTG GGGCAATTCTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT	21	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTCGCTAGGA ACCCTGGAA TGCTGCTCAC TCATTAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGGCCACCG CTGACCGGTT ACGCGGTGCC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCACCAGCAGG GCATCTGGG GCAGGAGGGCGT TGGAGCACTAT TGACACCTAT TGACACCTAT GGACACAGAAG	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCC TTCAAGGCCT GACCAAGACC ACGGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAGC CTTGAGTTGG GTTCATGCAGTAG AGATCCAAGA ATCCTTCTCAGGTAGAAAA ATCCTTTCTG GGGATGGCCA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	Coding sequilibrium sequilibriu	Lence: 14	D86 21	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTGCTCAC TCATTANAGA GAGGAGAGCT TGTATGGAAG GGGTGGTAA TGAACAAGAC CGGGCCACCG CTGACCGGTT ACGCGTGCC TGGATGACAT GGTTGACACT GGTTGACACT GGTTGACACT TGGATGACACT GGTTTAGACA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GCCCAGACCAG CCCTTCTGCC CCACGACCAG GCATCTCTGC CCACGACCAG GCATCTGGC CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGGCAGAGAG GCCCTTGGAGACAG CCCTTGGAGACAG CCCTTGGAGAC CCCTTGGAGAC	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAAGACCC TTCAAAGACCC ACAGTCTATT CCGATTGTTT AGTGCCTCT GGTATTCAGC GTTCATGCAGTAGT GTTCATGCAGAGAA ATCCTTTCTA AGATCCAAGA ATCCTTTCTCA TCGATGACCA TTTCTAACTG TTCTAACTG	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
50 55 60	Coding sequilibrium sequilibriu	Hence: 141 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CCCGTGCGCT CACTGCCAGG CAGCTGGCT TGACCAGAGG TATCAGCCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCATCTTC TATCAGTCTG AAAGCTCTCC TATTTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT TGATGAAGGT TCAATCATCT TCCATCATCTT TCCATCATCTT TCCATCATCTT TCCATCATCTT TCCATCATCTT TCCATCATCTT TCCATCATCTT	21 CCCAGCGCGG GCTGAGCGCG ACGCCCGGG CCTGGCCCGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC GCAAGCTGG ATTGACAACG TGGACATTTC GAAAGGAGCT GTCATCCATT CAGTATTTGA	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGCCACCG CTGACCAGGT ACGCGGTGCC TGGATGACAA ACCATATTGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCAGACGAG GGCTAATGAA AGGAGGCGCT CCTTCACCCA TGAGACTATT TGACACCTAT CGATGCAGAG GGCCAGGAAG GCCCAGGAAG ACCCTTGGAGT ATATCATGGA	CGAGCGCAAG TTCCAGACC CTACAGACCC TTCAAGGCCA ACAGTGGCTA ACAGTGGCTA ACAGTGCTATT AGTGCCCTCT GGTATTCAGC CTTGAGTGC GTTGAGTGC GTTGAGTTGC GTTGAGTTGC GTTCATGC AGATCCAAGA ATCCTTCTG GCGATGACTCA CGTAGATGCC AGATCCAAGA ATCCTTTCTG CGATGACCTC CATCGAGGCT CATCGAGGCT CATCGAGGCT CATCGAGGCT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
50 55	Coding sequilibrium control co	TCARGCACA AGCTGCCC CACTGCCC CATCGCCG CTACGGCGG CCAACTCCT GGGCAATTCT ATCAGGCAC TGATGTTGT ATCAGCCAC TGATGAGGT CCACTCTCC CCATCTCT CCACTCCT CCACTCCT CCACTCCT CCACTCCT CCCGGTATTC	21 CCCAGCGCGG GCTGAGCGCG GCTGAGCGCG GCTGAGCGCG ACGCCCCGGG ACGCCCCGCG ATGGGAGCTG ACTCTGACTTG ACTCTGACTG GGCAAGACAC GGCAAGACAC GCAAGACTG TAGGTACATTC GAAAGCAGCT GTCATCATT CAGTATTTCAGTATTCAGTATTTCAGTATTTCAGTATTCAGTAGAGAGAG	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGG GAGGGGTGAC CTGGGAGGCA GCTTCCTGG AACCTGGTA TCATTANAGA GAGGAGAGCT TGTATGGAG GGGTTGGTAA TGAACAAGAC GTGACCGGTT AGCGGTTGCC TGGATGACAT ACCATATTGACA ACCATATTGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTOTTCTGG GGCCACATCC CCCTGGCCAT CCACAGCAG GCATGCTGGG GCTGATGAA AGGAGGGGCGT TGACACCAA TGAGATATT TGACACCAA TGAGAGAGAG GCCAGGAAG CCTTGAGCA TGATGATAT TGACACTAT TGATGCAGAG TCATTGAGT TATTATCATGA	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCC TTCAAGGCCC ACGGTCTAT AGTGCCTCT GGTATTCAGC CTTGAGTTGC GTGCATGGCATG	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
50 55 60	Coding sequilibrium sequilibriu	TCAAGCAGAG TATCAGCAGAG AGCCAGCAG CCGCTTGCCC CCGCTGCGCT CACTGCCAGAGG CACTGCCAGAGG TATCGGCCAG CTCAGAGGGAA CTCAGAGGGAATTCC CTATGGTCTG AAAGCTCTGC CTATTTTTT ATCAGGCAA ACGTCTGGTC TGATGAGGGTATC CCATCATCT TCCATCATCT TCCATCATCT TCAGTCAGTTT TTCAGTCAGTCT TCCATCATCT TCCATCATCT TCAGTCAGTTT TTGAGTCAGTTT TTGAGTCAGTTT TTGAGTTGGTT TCAGTTGGTTT TGAGTTGGTTT TGAGTTGGTTT	D86 21 CCCAGCGCGG GCTGAGCGCG GCTGAGCCGG ACGCCCGGG ACGCCCGGG ACGCAGCTG ACTCTGACCC GCAAGCTGG ACTCATCT AAGTACATT AAGTACATTG CGAAAGGGGCT GTCATCATT CAGAGATTC GAAAGGAGCT GTCATCCATT CAGAGATTC CAGAGAGAGCT CTGCACCTTG TCAGTGGAAATC CTGCACCTTG CAGAGAGAGAGAGAGAGAGT CCGCACCTTG CAAGAGAGAGAGAGAGAGAGAGAGAGT CCGCACCTTG CAGAGAGAGCGCAGAAGACCCAAGAGAGGCT CCAAGAGAGGCT CCAAGAGAGTGGAAGCGCAGAGAGTGGAAGCGCAGAGAGTGGAAGCGCAGAGAGTGGAAGCGCAGAGAGTGGAAGCGCAGGAGGTGGACCTGCACCAGGAGAGTGGAAGCGCAGGAGGCGCAGAGAGGTGGACCTGCACCAGGAGAGGCGCCAAGACGCCAAGACGCCAAGACGCCCAAGACGCCCAAGACGCCCAAGACGCCCAAGACGCCCAAGACGCCCCAAGACGCCCAAGACGCCCCAAGACGCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCCAAGACGCCCCAAGACGCCCCCAAGACGCCCCAAGACGCCCCAAGACGCCCCCAAGACCCCCC	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTGCTGG AACCCTGGAA TGCTGCTCAC TGATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC CGGGCCACCG CTGACCGGTT ACGCGTTGCC TGGATGACAT GATTTTGAACA ACCATATTGA AGACAGAGCA AGGCACGGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CCCTTCTGCC CCACGAGCAGG GCATGCTGGG GCATGCTGGC CCTTCACCA TGGAGTATT TGACACCTAT TGACACCTAT TGACACTAT TGACACTAT TGACACGAGAAG CCCTTGGAGT ATATCATGGA TGGCGAATAT TGGCGAGAT TGGCGAATAT TGGCGTCCAT	CGAGGGGAAG TTCCAGACT CAGCGACCAG CTACAAGACCC TTCAAGGCCA GACCAAGACC ACAGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAGC GTTCATGCAGTGCA AGATCCAAGA ATCCTTCTA TTCTAACTCA CATCGAGGCT TTCTAACTG CATCGAGGCT TTCTAACTG CATCGAGGCT TTCAATGATT CATCATGAAAAA	120 180 240 300 350 420 540 600 660 720 780 840 900 1020 1080 1140 1200 1260
50 55 60	Coding sequilibrium sequilibriu	Lence: 141 11 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CACTGCCAC CACTGCCAGGCT TGACCAGAGC TATCAGCCAG CTAGAGCAGAGC	D86 21 CCCAGCGCGG GCTGAGCGCG GCTGAGCCGG ACGCCCGGG ACGCCCGGG ACGCAGCTG ACTCTGACTC CCTGAGTTGC GGCAAGCACA ACCATCATTT AAGTACATTC GAAAGAGGCT GTCATCCAATT CAGAAGTTGC ACCATTCATT AAGTACATTG AAGTACATTG AAGTACATTG AAGTACATTG AAGTACTTCAAATTC CAGAATTTGAAACG CTGCACCTTG AAGTACTTGAAATTC AAGTACATTGAAATTC AAGTACATTGAAATTC AAGTACATTGAAATTC AAGTACATTGAAATTTGAAATTGAAATTTTCAAATTGAAATTGAAATTGAAATTGAAATTGAAAATTTGAAAATTTGAAAATTGAAAAATTTTACAAAAATTTGAAAAATTTTACAAAAATTTGAAAAAATTTTACAAACGAAGAAGAAAAATTTTACAACACGAAAAAATTTTACAACACGAAGAACGAAGAAGAAAAATTTTACACCAAAAAAATTTTACACACAC	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGGGTGAC CTGGGAGGCA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA GGGGCACGG CTGACCAGGT ACGCGTGCC TGGATGACA ACCATATTGA ACCATATTGA AGCAGAGGCA AGTGGACGGA CAGACCTCTG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCATCCTCTTCTGCC CCAGACCAG GCATGCTGGCGT CCTTCTCGCC CCAGACCAG GCATGCTGGG GCTGATGAA AGGAGGGGT TGGAGTTATT TGACACCTAT CGATGGCAGACAG CCCTTGGAGT ATATCATGGA TGGGGAATAT TGGGAATAT TGGGAATAT GAAAGCTCAC	CGAGGGCAAG TTCCAGACC TTCAAGGCCA TTCAAGGCCA ACAGTGCTATT CGGATTCTAT GGTATTCAG GTTCATGC GTTCATGC GTTCATGC GTTCATGC GTTCATGC GTTCATGC TTCAGG TTCATGC AGATCCTT TCAGGATGCT TTCAGG TTCTTCT GTTTCTC TTCATGTC TTCAATGTT TCAATGTT TCAATGTTT CATGATAAAG CCAGGAAAAA	120 180 240 300 360 420 540 600 720 780 900 960 1020 1080 1140 1260 1320
50556065	Coding sequilibrium sequilibriu	TCAGGGGTATTC TGAGTGGGT TCAAGCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAGAGGAGA	21 CCCAGCGCGG GTTGAGCGCG ACGCCCCGGG ACGCCCCGGG ATGGGAGCTG ACTCTGACTTG CCTGAGTTGC GGCAAGACAC GGCAAGACAC GCAAGACAC TGGACATTT AAGTACATTT CAGAATTC CAGTATTTGAATTC TCACTTTT CTCACTTT CTCACTTT CTCACTTT CTCACTTT CTCACTTT CAGTATTTCAAATC CTGCACCTTG CAGTATTTCAAATC CAAGACGTGG AAATTGTCCCAAGACGTGT AAGTACATTC CAAGACATTC CAAGACATTT ATACAGCCCA	311 TGCTATCGGA GCCAGGGTCT AGCTCGCAGG GCTTCCCTGG ACCCTGGA ACCCTGGA ACCCTGGA TCATTANAGA TGCTGCTCAC TCATTANAGA TGAACAAGAC CTGGATGACA ACCATTATGAAA ACCATATTGA AGACAGAGCA AGTGGACGCA AGTGGACGCA AGTGGACGCA AGTGGACGCA AGTGGACGCA CCACACACCTCTG CTACAATGGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CTCTTCTGCG GGCTGATGAGA GCATGCTGGG GCATGCTGGG GCATGATGAA AGGAGGCGCT TGACACCA TGACACCAT TGACACCTAT TGACACCTAT TGACACCTAT TGACACTAT TGACACCTAT TGACACTAC TGGGAATAT TGGTTCGAT TGGGAATTAAC TGGGAATTAAC TGGGAATTAAC TGGGATTGAT	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGTTT AGTGCCTCT GGTATTCAGC CTTGAGTTCAG CTTAGTTCAG GTTATTCAG GTTATTCAG GTTCATTTCAG GTTCATTTCA AGATCCAAGA ATCCTTTCTC GCGATGACCA TTTCTAACTTT CATCGAGGCT TTCAATGTTT CATGAGAGCC TTCAATGTTT CATGAGAAAA CTCAGGACCG	120 180 240 300 360 420 540 600 660 720 780 840 960 1020 1080 1140 1200 1260 1320
50 55 60	Coding sequilibrium sequilibriu	Lence: 141 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CACTGCGCT CACTGCCC TATCGGCAG TATCGGCAG GCACATCCTG GCAATCCTG AAAGCTCTC CTATTTTTT ATCAGGCACA ACGTCTGGC CAAACACTC TCATCATCT TAAAGTTGAG TCCCATTGAT TAAAAGTGGG TCCCATTGAT CAAAAAAGGC	D86 21	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GGGTTGGTAA TGAACAAGAC GGGGCCACCG CTGACCGGTT ACGCGGTGC TGGATGACAT ACCATATTGA ACCATATTGA AGCATACAT AGCATACGGA AGCAGAGCA AGGAGCCA AGGACCTCTG CTACAATGGA GGTTTGCATAGGA GGTTTGCATTGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CCCTTCTGCC CCACGACGAG GCATACTAGA GCATACTAGA GCATACTAGA GCAGCAGCT TGACACTAT TGACACTAT TGACACTAT TGACAGAGAG CCCTTGGAGT ATATCATGGA TGGCGAGATAT TGGCGAGATAT GTGGTTCGAT GAAGCTCAC TGGAGTTACA CCTTCGAT CAGAGTTACACCA CTACGACCAC CTACCACCAC CTACCAC CTACCACCAC CTACCAC CTAC	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCC TTCAAGGCCC GACCAGACCC ACGGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAGC GTTCATGTCA AGATCCAAGA ATCCTTCTA CATCATGCC TTCTAACTC CATCGAGTTC CATCGAGTTC TTCTAACTC CATCGAGTCC TTCTAACTC CATCGAGGCT TTCTAACTC CATCGAGGCC TTCAAGGATCC CATCGAGGAAAAA CCCAGGAAAAAA CTCAGGCCC GGCAGACCCT	120 180 240 300 360 420 540 600 720 780 900 960 1020 1080 1140 1260 1320
50556065	Coding sequilibrium sequilibriu	Lence: 141 11 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CACTGCCCC CACTGCCAGG CACTGCCCAGGC TATCGGCCAG CTCAGAGGGA GCACATCCTG GGGCAATTTC CTATGGTCTG AAAGCTCTGC CTATTTTTT ATCAGGCACA ACGTCTGGTC TCAACAGGT TCAACACTTC TCAACAGT TCAACACTTC TCAACAGT TTAAAGGTTGGT TAAAGGTGGGT TCCCATCATCT TAAAGGTTGGGT TCCCATTGAT CAAAAAAGGC CCCTTTACGG CCCGTTACGG	D86 21 CCCAGCGCGG GCTGAGCGCG GCTGAGCCGG ACGCCCGGG ACGCCCGGG ACGCCAGCCCGG ACGCAGCTGACCT CCTGAGCTG GGCAAGCAC ACTACATT AAGTACATTG ACATCATTT CAGACATTT CAGACATTT CAGACATTT CAGTATTGCAAC TCTGACATT CAGTATTTGAAAC TCTGAAATC TCAGTATTTGAAATC TCAGTGGAAT TCTGCACTTG TCAGTGGAAG AAATTGTTCA AAATTGTTCA AAATTGTTCACATTGAAAC CAGAGACGTGG GAGAAAATTT ATACAGGCCA CAGGATTATA TTCCTCTGTG	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTGCTCAC TCATTANAGA GAGGAGAGCT TGTATGGAAG GGGTCGCACG CTGACCGGTT ACGCGTGCC CTGACCGGT TGGATGACA TGATTTGACA ACCATATTGA AGCATACCA ACCATATTGA AGCAGAGCA AGTGGACGGA CAGACCTCTG CTACAATGGA GGGTCCTCTG CTACAATGGA GGTTTGCTTG GGAAGCCTCTG	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CCCTTCTGCCA GCAGACGAG GCATGCTGGCGCACAGC GCAGACGAG GCATGCTGGC CCTTCACCA TGGAGTTATT TGACACTAT CGATGGAGGAGA CCCTTGGAGT ATATCATGGA TGGCGAATAT GTGGTTCAC TGGAGTTAAC CGAGGAGAG CCCTTGGAGT TGGAGTTAAC CGAGGAGAG CCCTTGGAGT CGCGAATAT CGCGCAGAGAG CCTACCACG GAGGCCCAAA	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGTTT AGTGCCTCT GGTATTCAGC CTTGAGTTCAG CTTGAGTTCAG GTTATTCAGC GTTGATTTCAG GTTCATGTCA AGATCCAAGA ATCCTTTCTC GCGATGACCA TTTCTAACTTC CATCGAGGCT TTCAATGTTT CATGAGAGCC TTCAATGTTT CATGATAAAG CCCAGGAAAAA CTCAGCACCG	120 180 240 300 360 420 600 660 780 840 900 1020 1020 1140 1200 1260 1380 1440
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5055606570	Coding sequilibrium control coding sequilibrium code code code code code code code code	Lence: 141 11 TCAAGCAGAG AGCCAGGGGG CCGCTTGCCC CACTGCCAGCAGGCTGCCT CACTGCCAGGCTGCCT TGACCAGAGC TATCGGCAG CTCAGAGGGAG CTCAGAGGGAATCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTCT TCATCATCT CCAGGTATTCT TCAAGAGC TCAACAGGGA CTCATCAGGGAC ACGTCTGGTCT CAACACTCC CCGGTATTCC TGATGAGGT TCAACACTCGGGCAG CCGTGTACGG CAATGTGAAC CCGTGTACGG CAATGTGAAC TCCCTGCAGA	D86 21 CCCAGCGCGG GCTGAGCGCG GCTGAGCCGG ACGCCCGGG ACGCCCGGG ACGCAGCTGACTG ACTCTGACTT CCTGAGTTGC GGCAAGCAC ACTCATATT AAGTACATTT GAACATTT CAGACATTT CAGACATT CAGACATT CAGACATT CAGACATT CAGACATT CAGACATT CAGACATT CAGACATT CAGACATT CAGACCATT CAGACCAT CAGACCATT CAGACCAT	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA CAGGCACGGT ACGCGGTAC CTGACAGGCA ACCATATTAACA ACCATATTAACA ACCATATTAACA ACCATATTAACA ACCATATTAACA ACTACAGGC CTACAATGGA CAGACCTCTG CTACAATGGA GGTTTGCTTG GGAAGCCTTTG CTACATTGGA CAGACCTCTG CTACATGGA CAGACCTCTG CTACATGGA CAGACCTCTG CTACATGGA CAGACCTCTG CTACATGGA CAGACCTCTG CTACATGGA CTGATTACTC CCCAACCAGGT CCCAACCAGGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGAT ACTGTCTCGG GGACTTCCTC GCCCGCCAT CCCTTCTGCC CCAGACCAGG GCATGCTGGC CCAGACCAGG GCATGCTGGC CCTTCTCGC CCTTCACCA TGGACTTATT TGACACCTAT CGATGGAGAGAG CCCTTGGAGT ATATCATGGA TGGCGATATAT TGACACCTAT CGATGCAGAGAG CCCTTGGAGT CTACCCAG GAAGCTCAC CTACGACCAG GAAGATTAAC CTACGACCGG GAGGCCCAAA GGATAATGTA CATGTACCAG CCAGAGAGG CCTACGACCGG CAGGCCCAAA GGATAATGTA CATGTACCAG CCGGCGGGGGGGGGG	CGAGGGGAAG TTCCAGACC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC GCACAGACCC ACGGTCTATT CCGATTGTTT AGTGCCTCT GGTATTCAGC GTTCATGTCA AGATCCAAGA ATCCTTCTC TCCATGCACC TTCAAGTCC TTCAATGTC TTCAATGTC TTCAATGTT TCATGTTT CATGATAAAG CCAGGAAAAA CTCAGCACG GGCAGAGCCT CTCACACCCG GGCAGACCAA CGCAGAACAAA GTCAAGGAACCAA GGCAAACCAA GTTGGCTTC	120 180 240 300 360 420 600 6600 720 780 840 960 1020 1140 1200 1320 1380 1440 1560 1620
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5055606570	Coding sequilibrium sequilibriu	Lence: 141 11 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CACTGCCAC CACTGCCAGGCAG CACTGCCAGGCAGGCAG TATCGGCAGGCAGCAGCAGCAGCAGCAGCAGCACATCCTG GGGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TCAACAGTCTGCT CAACACTCT CCATCATCT CCATCATCT CCATCATCT TCAACACTCC TAACTGGGGAG TCCCATTGAT TAAAGGTGGG CAATGCTGGCAGA CATCCTGCAGAG CATCCTGCAGAC CATCCTTGACC TTCCTTCCAGAC CATCCTGCAGAC CATCCTGCAGAC CATCCTGCAGAC CATCCTTGCAGAC CATCTTGCAGAC CATCCTTGCAGAC CATCCTTGCAGAC CATCCTTGCAGAC CATCCT	D86 21 CCCAGCGCGG GCTGAGCGCG GCTGAGCGCG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCAGCTGACCT CCTGAGCTG GCAAGCAC ACTATTT AAGTACATT AAGTACATTG CAGAAGCGGG ATCGACATTC GAAAGGAGCTGG GAAAGACGT GTCATCCATT CAGTATTGCA AATTGTCAATT ATCAGCCCA CAGGACTTGG GAGAAATCT CAGTGGAAG AATTGTCC AGTATTGT ATTCCTCTGTG CAGGACTTGG AGGACATTC ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT TCCTGGCCC GAGATAGACG ATGGGGGAGG ATGGGGAGG ATGGGGAGGC TTCGATACCT GGCACCGAGG	TIGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTGCTCAC TCATTANAGA GAGGAGAGCT TGTATGGAAG GGGTCGCACG CTGACCAGT ACCATATGA ACCATATTGA ACACAGAC ACCATATTGA AGACAGAGC TGACAGGGC CTGACCGGT CTGACAGGC CTGACAGGAC CTGACAGGT TGGAGGACAA CTGATTACGA CCCAACCAGGT TGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGAT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CCCTTCTGCC CCACGACAGG GCATCATCA CCATCACCA TGGATTATT TGACACCTAT TGACACCTAT CGATGGAGA CCCTTGGAGT ATATCATGGA GCAGAGTATAT TGACACCTAT CGATGGAGTTAAC TGGAGTTAAC CTACCACCA GGAGTTAAC CTACCACCA CAGAGTTAC CAGAGTTAC CAGAGTTAC CAGAGTTAC CAACACCC CAACAGTTG GGGCCCAAA TGGCCCCACA CCACCAAGTTG CCATCAAGTTG CAACTGCCC CAACAGTGCC CATCAAGTTG CGGGCCCAAC CCATCAAGTTG CGGGCCCAAC CCATCAAGTTG CAGCACCC CAACAGTGCC CAACAGCCC CATCAAGTGCC CATCAAGTGCC CATCAAGTGCC CAACAGCCC CACCAACACCC CAACAGCCC CAACAGCCC CAACAGCCC CAACAGCCC CAACAGCCC CAACAGCCC CAACAGCCAC CCCCC CCCCC CCCCCC CCCCC CACCACCC CACCAC	CGAGGGGAAG TTCCAGACC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC GCACAGACCC GCACAGACCC ACGGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAG GCTCATGTCA AGATCCAAGA ATCCTTCTA TTCAAGGCCA TTCTAACTG CATCGAGGCT TTCAATGTT CATGATAAAG CCAGGAAAAAA CTCAGCACCG GGCAGAACCA GGCAGAACCA GCAGAAAAC GCAGAAAAC GCAGAAAAC GCAGAAAACC CATCATGGG GCAGAGCT CTCACGCCC GGCAGACCA GGCAGACCA GCAGAAACCA GCTGGGGTTC CTCACGGCTC CTCTGCGGTT	120 180 240 300 360 420 540 660 720 780 960 1020 1320 1320 1320 1360 1560 1560 1620 1740 1860 1920
5055606570	Coding sequilibrium control coding sequilibrium control code code code code code code code code	Lence: 141 11 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CACTGCCAC CACTGCCAGGCT TACAGCAGGCT TACAGCAGGCT TACAGAGC TATCAGAGGC TATCAGAGGC CTATGGTCTG CTATGGTCTG CTATGGTCTG CTATGGTCTG TACAGCACAA ACGTCTGGTC TCATCATCT TCCTTGCAGA CATCTTGCAC ACACTTGGAG TTCCTTCCAC ACACTTGGAG TCACTTCCAC ACACTTCCAC ACACTTCCAC ACACTTCCAC	D86 21 CCCAGCGCGG GTTGAGCGCG GCTGAGCGCG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGCACA ACCATCATTT AAGTACATT GAAAGAGCT GTCATCCATT CAGTATTGACACT TCGAAATTCACACT TCGAAATTGACACT TCAGTATTTGACACT TCAGTATTTGACACT TCAGTATTTGACACT TCAGTACTTG TCAGTGGAGG GAGAAAATTT ATACAGGCCA CAGGATTATA TTCCTCTGTG AGCACCATTC ATTGCCAGTA TTCCTCTGTG AGCACCATTC ATTGCCAGTA TTCCTCTGTG GAGATAGACC GAGATAGACC ATTGGGGGAGG TTCAGTGGCCC GGGATAGACC GGGAGGAGG CTGGCCGGTC CGGCACGGGGCG CTGGCCCGCCC CTGGCCCGCCC CCCCAGCGCGCC CTGGCCCGCCC CCCCAGCGCGCC CTGGCCCGCCC CCCCAGCCCCC CCCCAGCCCCCC CCCCAGCCCCCC CCCCAGCCCCCCC CCCCAGCCCCCCC CCCCAGCCCCCCC CCCCAGCCCCCCCC	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGGGTAC CTGGGAGGCA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAG GGGTCGCGGC CTGACCGGTT ACGCGTGAC CTGACAGGC AGCCACGG CTGACCAGGT ACCCGGTT ACGCGTGC CTGACAGGC CTGACTTGGACGGA CAGACCTCTG GGAAGCCTCTG CTACAATGGA GGTTTGCTTG GGAACCTCTG GGAACCTCTG TGAACTTGGA CTGACTTACAT CTGACTACTC CTACACCAGGT TGGACGACAC TTGGGGCCAC TTGGGGCCAC TTGGGGCCAC TTGGGGCCAA TTGGGGCCAA TTGGGGCCAA TTGGGGCCAA TTGGGGCCAA TTGGGGCCAA TTGGGGCCAA TTGGGGCCAA TTGGAGCATAT TGTAGACACAG	CAGAGCCTGG GAACCCAGAT GCCTGGCGAT ACTGTCTCGG GGACTTCCTC GCCCAGACCAGG GCCACATCC CCCTGGCCAT CCCTTCTGCC CCAGACCAGG GGATGCTGGG GGATGCTGGG GGCTATGACAGA TGGAGTTATT TGACACCTAT CGATGGAGTAGAT GGCAGGAGAG GCCTAGGAGT GAAGCTCAC CTACCCAG GAAGATGAC CATGACTTACCAC GAAGATTACAT GAAAGCTCAC CTACGACCGG GAGGCCCAAA GGATAATGTA CATGTACCAC CATCAAGTTT GGGACGAGAG ATGCTACCCC CATCAAGTTT GGGAACGCGAA ATGCTACCCC CATCAAGTTT GGGAACACCC CATCAAGTTT GGGAACACCC CATCAAGTGCA AAGCGCAAGCG	CGAGGGGAAG TTCCAGACC TTCAAGGCCA TTCAAGGCCA TTCAAGGCCA TTCAAGGCCA GACCAAGACC ACGGTCTATT AGTGCCTCT GGTATTCAG GTTCATGCAGA ATCCTTTCA AGATCCAAGA ATCCTTTCTA AGATCCAAGA ATCCTTTCTA CGATGACTC TTCAATGTT TCAATGTT TCAATGTT TCAAGACCA GGCAGAGCCT TTCAACTGT TCAAGACCA GGCAGAGCCT CTCAGCACCG GGCAGAGCCT CTCAGCACCG GGCAGAGCCT CTCACACTCA GGCAAGACCA GGTCATGGA GCATGAGACCA TTCTAGCACCG GCCTCGCGAC CAGTCATGGA GCAGAACCA TTCTAGCACCG CTCTCAGCACCG CTCACAGTCA CTCGTCAGCCCG TCCACAGTCA CTCACAGTCA CGCTCTGGGAT CTCAGGAACCA CTCTCGGGACC TTCAGGACCA TTCAGGACCA CTCGTGGGTT CTCACAGTCA CTGGTGGGTT CTCAGGACCA CTGGTGGGTT CTGAGGCTC TTCAGGACCA	120 180 240 300 360 420 540 600 780 900 960 1020 1140 1200 1320 1380 1440 1500 1500 1740 1800 1740 1800 1920 1980
505560657075	Coding sequilibrium sequilibriu	Lence: 141 11 TCAAGCAGAG AGCCAGCAGG AGCCAGCAGG CCGCTTGCCC CACTGCCAGC CACTGCCAG CACCAGCAGG CTACCAGG CTACAGAGG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGAATTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC CAACACTC CCACTCATCAT CCAGTGTGAGG TCCCATTGAT CAAAAAAGGC CCATTGAT CAAAAAAGGC CCATTGCAGGAG CATCATTAGT TACCCTGCAGA CATCGGGGAA CATTGCAGGAG CATCATAGTGGT TTCCTTCCAGGAG CATCATTGAT CAACACTTC CCAGGGAAC CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG CACCTTCCAC CAGGGACCTC CAGGGACCTC CAGGGACCTC CCAGGGACCTC CAGGGACCTC CAGGGACCTC CAGGGACCTC CAGGGACCTC	D86 21 CCCAGCGCGG GTTGAGCGCG GCTGAGCGCG ACGCCCCGGG ACGCCCCGGG ACGCCCCGGG ACGCCCCGGG ACGCCCCGGG ACGCCCCGGG ACGCCCCGGG ACGCAGCTGAGTTGC GCAAGACAC GCAAGACAC GCAAGCTGG ACATTT AAGTACATTG TGAACATTC CAGTATTTCAAATTC CTGAACTTC CTGCACCTTG TCAGTGGAAAT TCCTCGAAAT TCCTCGACTT ATGCACCTTG AGCACTTTC CAGGATTATA TCCTCTGGCCC AGGATTATA TCCTCGGCCC ATTGCCAGTA TCCTGCGCCC CGGCACGAGC CTGGCCGGTC CTGCCCGGTC CTGCCCGGTC CTCCATCCATC	311 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGGCT ACGCGGCAC GCTTGCTAC TGTATGGAG GGGTTGGTAA TGAACCAGGC AGCCACGG CTGACCAGGT CAGCACCTCTG CTACAATGGA GGTTGCTTG CTACAATGGA GGTTGCTTG GGAGCCTCTG CTACAATGGA GGTTGCTTG GGAGCCTCTG CTACAATGGA GGTTGCTTG GGAGCCTCTG TGAAGCCTCTG TGAAGCCACA TTGGAGGACAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTOTTCTGC GGCCACATCC CCCTGGCCAT CCACACAGA GCATGCTGG GGCTGATGAA AGGAGGCGCAT CCTTCACCA TGGATTATT TGACACCTAT TGACACCTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGAGATTAT TGAGAATTAT TGGTTCGAT GAGAGTTAAC TAGAGCTCAA CAAAGTGCA CAAAGTGCA CAAAGTGCA CAAAGTGCA CAACACTAT CAAAGTGCA CAACACCAC CAACAAGTTAAC CAACACCC CATCAAGTTT GGGGAACACCAA AAAGGGGAGGT TACCCCC CATCAAGTTT CGGGGAAGGCA AAAGGGGAGGT TCCCTCCCTTCCCCT CATCACCTC CATCAAGTTT CGGGGAAGCACA AAAGGGGAGGT TCCCTCCCTTC	CGAGGGGAAG TTCCAGACCA TTCAAGGCCA TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC ACGGTCTATT AGTGCCTCT GGTATTCAGC CTTCAGTTCA GGTATTCAG GTTATTCAG GTTATTCAG GTTCATGTCA AGATCCAAGA ATCCATTCTACTG CATCAAGTCA TTCTAACTG TTCAATGTT CATGATAAAG CCAGGAAAAA CTCAGCCCG GGCAGAGCCT CTCACAGTCA CAGTCAATGGA CCAGTCAATGGA CCAGTCATGGA CCAGTCATGGA CCAGTCATGGA CCAGTCATGGA CCAGTCATGGA CCAGTCATGGA CCAGTCATGGA CCAGTCATGGA CTCAGGAACCA CTCTGGGGTT CTTCAGGACCC CTCTGGGAT CTGTGGGGTT CTTACAGCACC CTTCTGGGAT CTTGTGGGTTC TTACAGCACC CTTTGGGGTT CTTACAGCCAC CTTGTGGGTT CTTATGACCCAC CTTGTGGGTT CTTATGACCCAC	120 180 240 300 360 420 600 660 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1680 1740 1860 1860 1980 2040
5055606570	Coding sequilibrium sequilibriu	Lence: 141 TCAAGCAGAG AGCCAGCAGG AGCCAGCAGC CCCCTGCGCT CACTGCCC CACTGCCAGG TATCGGCAG GCACATCCTG GGCAATTTC CTATGGTCTG AAAGCTCTGC CTATTTTTT ATCAGGCAA ACTCTGGTCAG TGATCAGTGGT TCCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCATCT TAAAGGTCGG TCCCATTGAT TAAAGGTCGG TCCCATTGAT TAAAGGTCGG TCCCATTGAT TAAAGGTCGG TTCCTTGAT TCAAAAAGGC CATCTTGAT TCAATAATGG CATCTTGAGAC TCCCTGCAGA CATCTTGAG TTCCTTTGAG TTCCTTTGAG TTCCTTTGAG TTCCTTTGAG CAGGGACCT CCGGGGAG CACCTTTGAG CAGGGACCT CCAGGGACCT CCAGGTATCT CCAGGGACCT CCAGGTATCT CCAGGGACCT CCAGGGACCT CCAGGTTTCAAC CCAGGACCT CCAGGTTTCAAC CCAGGGACCT CCAGGTTTCAAC CCAGGACCT CCAGGTTTCAAC CCAGGTTTCAAC CCAGGACCT CCAGGTTTCAAC CCAGGACCT CCAGGACCT CCAGGTTTCAAC CCAGGACCT CCAGGACT CCAGGA	21 CCCAGCGCGG 21 CCCAGCGCGG GCTGAGCGCG GCTGAGCCGG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCAGCTGG GCAAGACAC GCAAGACAC ACCATCATTT AAGTACATTG CAGAAGTGG GAAAGACTGG GAAAGACTGG GAAAGACTTGACATTC CAGTATTGCAAATC CTGCACCTTG CCAGGAATTC TCAGTGGAAATC CTGCACCTTG CAAGACTTGCACTTG AAGTACTTGCAAGTATTGCAAGTAC TCCTCTGCGCCC GAGAAATCTTCTCTCTGTG AGGACCATTC ATTGCCAGTATTCCTCTGCGCCC GAGATAGACC CTGGCCCTC TCCTGCGCCCC CTCGCCCCCC CTCGCCCCGTC TCCATCCATC ACGGCAGGACC CTGGCCCGTC TCCATCCATC AAGGACCTTC AAGCACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGCACCTTC AAGGACCTTC AAGGACCTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGACCTTC AAGGA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGA CTGGGAGGCA TGCTGCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG CTGGATGGCCACG CTGACCGGT ACCCGGTACCACT GATTTAGACA ACCATATTGA AGACAGAC CTGACCGGT CTGACCGGT CTGACCTGG CTGACCGGT CTGACCTGG CTGACCGGT CTGACCTGG CTGACCTGT GGAGCCTGT CCAACCAGGT TGGAGCACAA TTGGAGGACAA TTGGAGGACAA ATGTAGACCAG ATGCAGCTATAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGAT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCACCAGAGAG GCATCCTCC CCTGGCCAT CCACCAGAGAG GCATCCTGG GGCCACACC CCTGGCCAT TGGAGTATAT TGACACCTAT CGATGGAGAG CCCTTGGAGT ATATCATGGA TGGCGAGTATAT GTGGTTCGAT GAAGCTCAC GAAGATATCAT GAAGCTCAC CACCAGAGAG GCATATCAT GAAGCTCAC CAGAGAGAG CCTTGGAGT ATATCATGGA ATATCATGGA ATATCATGGA CCACCAGAGAG CCACCAGAGAG CCATCAGACG GAAGCCCAAA GGATATATC CAGAGCGGGGGAG ATGCCCC AAAGTGCAC CACCAGGTTAC CATCAGGCAC CATCAGGCAC AAGGGGAGGA ATGCTACCC CATCAGGCAC CATCAGGTTAC CATCAGGTT CCCTGCGTC TCCCTGCGGT TCCCTGCGGT CCCTCTGGGGT CCCTCTGGGGCGCGC CTCCTTGGGCC CTCCTTGGGCC CTCCTTGGGCC CTCCTTGGGCC CTCCTTGGGCC CTCCTTGGGCC CTCCTTGGGCC CTCCTTGGGCC CTCCTTTGGGCC CTCCTTTGGGCC CTCCTTTGGGCC CTCCTTTGGGCC CTCCTTTGGGCC CTCCTTTGGGCC CTCCTTTTGGCC CTCCTTTTGGCC CTCCTTTTGGCC CTCCTTTTTGGCC CTCCTTTTTTGGCC CTCTTTTTTGGCC CTCTTTTTTGGCC CTCCTTTTTTGGCC CTCTTTTTTGGCC CTCTTTTTTGGCC CTCTTTTTTGGCC CTCTTTTTTGGCC CTCTTTTTTTGGCC CTCTTTTTTTGGCC CTCTTTTTTTGGCC CTCTTTTTTTGGCC CTCTTTTTTTT	CGAGGGGAAG TTCCAGGCC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC GCAGATTATT CGATTGTTT AGTGCCTCT GGTATTCAG GCTCATGCCC GTTCATGCC GTTCATGCC GTTCATGCC GTTCATGCC GTTCATGCC TTCAAGTCCA AGATCCAAGA ATCCTTTCTA CATCGAGGCC TTCAAGTCT TTCAATGTT CATGATAAAG CCAGGAAAAAA CTCAGGCCT CTCACAGCC GGCAGAACCA GGTAAGCCA GGCAGAACCA CATTGGGGTC TTCAAGTCA CTTGGGGTC TTCAAGTCA GCTCAGGACC TTACAGACC GCCAGGAAACCA GTTGGGCTC TACAGGACC TTACAGAACC CCTCTGGGGT CTCACAGTCCA CCTTGGGGTC TATGACCCAC CCTCTGGGGT CTCACAGTCCA CACAGTCCATG CACAGTCCATG CACAGTCCATG CACAGTCCATG	120 180 240 300 360 420 600 660 780 840 900 1020 1020 1140 1200 1320 1380 1440 1560 1740 1860 1740 1860 1920 1920 1920 1920 1930
505560657075	Coding sequilibrium sequilibriu	Lence: 14 11 TCAAGCAGAG AGCCAGCAGG AGCCAGCAGG CCGCTTGCCC CACTGCCAGGCT CACTGCCAGGCT TATCGGCAG GCACATCCTG GGGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCAGA ACGTCTGGTCT TCATCATCT CCAGGTATTCT TCAACACTT TCAACACTT CAACACTTC CCAGTCTTGT TAAAGGTCGG TCCCATTGAT TCAACACTTC CCGGTATCGT CAACACTTC TCATCATCT CAACACTTC TCATCATCATCT CAACACTTC TCATCATCT CAACACTTC CATCATTGTT TAAAGGTCGG CAATTGATG CAACACTTGATC CAGGGAACTTC TCCTTGCAGA CACCTTTGATC CAGGGAACCTC CAGGGAACCTC CTCCTTGCAGA CACCTTTGATC CAGGGACCTC CTTGTTGATC CTTGTTGATC CTTGTTGATC CTTGTTGATC CTTGGTGAGA	D86 21 CCCAGCGCGG GCTGAGCGCG GCTGAGCGCG GCTGAGCCGG ACGCCCGGG ACGCCCGGG ACGCCAGCTGAGCTG	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTGCTGGA GAGCAGGGT TGTATGAAGA GAGGAGAGCT TGTATGAAGA GGGTTGGTAA CAGGCT TGACCAGGT ACCCAGGT ACCAGTACCAGGT ACCAGACCAG	CAGAGCCTGG GAACCCAGAT GCCTGGCGAT ACTGTCTCGG GGACTTCCTC GCCCAGCAGAC CCCTGGCCAT CCCTTCTGCC CCACGACAGG GCATGCTGG GCATGATGAA AGGAGGGGCT CCTTCACCCA TGGATTATT TGACACTAT TGACACTAT TGACAGATAT TGACAGAGAG GCCTAGGAGAT TGGAGTTAAT TGACAGCAG GAAAGCTCAC TGGAGTTAAT CATGACCG GAGGCCCAAA GGATAATGTA CATGACCG GAGGCCCAAA GGATAATGTA CATGACCG CAACAAGTTT GGACTACCCC CATCAAGTT GGGACAGCG AGGCCCAAA TGCTACCCC CATCAAGTT GGGACAGCG CAACTGGCG CATCAGGT CATCTACCCC CATCAAGTT CCCTCTTTGGGC CTCTTTGGGC CTCTTTGGGC CTCTTTTGGGC CTGTTTTGGCC CTCTTTTGGGC CTGTTTTGGGC CTGTTTTGGGC	CGAGGGGAAG TTCCAGACC TTCAAGGCCA TTCAAGGCCA TTCAAGGCCA TTCAAGGCCA GACCAAGACC ACGGTCTATT CGGATTGTT AGTGCCTCT GGTATTCAG GTTCATGCA TTCATGTCA AGATCCAAGA ATCCTTTCTA GCGATGACCA TTCTAACTC TTCAATGTC CATCGAGCCT TTCAATGTC CATCGAGCCT CTCACAGTCA CAGGAAAAA CTCAGGACCT CTCACAGTCA GGCAGAGCCT CTCACAGTCA GGCAGAGCCT CTCACAGTCA CAGTCATGGA GCAGGAACCA GCTCGGGAT CTCACGGCTC TTCAAGGCTT CTCACGGCCT CTCACAGTCA CAGTCATGGA GCAGGAACCA CCTCTGGGGT CTCACGGCTC CTCACGGCTC CTCACGCTCC CTCACGCTCC CTCACGGCTC CTCACGGCTC CTCACGGCTC CTCACGGCTC CTCACGCTC CTCACGGCTC CTCACGCTC CTCACGCTC CTCTGGGGT CTCTGGGGT CTCTGGGGT CCCTGGGGT CCCTGTCTC CCCTTGTCC	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1500 1560 1620 1620 1680 1620 1620 1620 1620 1620 1620 1620 162
505560657075	Coding sequilibrium sequilibriu	Jence: 141 TCAAGCAGAG AGCCAGCAGG AGCCAGCAGG CCGCTTGCCC CCCGTGCGCT CACTGCCAGG CTACCAGGCAG CTACAGAGG CTAGAGGGAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTATTTTT ATCAGGCACA ACGTCTGGTC TGATCATCT CCAGTCATCT TCAATCATCT CCAGTATATCT TCAATCATCT CCAGTTATCT TGAAGGTATC CAAAAAAAGG CCTCCTCCAGAG CACTTCGAGG CAATTTTTT TAAAGGTAGGG CCATTGATC CCAGTGAAGG TCCCTTCCAGAG CAACATTGAG CATCATTAGT CTCCTTCCAGG TTCCTTCCAGG TTCCTTCCAGG CACCTTTGATC CAGGGACCT CCAGGGACCT CCAGGCCGGAG CCTCCTCCCCC CCCCCCCCCC	D86 21 CCCAGCGCGG GTTGAGCGCG GCTGAGCGCG ACGCCCCGGG ACGCCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC GGCAAGACTG ACTATTT AAGTACATTG GAAAGAGTT CTGAACTTC GAAAGAGTTC CAGTATTTGAACATT TCTCCAATT CAGTATTTGAACATT TCAGTATTCC CAGAATATT ATACAGCCAT CAGGAAAATTT ATACAGGCCA CAGGATTATA TCCTCTGCAC CAGGATTATA TCCTCTGCCCC CGGACACTC CGGACCTTC CGGACCTTC CGGACCTTC CGGACCGTC CTGCCCCC CGGACACCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCCC CTGCCCCCC CTGCCCCCCC CTCCCCCCCC	31 TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGGGTGAC CTGGGAGGCA ACCCTGGAA GCAGAGAGCT TGATTAAAGA GAGGAGAGCT AGCTGGAA GCGTTGCTAA GAGCACGG CTGACCAGGT ACGCGGTGC ACGCGGTGCC ACGCGGTTCCCTGGATGACAT ACGCGGTGCC ACTGACCAGGT CTACAATGAA ACTATATGAA GGATTACTTC CCAACCAGGT TGAACCATGT TGAAGCATAT TGAAGCACAC TTGAGGACAC TTGAGGACAC TTGAGGACAC TTGAGGACAC TTGAGGACAC TTGAGGACAC TTGAGGACAC TTGAGGACAC ATTGAGCAC ATTGAGCACAC ATGAGCACAC ACAGCAAGAT	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTTCTGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCACACGAG GCATGCTGGG GCATGCTGGG GCATGCTGGG GCATGATGAG GCATGCTGGG GCATGATGAA AGGAGGCGCT CCTTCACCA TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGACACTAT TGAGATTATCAT TGAGATTAT TGAGATTAT TGAGATTAT TGAGATTAT CATGTACGA TGGAGATTAT CATGTACCAG CAAAGTGGC CAAAGTGGC AAGGGCCCAAA ATGCTACCC CATCAAGTTT GGGACAGCAG ATGCTTCGGC TCCTTTTGGGC CTCTTTTGGGC CTGTCTTTGGGC	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGTTT AGTGCCTCT GGTATTCAG CCTTCAAGTCCA GGTGCATGG GTTCATGTCA AGATCCAAGA ATCCATGTT CATGACTAC TTCTAACTG CATGACTAC TTCAACTG TTCAACTGT CATGACAGACCA GCAGAAAA CTCAGCACCG GGCAGAGCCT CTCACAGTCA GGTAGCACGG GCAGAGCCT TTCACAGTCA CAGTCATGA GCTGGGCTTC TTCACAGTCA CAGTCATGA GCTGGGCTTC TACAGGAACCA CCAGTCATGA CTCGGCACC CAGTCATGA CTCGGGAT CTGGGCTTC TACAGAACC CAGTCATGA CTCGGGAT CTGGGAT CTGGTGGGT CTACAGTCAC CAGTCATGA CTCGTGGGAT CTGGTGGGT CTACAGACCAC CACAGTCATG CACAGTCATG CACAGTCCATG CACAGTCCATG CACAGTCCATG CACAGTCCATG CACAGTCCATG CACAGTCCATG CACAGTCCATG CTCCTTGTCA ATCACAGAGGG	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1860 1740 1860 1980 2040 2160 2220
50 55 60 65 70 75 80	Coding sequilibrium sequilibriu	Lence: 141 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CACTGCCCT CACTGCCCT CACTGCCAGGG TATCGGCAGG TATCGGCAG GCAATTCC CTATGGTCTG AAAGCTCTGC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATCAGTGGT CAAACACTTC TCATCATCT TTATGTTGGT CAAAAAAGGC CCTTGTTGAT CAAAAAAAGGC CCTTGTTGAT TCCTTGCAGA CATCTGGGGAG CATCTTCCAG CATCTTCAC CAGGGACCT CTGGTTCATCG CAGGGACCT CTGCTTCATCA CTGGGGAG CTTCCTTCAGAG CATCTTCAC CAGGGACCT CTGCTCCCCC CGGGTACATC	086 21	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGA CTGGGAGGCA TGCTCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA TGCTGCTGAA TGCTGCTGGAAGCA TGTATGGAAG GGGTTGGTAA TGAACAAGA CGGGGCCACCG CTGACCGGT ACCCATTTAGACA ACCATATTGA AGCATACCT GATTACCC CTGACCTGG CTGACTGG CTGACTTGC CCAACCAGGT TGGACCTAGG TGGAGCACT TGGGCTATAA CTTTTTGACCCA ACAGCAAGAT	CAGAGACCTGG GAACCCAGAT GCCTGGCGAT CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCCTGGCCAT CCACCAGAGAG GCATACTGG GCCACAGAGAG GCATACTAGA GGAGGCGCT TGACACTAT TGACACCTAT TGACACCTAT TGACACCTAT CGATGAGAGAG CCCTTGGAGT TATACATGGA TGGCGAATAT TGACACCTAT CAGAGAGAGCCCAAA TGGCGAATAT CTGGCTACCAC CAGAGAGAGCCCAAA TGGCGAATAT CTGGCGAATAT CTGGCGAATAT CTGACACCGG CAAAGTTACCAC CAAAGTTACCAC CAAAGTTACCACCAC CATCAAGTT CGCGCGCGCGCGCC CTCTTTGGGC CTCTTTTGGGC CTCTTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGGC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGCC CTCTTTTGCC CTCTTTTGCC CTCTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTTGCC CTCTTTTTTGCC CTCTTTTTTGCC CTCTTTTTTTGCC CTCTTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTTGCC CTCTTTTTTGCC CTCTTTTTTTT	CGAGGGGAAG TTCCAGGCCA TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC TTCAAGGCCC GCACAGACCC GCACAGACCC ACGGTCTATT CCGATTGTT AGTGCCTCT GGTATTCAG GCTATTCAGCCC GTTCATGCCATGC	120 180 240 300 360 420 600 660 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1680 1740 1860 1920 1980 2040 2100 2160 2220
505560657075	Coding sequilibrium sequilibriu	Lence: 141 TCAAGCAGAG AGCCAGCAGG CCGCTTGCCC CACTGCCAC CACTGCCAGGCAG TATCGGCAGG TATCGGCAGG CTAGAGGGAA GCACATCCTG GAGCATCCTG CATAGTTGT AAAGCTCTCC CTATTTTT ATCAGGCACA ACGTCTGGTC TCAACAGTC TCAACAGTC TCAACAGTC TCAACAGTC TCAACATCT CCATCATCT CCATCATCT CCATCATCATCT TCAACATCT TCCTTGCAGA CATCTTGCAC TCCTTGCAGA CATCTTGCAC TCCTTGCAGA CATCTTCCAC TCCTTCCCCC CGGGGACATC TTCCTTCCCCC CTTGTTGATC TTGGCCGGAGA CCTTCCTCCCC CGGGGTACATC TCCCTCCCCC CGGGGTACATC TCCCTCCCCC CGGGGTACATC TCCCAACAAC	21 21 21 21 21 21 21 21 21 21 21 21 21 2	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTGCTGGA GAGCCTGGAA TGCTGCTCAC TCATTANAGA GAGGAGAGCT TGTATGGAAG GGGTCGCACG CTGACCGGT ACCCGTGCACCGT ACCCATATGAA ACATATGA ACATATGA AGACAAGAC CAGACCTCT CTACAATGGA GGTTGCTGC CTACACGGT CTGACCGGT CTGACCGGT CTGACCAGGT GGAGCCTCT CTGACATGGA CAGACCTCT CTGACATGGA CAGACCTCT CTGACATGGA CTGATTACT CTGATTACT CCAACCAGGT TGGAGGACAA ATTGGGGCCA TGGAGCATAT ATGTAGACCA TTGAGCTATAT ATTTAGACCA CTGATTACT CTGATTACT CTCAACATGGA ATTGGGGCCA TGGAGCATAT ATGTAGACCA TTGAGCATAT ATTTTGACCA CTTGTTCCCC CTACACAGGT CTGAGCATAT ATGTAGACCA CTGGGGCCA TGGAGCATAT ATGTAGACCA CTGGGGCCA CTGGGCCAC CTGGGCCAC CTGGGCCCC CTGCGCCCC CTGCTCCCC CTGCTCCCCC CTGGGGCCCC CTGCTCCCCC CTGCTCCCCC CTGCGGCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCGCCCC CTGCTCCCCC CTCCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTCCCCCCC CTGCTCCCCC CTCCCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCC CTGCTCCCCCC CTGCTCCCCCC CTGCTCCCCC CTC	CAGAGCCTGG GAACCCAGAT GCCTGGCGAT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CCCTGGCCAT CCACCAGAGAG GCAGACGAG GCAGACGAG GCAGCCAGAG GCAGCCACACCAC TGGAGTTATT TGACACCTAT TGACACCTAT CGATGGAGAG CCCTTGGAGT ATATCATGGA GGAGATATC TGGAGTTAAC TGGAGTTAAC TGGAGTTAAC CAAACTCAC CAAACTGCAC GAGGCCCAAA GGATAATGT CAAGCTGCAC CATCAAGTT GCGCGGCGGAG ATGCTACCCC CATCAAGTT CCTCCTCCCC CATCAAGTT CCTCCTCCCCC CTCCTCCCCC CTCCTCCCCC CTCCTC	CGAGGGGAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGTTT AGTGCCTCT GGTATTCAG CCTTCAAGTCCA GGTGCATGG GTTCATGTCA AGATCCAAGA ATCCATGTT CATGACTAC TTCTAACTG CATGACTAC TTCAACTG TTCAACTGT CATGACAGACCA GCAGAAAA CTCAGCACCG GGCAGAGCCT CTCACAGTCA GGTAGCACGG GCAGAGCCT TTCACAGTCA CAGTCATGGA CCAGTCATGGA CCAGTGATGGA CCAGTGATGGA CCAGTGATGGA CCAGTGATGGA CCAGTCATGGA CTCAGGAACCA CAGTCATGGA CTCAGGAACCA CAGTCATGGA CTCAGGACCAC CAGTCATGGA CTCAGGAACCA CTCAGGAACCA CTCAGGAACCC CAGTCATGGA CTCAGGACCAC CAGTCATGGA CTCAGGAACCC CAGTCATGCA CCAGTCCTTCC CACTGCTCC CACTGCTCC CACTGCTTCT CTCCTTGTCA ATCACAGAGGG ATCACAGAGGG ATCACAGAGGC ATCACAGAGGC ATCACAGAGGC ATCACAGAGGC ATCACAGAGGC ATCACAGAGGC ATCACAGAGGC ATCACAGAGGC ATCACAGAGGC TTCACAGAGAGC ATCACAGAGGC ATCACAGAGGC TTCACAGAACC ATCACAGAGGC ATCACAGAGC ATCACAGAGC TTCACAGAGC TTCACAGAGC ATCACAGAGC TTCACAGAGC TTCACAGAACC ACAGTCCATG CTCCTTGTCA ATCACAGAGGC TTCACAGAGAGC TTCACAGAGGC TTCACAGAACC ACAGTCCATG CTCCTTGTCA ATCACAGAGGC TTCACAGAGCC TTCACAGACAC ATCACAGAGC TTCACAGACAC ACAGTCCATG CTCCTTGTCA ATCACAGAGGC TTCACAGACAC ATCACAGAGC TTCACAGACAC ACAGTCCATG CTCCTTGTCA ATCACAGAGC	120 180 240 300 360 420 600 660 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1680 1740 1860 1920 1980 2040 2100 2160 2220

•						TCCAACTACC	
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•						CAAGAGATAA	2760
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		CCCCCATAAC					3060
		CTTCGGAGAG GTTCCATGAC					3120 3180
		CAACTGGCTG					3240
15		CAGTGGGTGC					3300
		GATCATCAAG					3360
						AAGGGCTACA	3420
		GGACCAGACG					3480
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		GTTGTTCCTG				TGGGACGAGG	3660 3720
						AACGCAGGCG	3780
		CACAGCCACA					3840
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	AGATGGAGAG	TTCCAAGCAG	CACTTCTTCC	AČCTCTGGAA	CGACTTCGCT	TACATTGAAG	3960
		GAAGTACCCC					4020
		CGTGGTGAGC					4080
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						TTCCGGCCCA	4320
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						CAGCCCCTGC	4440
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		TGCCACCTGC					4560
						CCTATCTGTG	4620
						ACAGCAAAGA	4680 4740
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		TCTTTACTCC					4860
						ACCTTTCAGG	4920
		TGGCAGGTTT					4980
	GAGATTCCAG	AAATCTGCTG	CATTTCACAT	GGTACCTGGA	ACCCAACAGT	TCATGGATAT	5040
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						GTGCACTGCA	5160
		GAGAAATCAC					5220
		GCTTCTTGCT CTGGAATGGC					5280 5340
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		AGCAATGGGC					5460
						CTTAGGGCCT	5520
		TCATCCAGGG					5580
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						TGCTCCCAGC	5880
		CCGCCCTCCC					5940
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						CAAAGGCCAG	
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						GAATGTCTTT	6660
						CATATGTTTC	
						AGCCAATATC	
75						TCCTTGTTAT	-
, ,						CTCTGAAATG TGTATAGAGT	
						TTCTATTTAT	
						CTTAAATGTC	
00							
80		95 Protein					
		cession #:					
	1	11	21	31	41	51	
	MCAACRODEL	Premitation	 TI.TCPDGATO	TWANCEDOC	 	I DODHENGICO	60
85						DQDHHVHIGQ SALCPFQGNF	
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	ERSWGHRGVI	GIQPDPYYGL VHVIDPKSGT	VIHSDRFDTY	RSKKESERLV	QYLNAVPDGR	ILSVAVNDEG	180 240
		AMTKLGSKHP PNVSLSSEWV					300 360
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		VGLLSRNIIV					540
		LVGQYPIHFH HCFFTEDGPE					600 660
10		STFWMANPNN					720
		SNYRAGMIID					780
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		NNAWQSCPHN					960
15		SYLTKNDNWL					1020
		EGALTRSTHY					1080
		SILSDVHNRL FAFCSMKGCE					1140 1200
		LEVKMESSKQ					1260
20		GIPWQLFNYV					1320
	QMAFVGFKGS	FRPIWVTLDT	EDHKAKIFQV	ABIBAAKKK	L		
		96 DNA sequid Accession		136 and AVA	11 666		
25		mence: 63-32		iso and Akvi	71000		
	1	11	21	3 J.	41 I	51 1	
	CAGGAATTTG	TGGCGGAGAG	GGCAAATAAC	TGCGGCTCTC	cccccccc	GATGCTCGCA	60
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30		GCAGCAGCAG					180 240
		GGGTGCTCCA AAAGCGGCTT					300
		CATCTCTGAG					360
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		CTCCCACGCC CATGTCTCAG					840 900
		TCTGTCTCTG					960
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		CTTCCAGAGC ACCGAACATC					1140 1200
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		CCCCATAGAT					1440 1500
		AGGGCTACCT					1560
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		GCCAGGGTCA TGATCCCAAC					1740 1800
		GCATTATCGC					1860
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60		GACGCAGCAT ACATATTCGG					1980 2040
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		CCATGATGAT					2160
65		CAGCTCCTCC					2220
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		ATCCTTCCAG					2460
70		CGATGCTGGG					2520
70		CAGTCTCCCT					2580
		CACATTTGTG					2640 2700
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		TACGGACGGA TGTGGACCCT					2940 3000
		GACCAATGAG					3060
00	TTTCCTTGGG	GGCCACCTCC	GTTGTGAATA	ACCCACTGT	CTCCAAGATG	GATGGCTCCC	3120
80		CAGTGCAGAT					3180
		CTTCCTGGAA GCAGACACAG					3240 3300
		TTCTTTTTCT					3360
0.5		GCAAGTGCTA					
85						_	
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		97 Proteir					
	Protein Acc	ession #: N 11	P_065169.1 21	31	41	51	
5	MSRRKQAKPQ	HINSEEDQGE	QQPQQQTPEF	ADAAPAAPAA	GELGAPVNHP	 GNDEVASEDE	60
				KKNCTKNPPV SVVYLKTETA			120 180
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10				AVALLSQKAG PSALLPQAPG			300 360
••	GKPPNISAVD	VKPKDEAALY	KHKCKYCSKV	FGTDSSLQIH	LRSHTGERPF	VCSVCGHRFT	420
				AGNGIPYALS PSPESEGGPT			480 540
1.5	TPEPGSETLK	LQQLVENIDK	ATTOPNECLI	CHRVLSCQSS	LKMHYRTHTG	ERPFQCKICG	600
15				CQKKPTNAVM IDVEEVSSQB			660 720
	TLGFAMMASL	DAPGKVGPAP	PNLQRQGSRE	NGSVESDGLT	NDSSSLMGDQ	EYQSRSPDIL	780
				SSENSRTEME			840 900
20	NICGRAFTTK	GNLKVHYMTH	GANNINSARRG	RKLAIENTMA	LLGTDGKRVS	EIFPKEILAP	960
		SATDGVPKHQ		QSGGVPTLPV AVS	SLGATSVVNN	ATVSKMDGSQ	1020
25		98 DNA sequ		•			
25		ld Accession Jence: 553		512.2			
	1	11	21	31	41	51	
20	TTCTCCCGCA	ACCTTCCCTT	CGCTCCCTCC	CGTCCCCCCC	AGCTCCTAGC	CTCCGACTCC	60
30				CGCCGAACCA			120 180
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				CTGACCTCAT CCCGAAGACA			300 360
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40				GAGGCGTTCA GCCCACGGGG			1020 1080
				GTCTGCAGCC			1140
50				TTCCATCCCG			1200 1260
50		CTCCATCGGG AAACACCCTT		ACAGCAGCAT CCCCCC	CTTCAAACAT	GTACAAAATC	1320
	Seg ID NO:	99 Protein	sequence				
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55	1	11 	21 	31 	41	Ï	
				TLCGGELVDT ERDVSTPPTV			60 120
60				EAKRHRPLIA			
UU	Sea ID NO:	100 DNA se	nuence				
	Nucleic Ac	id Accessio	n #: NM_004	217.1			
	Coding seq	uence: 58 11	1092 21	31	41	51	
65		(777)		AGCTCTCCTC	000000000	TOTALCOATO	60
						ATCTGGCCTG	120
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70	AGTGGGACAC	CCGACATCTT	AACGCGGCAC	TTCACAATTG	ATGACTTTGA	GATTGGGCGT	300
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80	CCAGAGATGA	TTGAGGGGCG	CATGCACAAT	GAGAAGGTGG	ATCTGTGGTG	CATTGGAGTG	840
οU						CAACGAGACC GGGAGCCCAG	900 960
	GACCTCATCT	CCAAACTGCT	CAGGCATAAC	CCCTCGGAAC	GGCTGCCCCT	GGCCCAGGTC	1020
^-						TGCCCTTCAA	
85						CCTCCTTTGT	1200

TTAATAAAGG CTGAAGCTTT TTGT

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Seq ID NO: 101 Protein sequence
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                    11
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                                                                                     60
        SSGTPDILTR HPTIDDFEIG RPLGKGKFGN VYLAREKKSH PIVALKVLPK SQIEKEGVEH
                                                                                   120
        QLRREIEIQA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI
                                                                                    180
10
        MEBLADALMY CHGKKVIHRD IKPENLLIGL KGELKIADPG WSVHAPSLRR KTMCGTLDYL
        PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA
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25
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                                                                                    480
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        GTCCCTGGCG CTGATCTTCA ATAGCCTCCA AGGCCAACTT CATCCAACAC CTGATCTGAA
30
       GCCCTTGCTC TCCAATGAGG TAATCTGGCT AGACAGCAAG CAGATCCGAC AGGAGGAAAT
                                                                                    720
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                                                                                    780
        GAGGAGTGTC TACATCGAAA GTCGGATAGG TACCAGCACC AGCTTCGACA GTGGCATTGC
                                                                                    840
        TGGGCTCTCT TCTATCAGTC AGTGTACCAG CAGTAGCCAG CTGGATGAAA CAAGTCATCG
                                                                                    900
        ATGGGCACAG CCAGACACTG CCCCACTACC TGTCCCGGCA AACATTCGCT TCTCCATCTG
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70		115 Protein		_			
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45	TGTTTATTTC GATACGCACC CCTCTGCCCT	CTCCTCCTTG CACAGTGGCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT	ATAAATGTTA TAACCGTGTC GAGTGAGGCT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG	CCCACACTCG AACACTGGCA CGCTGGCTCC	120 180
45	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT	120 180 240 300
45	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC	120 180 240 300 360
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG	120 180 240 300 360 420
45 50	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG	120 180 240 300 360
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC GTCCACACGG	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG	120 180 240 300 360 420 480
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGAGGCTTCCC	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCCGA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA	120 180 240 300 360 420 480 540
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCCGG GTCTTCCTGC AATCCAGCCC CCCGGGACCGC GATCTGCCCT GTAACGGATG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGCAGACCCG CGAGCTTCCC TGTACCGGAG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC	CACGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT	120 180 240 300 360 420 480 540
	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCCGG GTCTTCCTGC AATCCAGCCC CCCGGGACCGC GATCTGCCCT GTAACGGATG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT	ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGCAGACCCG CGAGCTTCCC TGTACCGGAG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC	CACGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT	120 180 240 300 360 420 480 540
50	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAGA AGACCTAATA	ACGTCTCCAT GATTOGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGACCCG CGAGCTTCCC TGTACCGGAG GTCACACCAG	ATAAATGTTA TAACCGTGTC GAGTGAGGCGG CCAGTCTCCG CCTCGGGCAC GTCCACAGG TCGTGGCCGG AAGGAGGATC CTACCATTTT	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CCGGAACAATG AAAAGAGGTG AAAGGAAAAA	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA	120 180 240 300 360 420 480 540 600 660
50	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCCAGGT AGACCTAATA TTTTGGAACT	ACGTCTCCAT GATTOGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACCG	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACCGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT	CACGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGAAAAA GACGGTGGAG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGGACCCCA TGGTCCTCAG	120 180 240 300 360 420 480 540 600 660 720
	TGTTTATTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGATCCC TGTACCGGAG GTCTACACCAG GTGTTCACGGAG CATATCAAGC	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCG CGAGTCTCCG CTCCACACGG TCCTCACACGG AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCAGAGG TCCCCAGGT CCAGGGGCTA CAGAACAATG AAAAGAGAAAAA AAAGGAAAAAA CACGGTGGAG CCTGTCATTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCAG CACCTTGGT CACCTGGCT	120 180 240 300 360 420 480 540 600 660 720 780
50	TGTTTATTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCCAGGT AGACCTAATA TTTTGGAACT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CCAGACCCG CCAGACCCG GTACCACCAG GTCTCACGCAG GTGTTCACGCAG CATATCAAGC	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCG CGAGTCTCCG CTCCACACGG TCCTCACACGG AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA	CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCAGAGG TCCCCAGGT CCAGGGGCTA CAGAACAATG AAAAGAGAAAAA AAAGGAAAAAA CACGGTGGAG CCTGTCATTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCAG CACCTTGGT CACCTGGCT	120 180 240 300 360 420 480 540 600 660 720
50	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCAGAAACCT GCACTATGCA	ACGTCTCCAT GATTCGGGGG ACTCACCAT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGAGACCCG TGTACCGGAG GTCACACCAG GTGTTCACCG GTGTTCACAG GTGTACAGG GTGGAATTAT	ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCG GCACTCTCCG GTCCACACGG TCCTACGCGA AAGGAGGATC CTACCATTT ATCATATGC TCTTCAGAA TTGAAGGATT	CACGGGCATC ATTTGCTTGC CGGGTCTGGGGGAGG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGGAAAAA GACGGTGGAG GCTGTCATTG GAAGGCATTT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CCAGGGAGTAG	120 180 240 300 360 420 480 540 600 660 720 780
50	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGAT TTAAGGGTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCAGAAAACCT GCAGAAACCT ATCGACTGCTTTT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CCCAGACCCG CGAGCTTCCC TGTACCGGA GTCACCCAG GTGTTCACGG CATATCAAGC CATATCAAGC CTGGAATTAT CAGCCAAACC	ATAAATGTTA TAACCGTGTTA GAGTGAGGCG CAGGGGCGC CCTCGGGCAC GTCCACACGG TCGTGGCGAC CTACCATTT ATCATATGCT CTCTTCAGAA TTGAAGGATT TCAACATGGA	CACGGGCATC ATTIGCTIGC CGGGTCTIGGG CCTGGGGGAG CCGCAGAGG TGCCCAGGT CCAGGGGCA CAGGACAATG AAAAGAGGTG AAAGGGAAAAA GACGGTGAG CCTTCATTIG AAAGCATTT TAGAATGTAT	CCCACACTCG AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGG CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAGGAGGTAG CACCCTGGCT CAGGAGGTAG CGCTCTGCTG	120 180 240 300 420 480 540 600 660 720 780 840 900
50	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTT GCCCACGAGT CTCCGCAGAG AGACCTAATA ATTTTGGAACT GCAGTAGCACTATGCA GCACTATGCA TCCACTAGTT TCTGCCGGTA	ACGTCTCCAT GATTCGGGGG ACTCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACGG CATATCAAGC CTGGAATTAT CAGCCAAACC TTTGACAACAC	ATAAATGTTA TAACGGTGTC GAGTGAGGCTG CTGGGGGGG CGAGTCTCCG CTCCGGCGA AGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGGAT TCAACATCT TCAACATCT TCAACATCT TCAACATCT TCAACATCT TCAACATCT TCAACATCT TCAACATGGA AAGAGCTCTT	CACGGCATC ATTIGCTIGC CGGGTCTGGGCAG CCCGAGGAG CCGCAGAGG TGCCCCAGGT CCAGGGGCTA CAGGACAATG AAAGAGATA AAAGAGATA AAAGGATAA ACCGTACATG GAAGGATTAT TAGAATGTAT AGAGTGTATT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGGGACTT CGAGGGGTT CCAGACCTCAG CACCTTGGT CACCCTGGCT CGAGGACTTG CACCCTGGCT CGAGGACTTG CACCAGGTTTG	120 180 240 300 420 480 540 600 660 720 780 840 900 960
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATG TTTTGGAACT GCAGAAACCT TCGACATGTA TCGACATGTT TCTGCCGGTA TCAAGAATGG TCAAGAATGG	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CCAGACCCG CCAGACCCG TGTACCGAG GTCACACCAG GTCACACCAG CATATCAAG GTGGAATTAT CAGCCAAAC GTCCCATATT	ATAAATGTTA TAACCGTGTC GAGTGAGGCTC CTGGGGGGCGC CGACTCTCCG CTCCACACGG TCCTCGGCAC TCCTCACACTGT ATCATATGCT CTCTCAGAA TTGAAGGATT TCAACATGT TCAACATGT TCAACATGT CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC	CACGGCATC ATTIGCTIGC CGGGTCTTGGC CGGGTCTGGGGGAG CCGCGAGAGG CCCAGGGCTA CCAGGGCTA AAAGAGGTG AAAGAAATG AAAGAGTT TAGAATGTAT TAGTCTGTAT TAGTCTGTAT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GGACCCTTGG AAGGATTGCA GTGGGACCTCA GTGGGACCCCA CGACCCCA CGACCCCA CGACCCCA CACCTGGCT CGAGGAGTAG CGCTCTGCT CAACAGCTTCA ATTCGTCCTA ATTCGTCCTA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATG TTTTGGAACT GCAGAAACCT TCGACATGTA TCGACATGTT TCTGCCGGTA TCAAGAATGG TCAAGAATGG	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CCAGACCCG CCAGACCCG TGTACCGAG GTCACACCAG GTCACACCAG CATATCAAG GTGGAATTAT CAGCCAAAC GTCCCATATT	ATAAATGTTA TAACCGTGTC GAGTGAGGCTC CTGGGGGGCGC CGACTCTCCG CTCCACACGG TCCTCGGCAC TCCTCACACTGT ATCATATGCT CTCTCAGAA TTGAAGGATT TCAACATGT TCAACATGT TCAACATGT CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC	CACGGCATC ATTIGCTIGC CGGGTCTTGGC CGGGTCTGGGGGAG CCGCGAGAGG CCCAGGGCTA CCAGGGCTA AAAGAGGTG AAAGAAATG AAAGAGTT TAGAATGTAT TAGTCTGTAT TAGTCTGTAT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GGACCCTTGG AAGGATTGCA GTGGGACCTCA GTGGGACCCCA CGACCCCA CGACCCCA CGACCCCA CACCTGGCT CGAGGAGTAG CGCTCTGCT CAACAGCTTCA ATTCGTCCTA ATTCGTCCTA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATCATTGG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCACGTGTA GCTCTGCAGCT CTCCGCAGGA AGACCTAATA TTTTGGAACT GCAGAGAAACCT TCGCAGGA TCGACTGCTTT TCTGCCGGTA TCGACTGTTT TCTGCCGGTA TCAAGAATGG AACTGTTT TCTGCCGGTA ACAAGAATGG	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGCCCC TGTACCGGA GTCACCCAG GTGTTCACCG GTGTTCACCG GTGTACCACAC GTGTTCACCG CTTATCAAGG CTTGACAAAC TTTGACAAAC TTTGACAAAG TCTCTTGGAA TCTCTTGGAA	ATAAATGTTA TAACCGTGTTC GAGTGAGGCG CCTCGGGCAC CCTCGGGCAC GTCCACACGG TCGTGGCGAC CTACCATTTT ATCATATGCT CTCTTCAGAAT TCGAACATGGA AAGAGCTCTT CAACATCGC TCAACATGGA AAGAGCTCTT CAACATCTGC TCAAGAAGCC	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAAGAGATG GAAGGCATT TAGAATGTAT TAGAATGTAT TAGCAAAGCC TAGCTCGTATT TAGCAAAGCC TAGCTCGTATT TAGCAAAGCC	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGACCTC TCAGACCCCA TGGTCCCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCTG CAACAGCTTG CAACAGCTTG CAACAGCTTG CATCGTCCTA CTGCTCTAG CTGCTCTTTG CTCCTTAG CTGCTCTTTTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50 55	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGATA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TATATTGAAT TGATTGGT TGATTCATTGG TACTCTTGAG	CTCCTCCTTG CACAGTGGCI GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCAGTAGTA GCACTATCA TCACCTGTTT TCTGCCGGTA TCAAGAATGG AACTGAGCCT CCCAGTGGGA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CCCGCGCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACGG CATATCAAGC GTGGAATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG	ATAAATGTTA TAACCGTGTTC GAGTGAGGCGG CGAGTCTCCG CCTCCGGGCGA TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA TTGAAGGATT TCAACATCGGA AAGAGCTCTT CAACATCTGC CAACATCTGC CAAGAAGCC CCAAGTAGAAC	CACGGCATC ATTIGCTIGC CGGGTCTIGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGATG AAAGAGATG GAAGGATAAA GACGTGGAG CCTGTCATTG GAAGGCATTT TAGAATGTAT TAGATGTAT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA	CCCACACTCG AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGG GCACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGT CGACACCTGGT CGACACCTGGT CACACCTGGT CACACCTGGT ATTCGTCCTG ATTCGTCCTG GTGCTCTTTG GTGTCCTTTTG GTGTCCTTTTG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1140
50 55	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTTA TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT TGAAGGCAAC TGAAATTGGA CATTCATTGG TATCATTGG TATCATTGG CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG GGGCCAATCC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTTA GCTCTGCAGAC CTCCGCAGAGA AGACCTAATA ATTTTGGAACT GGAGAAACCT GGAGAAACCT TCTGCCGGTA TCTGCCGGTA TCAGGAGATA TCTTGCCGGTA CCCAGTGGGA CAAGTATGTA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCCC GTACCACC GTGTTCACCGGAG GTCATCACACCAC GTGTTCACAGC CATATCAAGC CATATCAAGC TTTGACAAACC TTTGACAAACC TTTGACAAACC CTTTGACAAACC CTTTGACAAACC CTTTACTTGAGA CCCTTATTTT AGAGCCTGGA	ATAAATGTTA TAACGGTGTC GAGTGAGGGCG CGAGTCTCCG CCTCCGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA TTCAACATGCT TCAACATGT AAGAAGCTCTT CAACATCTGC TCAAGAAGC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC	CACGGGCATC ATTIGCTIGC CGGGTCTTGGGCAG CCCGGGAGAGG CCCCAGGT CCAGGGGCA CCGGACAATG AAAGAGGTG AAAGAGAAAA ACGGAACAATG AAAGAGAAAA ACGGAACAATG AAAGAGAATT AAAGAGATT AAGATGTAT AGAATGTAT TAGAATGTAT TAGCAAAGCC TTTTAATCCA TGGGGACTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCTGGCT CGAGGAGTAG CGCTCTGGTG CACCTGGTC CAACAGCTTG ATTOGTCCTA CTGCTCTTA ATTOGTCCTA ATTOGTCCTTA AAGATGGAG	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1080 1140
50 55	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTTA TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT TGAAGGCAAC TGAAATTGGA CATTCATTGG TATCATTGG TATCATTGG CATCATTGAG CATCATTGAG CATCATTGAG CATCATTGAG GGGCCAATCC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTTA GCTCTGCAGAC CTCCGCAGAGA AGACCTAATA ATTTTGGAACT GGAGAAACCT GGAGAAACCT TCTGCCGGTA TCTGCCGGTA TCAGGAGATA TCTTGCCGGTA CCCAGTGGGA CAAGTATGTA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC CGAGCCCC GTACCACC GTGTTCACCGGAG GTCATCACACCAC GTGTTCACAGC CATATCAAGC CATATCAAGC TTTGACAAACC TTTGACAAACC TTTGACAAACC CTTTGACAAACC CTTTGACAAACC CTTTACTTGAGA CCCTTATTTT AGAGCCTGGA	ATAAATGTTA TAACGGTGTC GAGTGAGGGCG CGAGTCTCCG CCTCCGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA TTCAACATGCT TCAACATGT AAGAAGCTCTT CAACATCTGC TCAAGAAGC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC	CACGGGCATC ATTIGCTIGC CGGGTCTTGGGCAG CCCGGGAGAGG CCCCAGGT CCAGGGGCA CCGGACAATG AAAGAGGTG AAAGAGAAAA ACGGAACAATG AAAGAGAAAA ACGGAACAATG AAAGAGAATT AAAGAGATT AAGATGTAT AGAATGTAT TAGAATGTAT TAGCAAAGCC TTTTAATCCA TGGGGACTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCTGGCT CGAGGAGTAG CGCTCTGGTG CACCTGGTC CAACAGCTTG ATTOGTCCTA CTGCTCTTA ATTOGTCCTA ATTOGTCCTTA AAGATGGAG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1140
50 55	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAA TGAATTGGA CATTCATGG TACTCTTGGA CATCCTTGG TACTCTTGGA GGGCCAATCC GGAATTACCG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATGCA TTTTGGAACT GCACTATGCA TCGACAGTGTA TCAGCAGTGTA TCAGCAGTGTA TCAGCAGTGTA TCAGCAGTGTA CCAGTGGGTA TCAAGAATGG AACTGAGCCT CCCAGTGGGA CAAGTATGTA CAAGTATGTA CTCATCTCTT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CCAGACCCG CCAGACCCG GTACCACACCAG GTCACACCAG GTCACACCAG CATATCAAGC GTGGAATTAT CAGCCAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGA TTTGCCCAAT TTTGCCCAAT	ATAAATGTTA TAACCGTGTC GAGTGAGGCTC CTGGGGGGCG CGAGTCTCCG CTCCACACGG TCCTCACACGG TCCTCACACTTTT ATCATATGCT CTCTCAGAA TTGAACGATT TCAACATGTT CAACATCTT CAACATCGT CAACATCGC TCAAGAAGCC CAAGTGGAAC GTGAACATGGAAC GTGAACATGGAAC GTGAACATGGAAC	CACGGCATC ATTIGCTIGC CGGGTCTTGGC CCGGGGGGAGG CCGCGAGAGG CCCACGGT CCACGGGCTA AAAGAGAAAG AAAGAGGTG AAAGGAAAAG CCTGTCATTG GAAGCATTT TAGAATGTAT TAGCCAAAGC CTTTAATCCA AGGGTACTGC AGGACATCG AGGACATCG AGGACATCG AGATAATCGG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA CACCCTGGCT CGAGGAGTAG CACCTTGGT CAACAGCTT CAAGGATTGC AATTCGTCTTA ATTCGTCCTTA ATTCGTCCTTA CTGCTCTTTG GTGTCCCTGGT TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1260
50 55 60	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGAT ATAACGAT ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGGAATTACGG TCCTGTGGCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCGACTATTT TCTGCCGGTA TCAAGAATAGCA TCAAGAATAGCA TCAAGAATAGCA TCAAGAATAGCA TCAAGAATAGCA ACTGAGCCT CCCAGTGGGA CAAGTATGTT CTATGAGAGAGAGAGAGAAGAATAGTAT CTATGGAGAGA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCG CCAGACCCG CGAGCTTCCC TGTACCGGA GTCTACCGAG GTGTTCACCGG GTGTTCACGG CATATCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAAC CTTTGACAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT ACAGCCTGAA TTTGCCCAAT GACCATCAGA GACCATCAGA	ATAATGTTA TAACGGTGTTA GAGTGAGGCG CCTCGGGCAC CCTCGGGCAC GTCCACACGG TCGTGGCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA ATTGAAGGATT CAACATCTG AAGAGCTCTT CAACATCTGC AAGAGCCC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC AGGTAGAAC TCACTGAAGT TCACTGAAGT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGGTG AAAGGGTAG GAGGCATTT TAGAATGTAT TAGATGTAT TAGGATATGCA GGGAATTGC GGGAACTATG	CCCACACTCG AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGG CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAGCACCTGGCT CAGCAGGTTAG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTTA ATTCGTCCTTA AAGATGGCAG AATCTTTTC	120 180 240 300 360 480 540 660 720 780 840 900 960 1080 1140 1200 1260
50 55	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGAT ATAACGAT ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGGAATTACGG TCCTGTGGCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCGACTATTT TCTGCCGGTA TCAAGAATAGCA TCAAGAATAGCA TCAAGAATAGCA TCAAGAATAGCA TCAAGAATAGCA ACTGAGCCT CCCAGTGGGA CAAGTATGTT CTATGAGAGAGAGAGAGAAGAATAGTAT CTATGGAGAGA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCG CCAGACCCG CGAGCTTCCC TGTACCGGA GTCTACCGAG GTGTTCACCGG GTGTTCACGG CATATCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAAC CTTTGACAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT ACAGCCTGAA TTTGCCCAAT GACCATCAGA GACCATCAGA	ATAATGTTA TAACGGTGTTA GAGTGAGGCG CCTCGGGCAC CCTCGGGCAC GTCCACACGG TCGTGGCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA ATTGAAGGATT CAACATCTG AAGAGCTCTT CAACATCTGC AAGAGCCC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC AGGTAGAAC TCACTGAAGT TCACTGAAGT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGGTG AAAGGGTAG GAGGCATTT TAGAATGTAT TAGATGTAT TAGGATATGCA GGGAATTGC GGGAACTATG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA CACCCTGGCT CGAGGAGTAG CACCTTGGT CAACAGCTT CAAGGATTGC CAACAGCTT CAACAGCTT ATTCGTCCTA CTACCTCTTT GTGTCCTCTA CTGCTCTTTG GTGTCCTCTA GTGTCCTCTA GTGTCCCTGGT TGTCAGCAGG TGTCAGCAGG	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1260
50 55 60	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GCGCCAATCC GGAATTACG TCCTGTGGCT TTTACTGGAT TTTACTGGAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCTCTGCAGCT CTCCGCAGAG AGACCTAATA ATTTTGGAACT GCAGTAGTAT TCTGCCGGTA TCAAGAATGT TCTGCCGGTA TCAAGAATGA CCCAGTGGTA CCCAGTGGTA CCCAGTGGGA CAAGTATGAA CTCATCTCTT CTCATCGCGGA AAATGAAGAT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CCCCACCAC CGCAGCCCGC CGAGCTCCC CGAGCTCCC CGAGCTCCC CGAGCTCCC CGAGCTCCC CGAGCTCCC CGAGCTTCCC TGTACCGAG GTCTCACCAG GTCTCACAG GTCTCACAG GTCGAATTAT TCAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTTT AGAGCCTGGA TTTGCCCAT TTTGCCCAAT CGACCATCAGA GGCATCAGA GGAGAAGAAA	ATAAATGTTA TAACGGTGTC GAGTGAGGGCG GAGTCTCCG CCTCCGGGCA TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGAGT TCAACATCTGC AAGAGCTCTT CAACATCTGC TCAAGAAGCC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC AAGTGGAAC AAGTGGAAC AACTGGCAAC	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGATG AAAGAGAAA AACGGTGGAG CCTGTCATTG GAAGCATTT TAGATGTAT TAGATGTAT TACCAAAGCC TTTTAATCCA TGGGGACTCC TGGGGACTAC TCCTCCACTA TCCTCCACTA	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGGTT CGAGAGCTTG CACCTGGCT CACCCTGCT CAACAGCTTG ATTCGTCCTA CTGCTCTTTG GTGTCCTCTTTA AGATGGAG TGTCAGCAGG AATCTTTTTC GATGGCATCA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1232 1380
50 55 60	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCCG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGTTA TTAAGGCTTA ATAATCTGGT ACTTTGGATG CATCAGCTTT ATAATAATA TGAGGGCAAC TGAAATTGGA GAATTCATGG GTCTTTGAG GCGCCAATCC GGAATTACGG TCTTTGGGT TTTTACTGGAT TTTTCCAGG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTTA GCTCTGCAGCT CTCCGCAGAGA AGACCTAATCA GGAGAAACCT TCTGGAGCT TCTGCAGT TCTGCAGTT TCTGCCGGTA TCAGCATGTTT TCTGCCGGTA TCAGCAGTGTTT CCAGTGGGA ACTGAGCCT ACTGAGCAT CCAGTGGGA ACTGAGCAT CCAGTGGGA ACTGAGCAT CCAGTGGGA ACTGAGCAT CTCATCTCTT CTATGGAGAG AAATGAGAGA AGTGACAAGG	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCCTCC TGTACCGGAG GTCACACCAG GTCTACACAC GTGAATTACAGG CATATCAAGC CATATCAAGC CATGCCAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGAA TTTGCCCAAT GACCATCGA TTTGCCCAAT CACCATCAGA CACCATCACAC CACCATCACAC CACCATCACAC CACCATCACAC CACCATCACAC CACCATCA	ATAAATGTTA TAACGGTGTC GAGTGAGGGCGG CGAGTCTCCG CCTCCGGGCAC CTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA TTCAACGATT TCAACATGGA AAGGACTCTT CAACATCTGC TCAAGAAGCCC TCAAGAAGCC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC AAGGTGGAAC TCACTGACGA TCACTGACGA TCACTGACGAC TCACTGACGAC TCACTGACGAC TCACTGACGAC TCACTGACGAC TCACTGACGAC TCACTGACGAC TCACTGCACAC TCGACCTGGCAC	CACGGGCATC ATTTGCTTGC CGGGTCTTGGGGGAG CCCGGGGAGAG CCCCAGGT CCAGGGGCA CCAGGGCAA AAAGAGGTG AAAAGAGGTG AAAGGAAAA AGAGGAATA TAGAATTTA TAGAATTTA TAGAATGTAT TAGAATGTAT TAGCAAAGCC CTTTAATCCA TGGGGACTGC AGATAATGGG GGAACTATG TCCTCCACTA ACATCAGTGG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTGG AAGGATTGCA GTGGGACCTCA GTGGGGACTCA GCCCTGGCT CAGCACCCCA TGGTCCTCAG CACCTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTTA ATTCGTCCTTTTG ATTCGTCCTTTTG AAGATGGCAG TGTCAGCAGG AATCTTTTTC AATGGCATCA GGTGAATTTA	120 180 240 300 360 420 660 660 720 780 840 900 1020 1020 1140 1200 1260 1320 1380 1440
50 55 60	TGTTTATTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGACCGC GATCTGCCT GTAACGGAT TTAAGGATA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATCATTGG TACTCATTGG TACTCATTGG TCCTGTGGCT TTTACTGGAT TTTCTTCAGG AGGTCTTCAGAG AGGTGTCAGA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCACAGTGTA GCTCTGCAGC CTCCGCAGGA AGACCTAATA TTTTGGAACT TCTGCAGTA TCAGATGCA TCACAGTTT TCTGCCGGTA TCAAGAATGC AACTGAGTC CCCAGTGGGA CAAGTATGTT CTATGAGCCT CCCAGTGGGA AATGAGAGA AATGAAGAG AAATGAAGAG GAGATACCTC	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCG CCAGACCCG CGAGCTTCCC TGTACCGGA GTCTACCGGA GTGTTCACGG GTGTTCACGG GTGTACAACC TTTGACAAACC TTTGACAAAC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCAAT TTTGCCAAT GACCATCAAA GCGTGCATTCACAAA GCGTGCATTCACAAAC CTTATTTTT AGAGCCTGGAT GACCATCAAA	ATAATGTTA TAACCGTGTTA GAGTGAGGCG CCTCGGGCAC CCTCGGGCAC CTACCACACGG TCCTACCATTT ATCATATGCT CTCTTCAGAA AAGAGGATCTTT CAACATCGA AAGAGCTCTT CAACATCTGC CAAGTGGAAC AAGTGGAAC AAGTGGAAC AAGTGGAAC AAGTGGAAC TCACTGAAGT TCACTGAAAGAT TCACTGACATCTAC AACTGGCAAC AAGTGGAAC TCACTGAAGT AACTGGCAAC TCACTGAAAC TCGACTGGCAAC TCGACTGGCAAC TCGACTGAAAC TCGACTGGCAAC TCGACTGAAAC TCGACTGAAAC	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG ANAAGAGGTG ANAAGAGATG ANAGGAAAAA GACGTGGAG CCTTCATTG TAGAATGTAT TAGACTGTAT TAGACTGTAT TAGCAAAACC CTTTAATCCA TGGGACTGC TGTTAATCGA GAGTAATTGGAGACTAT TCCTCACTA ACATCAGTGG	CCCACACTCG AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC CAGCCTTGGTGCAG CGACCCTTGG AAGGATTGCA CTGGTCCCAC CGGTCCTCAG CACCCTGGCT CAGAGACTCCA CGCTCTGCTG CAACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTT AAGATGGGAG TGTCAGCAGG AATCTTTTC GATGGCATCA CGTGAATTTA CGGGAACAGGG	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1260 1320 1320 1440 1500
50 55 60	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGATG ATATTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCTTGAG GGGCCAATCC GGAATTACG TCCTTTGGT TCTTCCAGG AGGTGTCAGA TTTACTGGAT TTTACTGGAT TTTTCTCCAGG AGGTGTCAGA TGAAGAGAGAT TTGAAGAGAGAT TGAAGAGAGAT TGAAGAGAGAG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTAATA TCTTGCAGCT TCTGCAGGT TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA CACAGTGGA CAAGTATGTA CTCATCTCT TCTTGGAGCG CAAGTATGTA TCTAGGAGAG CAAGTATGTA CTCATCTCTT TCTTGGAGAG AAATGAAGAT AGTGACAAGG GGGATACCTC GTTTGGCTCT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACCGG GTGACACCAG GTGTTCACAGAG CTTGACAAAG CTTGACAAAG CTTGACAAAG CTTTGACAAAG CTTTGACAAAG CTTTGACAAAG CTTTATTTT ACAGCCTGAA TTTCCCCAATTT ACAGCCTGAA CCGTACATCAGA CGGAGAAGAAG CGTGCATCAGA CGGTGCATCC ACCATGGAT GGTACAGCC GGTACAGCC GCGATGGATG GGTACAGCC	ATAATGTTA TAACGGTGTC GAGTGAGGGCG CCTGGGGCGC CCTCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA TTCAACATCGG AAGAGCTCTT CAACATCTGC CAACATCTGC CAACATCTGC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC CAAGAAGCAC TCAAGAAGCAC TCAAGAAGCAC GTGAAGCAC ACTGGAAC GTGTGAACA GTGTGAAC GTGTGACAC GTGTTGACAC GTGTTGACAC GTGTTGACAC GTGTTGTTTG	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGAATA GACGTGGAG CCTTCATTG GAAGGCATTT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGCAAAGC CTTTAATCCA TGGGGACTAC GGGAACTAT TCCTCACTA ACATCAGTGG GCCAGTTTCT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGG CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGTT CGAGACCTC CAGCGTCTTG CAACAGCTTG ATTCGTCCTG ATTCGTCCTG ATTCGTCCTA ATTCGTCCTT AGAGAGGAGA ATCTTTTTC GATGGCATCA GGTGAATTTA GGGAACAGAG GATATACTGT	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500 1560
50 55 60 65	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGATG ATATTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCTTGAG GGGCCAATCC GGAATTACG TCCTTTGGT TCTTCCAGG AGGTGTCAGA TTTACTGGAT TTTACTGGAT TTTTCTCCAGG AGGTGTCAGA TGAAGAGAGAT TTGAAGAGAGAT TGAAGAGAGAT TGAAGAGAGAG	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTAATA TCTTGCAGCT TCTGCAGGT TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA CACAGTGGA CAAGTATGTA CTCATCTCT TCTTGGAGCG CAAGTATGTA TCTAGGAGAG CAAGTATGTA CTCATCTCTT TCTTGGAGAG AAATGAAGAT AGTGACAAGG GGGATACCTC GTTTGGCTCT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACCGG GTGACACCAG GTGTTCACAGAG CTTGACAAAG CTTGACAAAG CTTGACAAAG CTTTGACAAAG CTTTGACAAAG CTTTGACAAAG CTTTATTTT ACAGCCTGAA TTTCCCCAATTT ACAGCCTGAA CCGTACATCAGA CGGAGAAGAAG CGTGCATCAGA CGGTGCATCC ACCATGGAT GGTACAGCC GGTACAGCC GCGATGGATG GGTACAGCC	ATAATGTTA TAACGGTGTC GAGTGAGGGCG CCTGGGGCGC CCTCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA TTCAACATCGG AAGAGCTCTT CAACATCTGC CAACATCTGC CAACATCTGC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC TCAAGAAGCC CAAGAAGCAC TCAAGAAGCAC TCAAGAAGCAC GTGAAGCAC ACTGGAAC GTGTGAACA GTGTGAAC GTGTGACAC GTGTTGACAC GTGTTGACAC GTGTTGACAC GTGTTGTTTG	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGAAAAA GACGTGGAG CCTTCATTG AAAGGATTT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGCAAAGC CTTTAATCCA TGGGGACTAC TGGGGACTAT TCCTCACTA ACATCAGTGG GCGAACTAT CCCCCTA ACATCAGTGG CCCAGTTTCT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGG CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGTT CGAGACCTC CAGCGTCTTG CAACAGCTTG ATTCGTCCTG ATTCGTCCTG ATTCGTCCTA ATTCGTCCTT AGAGAGGAGA ATCTTTTTC GATGGCATCA GGTGAATTTA GGGAACAGAG GATATACTGT	120 180 240 300 360 420 600 660 720 780 840 900 1020 1080 1140 1260 1320 1320 1440 1500
50 55 60 65	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGTA TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG GGGCCAATCC GGAATTACGG TCCTGTGGCT TTTACTGGAT TCTTCAGG AGGTGTCAGA AGGAGAGAT ACAAAGGCGA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCCAGAGT TCTCCGCAGAG AGACCTAATA ATTTTGGAACT GCACTATGCA TCACCTGTT TCTGCCGGTA TCAGAGAATACT TCAGCAGGC CACTATGCA CACATATGCA CACATATGCA ACTAGATAT TCTACCGGTA TCAAGATGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATGAAGAT AGTGACAAGG GAGAATACCTC GACAATACAC	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CGCGCCCC CGAGCCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CTTACCGGAG GTCTCACACAC CTTGACAACC TTTGACAACG TTTGACAACG TTTGACAACG TTTGCCAATT TCTCTTGGAG TCTTTGCCAATT TCTCTTGGAG CCTTATTTT AGAGCCTGA TTTGCCCAATT GACCATCAGA GGGAAAGAAA CGGTGCATTC ACCATCGAT CGGTGCATTC ACCATCGATC ATTCCAACTA	ATAAATGTTA TAACGGTGTC GAGTGAGGGCG CCTCCGGGCAG CCTCCGGCAG AGGAGGATCCCG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTACCATTTT TCAACATCTTC CAACATCTGC TCAAGAAGC TCACTGAAG ACTTGGCAAC TCGACTGGC ACTTGACAAC TCGACTGGC ACTTGACAAC TGGACTGGC CTGTTGTTTTT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CAGGACAATG AAAGAGATG AAAGGAAAA AACGGATAA GACGGTGAGG CCTGTCATTG GAAGGCATTAT TAGAATGTAT TAGAATGTAT TACCAAAGCC TCTTTAATCCA TGGGGACTGC AGATAATCGG GGGAACTATG TCCTCCACTA ACATCAGTGG AGCCTGGAG AGCCTGCAGT CCCAGTTTTT TCCTAAGCTG CCCAGTTTTT TCCTAAGCTG	CCCACACTCG AACACTGGCA CGGTGGCTCC CAGCCTTAGT GCCGGTCTGC GCACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACCCTGGCT CACCCTGCTC CAACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTT AAGATGGAG TGTCAGCAGG AATCTTTTT GGGAACACACA GGTGAATTTA GGGAACACACA GGTGAATTTA GGGAACACACA GGTGAATTTA GGGAACACACA GATATACTGT GCAAGCCCCA	120 180 240 300 360 420 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560
50 55 60	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC GATCTGCCCT GTAACGGACGC GATCTGCCCT GTAACGGATA ATAATCTGGT AGTTTGGATG AGTTTGGATG ATAATAATA TGAGGGCAAC TGAAATTGG TACTTTGG TACTTTGG TACTCTTGG TACTCTTGG TACTCTTGG TACTCTTGGAT TCTTCCAGG TCTTCAGGAT TTTACTGGAT TTTACTGGAT AGGAGAGAAT ACAAAGGGA ACATGAGCAA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGACCTAATGC CTCCGCAGAG AGACCTAATGCA TCTTGGAACCT TCTGGCAGT TCTGGCAGT TCAGCATGTT TCTGCCGGTA TCAGCATGTTT TCTGCCGGTA TCAGCATGTTT TCTGCCGGTA ACTGAGCT CCCAGTGGGA AAATGAAGAT AATGAAGAT AATGAAGAT AAATGAAGAT AATGAACACG GAGAATACCTC GTTTGGCTCT GCCAATCACG ATTAACTGAT	ACGTCTCCAT GATTOGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTCACACCAG GTGTACAGCAG CATATCAAGC CATATCAAGC CATGCCAAACC ACCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG TTTGCCCAAT ACCATCAGA GAGAAGAAG GAGAAGAAG GAGAAGAAG CGGTGCATTC ACCATGGAT ATCCAACTA ATCCAACTA ATCCAACTAT ATCCAACTAT ATCCAACTAT ATCCAACTAT	ATAAATGTTA TAACGGTGTC GAGTGAGGGGG CGAGTCTCCG CCTCCGGGCAC CTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT TCAACATGGT TCAACATGGAT TCAACATGGAT TCAACATGGAT TCAACATGGAT CAACATCTGC CAAGTGGAAC GTGAAGCAGT TCAACGAGAC GTGAAGCAGT CACTGGAGAC GTGAAGCAGT CACTGGAGAC GTGAAGCAGT CACTGGAGAC GTGAAGCAGGAC ACTTGACAAC GTGTTGTTTG TGGAGCATGGAAC GTGTTGTTTG GGAGGAAGGA GAAGGAAGGA	CACGGGCATC ATTTGCTTGC CGGGTCTTGGGGGAG CCGCGAGAGG CCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGAGAAA AGAGGAAAA GACGTCATTG GAAGGAATT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTAC GGAACATGGGGACTGC AGATATCGG GGAACTATC ACATCACTA ACCACAGTG ACCCTGGAG CCCAGTTTCT TCCTAAGCTG GAGCGACTGC GAGCGACTGC GAGCGACTGC	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTGG AAGGATTGCA GTGGGACCTCA GTGGGACCTCA CACCCTGGCT CAGCGCTA CACCCTGGCT CAGCGCTA CACCCTGGCT CAGCGCTA ATTCGTCCTA ATTCGTCCTTA ATTCGTCCTTTG GTGTCCCTGT ATTCGTCCTTTT GTGTCCCTGT AAGATGGGAG TGTCAGCAGG AATTCTTTTC GATGGCATCA GGGAACAGAG GATATACTTTA GGGAACAGAG GATATATCTGC ACCACCCCCA ACAATTGTGC	120 180 240 300 360 420 6600 6600 720 780 840 900 1020 1140 1260 1320 1380 1440 1500 1560 1620 1680
50 55 60 65	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC GATCTGCCCT GTAACGGACGC GATCTGCCCT GTAACGGATA ATAATCTGGT AGTTTGGATG AGTTTGGATG ATAATAATA TGAGGGCAAC TGAAATTGG TACTTTGG TACTTTGG TACTCTTGG TACTCTTGG TACTCTTGG TACTCTTGGAT TCTTCCAGG TCTTCAGGAT TTTACTGGAT TTTACTGGAT AGGAGAGAAT ACAAAGGGA ACATGAGCAA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCCAGAGT TCTCCGCAGAG AGACCTAATA ATTTTGGAACT GCACTATGCA TCACCTGTT TCTGCCGGTA TCAGAGAATACT TCAGCAGGC CACTATGCA CACATATGCA CACATATGCA ACTAGATAT TCTACCGGTA TCAAGATGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATGAAGAT AGTGACAAGG GAGAATACCTC GACAATACAC	ACGTCTCCAT GATTOGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTCACACCAG GTGTACAGCAG CATATCAAGC CATATCAAGC CATGCCAAACC ACCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG TTTGCCCAAT ACCATCAGA GAGAAGAAG GAGAAGAAG GAGAAGAAG CGGTGCATTC ACCATGGAT ATCCAACTA ATCCAACTA ATCCAACTAT ATCCAACTAT ATCCAACTAT ATCCAACTAT	ATAAATGTTA TAACGGTGTC GAGTGAGGGGG CGAGTCTCCG CCTCCGGGCAC CTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT TCAACATGGT TCAACATGGAT TCAACATGGAT TCAACATGGAT TCAACATGGAT CAACATCTGC CAAGTGGAAC GTGAAGCAGT TCAACGAGAC GTGAAGCAGT CACTGGAGAC GTGAAGCAGT CACTGGAGAC GTGAAGCAGT CACTGGAGAC GTGAAGCAGGAC ACTTGACAAC GTGTTGTTTG TGGAGCATGGAAC GTGTTGTTTG GGAGGAAGGA GAAGGAAGGA	CACGGGCATC ATTTGCTTGC CGGGTCTTGGGGGAG CCGCGAGAGG CCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGAGAAA AGAGGAAAA GACGTCATTG GAAGGAATT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTAC GGAACATGGGGACTGC AGATATCGG GGAACTATC ACATCACTA ACCACAGTG ACCCTGGAG CCCAGTTTCT TCCTAAGCTG GAGCGACTGC GAGCGACTGC GAGCGACTGC	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTGG AAGGATTGCA GTGGGACCTCA GTGGGACCTCA CACCCTGGCT CAGCGCTA CACCCTGGCT CAGCGCTA CACCCTGGCT CAGCGCTA ATTCGTCCTA ATTCGTCCTTA ATTCGTCCTTTG GTGTCCCTGT ATTCGTCCTTTT GTGTCCCTGT AAGATGGGAG TGTCAGCAGG AATTCTTTTC GATGGCATCA GGGAACAGAG GATATACTTTA GGGAACAGAG GATATATCTGC ACCACCCCCA ACAATTGTGC	120 180 240 300 360 420 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560
50 55 60 65	TGTTTATTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGACT GTAACGACT GTAACGACT ATATTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC CATCATTGG TACTCATTGG TACTCATTGG TACTCATTGG TACTCATTGG TCCTTTGAG GGGCAATCC GGAATTACGGAT TTTTACTGGAT TTTTTCAGG TCCTTTGAG AGGTGTCAGA TGAGAGAGAT TTTTTCAGGAT TTTTTCAGAG TGAGAGAGAT TTTTACTGAG TGAGAGAGAT TTTTACTGAG TGAGAGAGAT TTTTAGGAT TTTTAGGAAT TCTTGAGCAA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCGACTGCTT TCTGCCGGTA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCT CCCAGTGGGA CAAGTATGTA CTCATCTCT CTATGGAGAG AAATGAAGAG GAGATACCTC GTTTGGCTCT GACAATACTG ATTAACTGAT GCAAATAGA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CCCAGACCCG CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC GTGTACCGGA GTGTTCACGG GTGTATCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAAC TCTCTTGGAG TCTCCATATT AGAGCCTGAA TTTGCCCAAT TTTCCCATAT GACCATCAGA GGGAGAAGAAC CGTTGCATTC ACCATCAGA GGGAGAAGAAC CGTTCATTC ACCATCAGA GGTACATC ACCATCAGA GGTACACC ATTCCAACTA GGTACACTA GGTACACTA GGTACAGTAG GGTACAGCT ATTCCAACTA GGTACAGTAG GGTACAG GGT	ATAATGTTA TAACCGTGTTA TAACCGTGTTA GAGTGAGGCG CCTCGGGCCG CCTCGGGCAC GTCCACACGG TCGTGGCGAA AAGGAGATC CTACCATTT ATCATATGCT CTCTCAGAA ATTGAAGGATT CAACATCTGC TCAAGAAGCC CAAGTGGAAC AAGGTGGAAC AGGTGAAC AGGTGGAAC AGGTGGAAC AGGTGGAAC AGGTGGAAC AGGTGGAAC GTGACTGCAC TCACTGAAGCAC TCACTGAAGCAC TCACTGAAGCAC TCACTGAAGCAC TCACTGAAGCAC GTGTTGTTTG TGGAGAATAGA GAAATAGAG GAAAGAAGAA	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGGTG AAAGGGATA GACGGTGAGA GACGGTGAGG CCTTCATTG TAGAATGTAT TAGATGTAT TAGACTGTAT TAGCAAAGC CTTTAATCCA TGGGACTAC GGGAACTAT TCCTCACTA ACACCTAGGG CCCAGTTTCT TCCTAAGCTG CCCAGTTCT TCCTAAGCTG GACCACTG GACCACTG GACCACTG GACCACTG GACCACTG GACCACTG GACCACTG GATACCACG	CCCACACTCG AACACTGGCA ACACTTGGCAGCCTTAGT GCCGGTCTGG CAGCCTTAGT GCAGCCTTAGT CAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTAG CACCCTGGTT CAGACCCCA TGGTCCTCAG CACCCTGGTT CAACAGCTTG AATTCGTCCTA ATTCGTCCTA ATTCGTCCTT AAGATGGGAG TGTCAGCAG TGTCAGCAG GATCATCATTTC GATGGCATCA GGTGAATTTA GGGAACAGAG GATATACTGT GCAAGCCCCA ACAATTGTGC CTATGGTACT	120 180 240 300 360 480 540 660 720 780 960 1020 1140 1260 1320 1380 1440 1560 1560 1680 1740
50 55 60 65	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA GCGCCAATCC GGAATTACGG TCCTGTGGCT TTTACTGGAT TCTTCCAGG AGGTGTCAGA TGTCTTCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTGAGAT TCTTCAGAG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCCTTGAGAT ACAAAGGCGA TCCTTGAGAAT ACAAAGGCGA TCCTTGAGAAT ACAAAGGCGA TCCTTGAGAAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCTCAGCG CTCCGCAGAG AGACCTAATA ATTTTGGAACT GCAGAATACT TCTGCCGGTA TCTACTGTTT TCTGCCGGTA ACTGATGTT TCTGCCGGTA ACTGATGTT TCTACGGGA AACTGATGTT CTATGAGAG AACTATGA CTCATCTCTT CTATGAGAG AAATACAC GATATACAGAG ATTAACTGAT GTTAGCTTTT GCCAATTCT GTTTTGCTCTT GACAATACAC ATTAACTGAT GGAAAATACAC ATTAACTGAT GTTTGCATTTTG	ACGTCTCCAT GATTCGGGGG ACTCCACCAC ACTCCACCAC CGCGCGCCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTCC CGAGCTTCACCGGAG GTCTCACCGGAG GTCTCACCGGA GTGTTCACGG CATATTAT TCGCCAAAC TTTGCCAATAT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCCAT TTGCCCAT ACCATCAGA CGGTGCATC ACCATCAGA CGGTACAGCC ATTCCAACTA ACCATCAGA ACCATCAGA ACCATCAGA ACCATCAGA ACCATCAGA ACCATCAGA ACCATCAGAT ATCCAGTATG GGTACAGCT ATTCCAACTA ATCCAGTATG GAATACAATG AATTGTGATA	ATAATGTTA TAACGGTGTC GAGTGAGGGCG CCTCGGGCAG CCTCCGGCAG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGATT TCAACATCTGC TCAACATCGT CAACATCTGT CAACATCTGT CAACATCTGC TCAAGAAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC AAGTGGAAC AAGTGGAAC AGGTGGAAC AGGTGGAAC TGAAGCAGT TCACTGACAC TCAAGAAGT TCACTGACAC TGGACTGGCAC TGGACTTGCCAA TTGACAAGT TCACTGACAC TGGACTTGGCAAC TGGACTTGGCAAC TGGACTTGGCAAC TGGACTTGGCAAC TGGACTTGGCAAC TGGACTTGGCAAC TGGACATGGAAC ACTTTGACAAC TGGACATGGAAC TGGACATGGAAC TGGACATGGAAC TGGACATGGCAAC TGTTTTTTTTTT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT TGCCCCAGGT CCAGGGGCTA CAGGACAATG AAAGAGATG AAAGAGATA GACGGTGAAG CCTGTCATTG GAAGCATTA TAGATGTAT TAGATGTAT TACCAAAGCC TCTTAATCCA TGGGGACTAC TCCTCCACTA ACATCAGTGG ACCCTGCAG CCCAGTTTTT TCCTAAGCT GAGCACTGG GCCACTTTC TCCTAACCT GAGCACTGG GATACCACTG GATACCAACT CCTACCTTG GAGCACTGG GATACCACTG GCTACCTCTG GCTACCTCTG GCTACCTCTG GCCACTTGC GCTACCTCTG GCCACTTCG GCCACTTGC GCCACTTCG GCCACTTCG GCCACTCG GCCACCTCTG GCCACCTCT GCCTACCTCT GCCTACCTCT GCCACCTCT GCCCACCTCT GCCTACCTCT GCCCACCT CCTCCCTCT GCCCACCT GCCCCCCT GCCCCCCC CCCCCCT CCCCCCCC CCCCCCCC	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACCCTGGCT CACCCTGGCT CACCCTGGCT CACCCTGGT ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA AGATGGCAG AACATTTTC GATGGCATCA GGGAACTAG GGTGAATTTA GGGAACAGG GATATACTGT GCAAGCCCCA ACAATTGTGC CATAATGTAG	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1680 1740
50 55 60 65	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC GGAATTCCTGAG GGGCCAATCC GGAATTACGG TACTTTGAG TCCTTGTGGT TTTTACTGGAT TTTTCCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTGAGCAA TATCCTGAGC TCTTGAGCAA TATCCTGAGT TCTTCAGCAA TATCCTGAAT TTTTTAGTAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCCCAGGGT CTCCGCAGAG AGACCTAATC GCACTATGCAA TTTTTGGAACT GCACTATGCA TCACTATGTT TCTGCCGGTA TCAGCTGGTA TCAGCAGTGTTT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAAGA AATGAAGAT AATGAAGAT AGTGACCAC GTTTGGCTCT GCAATACCC GTTTGGCTCT GCAAATACAC ATTAACTGAT GGAAAATAGA ATTAACTGAT CTATGCATTTG	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCGCCCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCAC GTCTACCGGAG GTCACACCAG GTCTTCACCAG CATATCAAGC CATATCAAGC CCTTATTTT AGAGCCTAAT TCTCTTGGAG TTTGCCCATAT ACCACCATAGA CCCTCATATT CACCATCAGA CCGTGCATTC ACCATCAGA CCGTGCATTC ACCATCAGA CGGTGCATTC ACCATCAGA CGGTGCATTC ACCATCAGA CGGTACAGCA ATCCAGTATG ATCCAGTATG CGATACAACC ATTCCAACTA ATCCAGTATG CAAGGAGGAT CAAGGAGGAT CAAGGAGGAT CAAGGAGGAT CAAGGATGATA CAAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGAGGAT CAAGAGGAGAT CAAGAGGAGAT CAAGAGAGGAT CAAGAGAGAGAT CAAGAAGAGAGAT CAAGAGAGAGAT CAAGAGAGGAT CAAGAGAGAGAT CAAGAGAGAGAGAT CAAGAGAGAGAGAT CAAGAGAGAGAT CAAGAGAGAGAT CAAGAGAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGA	ATAAATGTTA TAACGGTGTC GAGTGAGGGCG CCTCGGGACC CTCCGGCAC GTCCACAGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA TTCAACGATCT CAACATCTGC TCAAGAGACC TCAAGAGACC TCAAGAGACC TCAAGAGACC TCAAGAGCC TCAAGAGACC GTGAAGCAGT TCACTGAAG TCACTGAAG TCACTGAAG GGACTTGC ACTTGACAC TCGACTTGC ACTTGACAC TCGACTTGC ACTTGACAG ACTTGACAG GACTTGACAC GTGTTTTTT TGGGGAATAGAG GAAAATAGAG GAATATAGAG GATTTCTTC	CACGGGCATC ATTIGCTIGC CGGGTCTTGGGGAG CCCGGGGAGAGG CCCCAGGT CCAGGGGCA CCAGGGCAA AAAGAGGTG AAAAGAGGTG AAAAGAGAAAA AGAGGTATT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGACTATATCA CCTTTAATCA TCCTCACTA ACATCAGTGA AGCCTGTGGG AGCCTGGGG CCCAGTTTCT TCCTCACTA ACATCAGTGG AGCCACTGGG CCCAGTTCT TCCTAAGCTG GAGCGACTGG GATACCACTG GAGCGACTGG GATACCACTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGT CACCTGGT CACCTGGT ATTOGTCCTA ATTOGTCCTA ATTOGTCCTA ATTOGTCCTA ATTOGTCCTA CTGCTCTTTG ATTOGTCCTTA AGATGGCAG GATTACTTTTA GGGAACAGAG GATATACTGT GCAAGCCGCA ACAATTGTGC GTATGCTACT ACATTGTAC ATTAGTACT ATTAGTACT ACATTGTAC ACATTGTAC ATTAGTAC AATTGTAC AATGTAG AATGTAG AATGTACT AATGTAG AATGT	120 180 240 300 360 420 6600 6600 720 780 840 900 1020 1140 1200 1140 1320 1440 1500 1560 1620 1680 1740 1800 1800
50 55 60 65 70	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC GGAATTCCTGAG GGGCCAATCC GGAATTACGG TACTTTGAG TCCTTGTGGT TTTTACTGGAT TTTTCCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTGAGCAA TATCCTGAGC TCTTGAGCAA TATCCTGAGT TCTTCAGCAA TATCCTGAAT TTTTTAGTAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCCCAGGGT CTCCGCAGAG AGACCTAATC GCACTATGCAA TTTTTGGAACT GCACTATGCA TCACTATGTT TCTGCCGGTA TCAGCTGGTA TCAGCAGTGTTT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAAGA AATGAAGAT AATGAAGAT AGTGACCAC GTTTGGCTCT GCAATACCC GTTTGGCTCT GCAAATACAC ATTAACTGAT GGAAAATAGA ATTAACTGAT CTATGCATTTG	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCGCCCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCTCC CGAGCCAC GTCTACCGGAG GTCACACCAG GTCTTCACCAG CATATCAAGC CATATCAAGC CCTTATTTT AGAGCCTAAT TCTCTTGGAG TTTGCCCATAT ACCACCATAGA CCCTCATATT CACCATCAGA CCGTGCATTC ACCATCAGA CCGTGCATTC ACCATCAGA CGGTGCATTC ACCATCAGA CGGTGCATTC ACCATCAGA CGGTACAGCA ATCCAGTATG ATCCAGTATG CGATACAACC ATTCCAACTA ATCCAGTATG CAAGGAGGAT CAAGGAGGAT CAAGGAGGAT CAAGGAGGAT CAAGGATGATA CAAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGGAGGAT CAAGAGAGGAT CAAGAGGAGAT CAAGAGGAGAT CAAGAGAGGAT CAAGAGAGAGAT CAAGAAGAGAGAT CAAGAGAGAGAT CAAGAGAGGAT CAAGAGAGAGAT CAAGAGAGAGAGAT CAAGAGAGAGAGAT CAAGAGAGAGAT CAAGAGAGAGAT CAAGAGAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGA	ATAAATGTTA TAACGGTGTC GAGTGAGGGCG CCTCGGGACC CTCCGGCAC GTCCACAGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA TTCAACGATCT CAACATCTGC TCAAGAGACC TCAAGAGACC TCAAGAGACC TCAAGAGACC TCAAGAGCC TCAAGAGACC GTGAAGCAGT TCACTGAAG TCACTGAAG TCACTGAAG GGACTTGC ACTTGACAC TCGACTTGC ACTTGACAC TCGACTTGC ACTTGACAG ACTTGACAG GACTTGACAC GTGTTTTTT TGGGGAATAGAG GAAAATAGAG GAATATAGAG GATTTCTTC	CACGGGCATC ATTIGCTIGC CGGGTCTTGGGGAG CCCGGGGAGAGG CCCCAGGT CCAGGGGCA CCAGGGCAA AAAGAGGTG AAAAGAGGTG AAAAGAGAAAA AGAGGTATT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGACTATATCA CCTTTAATCA TCCTCACTA ACATCAGTGA AGCCTGTGGG AGCCTGGGG CCCAGTTTCT TCCTCACTA ACATCAGTGG AGCCACTGGG CCCAGTTCT TCCTAAGCTG GAGCGACTGG GATACCACTG GAGCGACTGG GATACCACTG	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACCCTGGCT CACCCTGGCT CACCCTGGCT CACCCTGGT ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA AGATGGCAG AACATTTTC GATGGCATCA GGGAACTAG GGTGAATTTA GGGAACAGG GATATACTGT GCAAGCCCCA ACAATTGTGC CATAATGTAG	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1680 1740
50 55 60 65 70	TGTTTATTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGAT ATAACGGAT ATAACTGGAT ATAATCTGGT ATAATAAAAT TGAGGGCAAC TGAAATTGGA TGAATTGGA TGATCATTGG TACTCATTGG TACTCATTGG TACTCATTGG TCCTGTGGCT TTTACTGGAT TTCTTCAGG AGGTGTCAGA TGAGAGAGAT TCTTCAGA TGAGAGAGAT TCTTCAGA TGAGAGAGAT TCTTCAGA TGAGAGAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TCTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TTTTTAGTAT AATCATCAAA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCACGTGTA GCTCTGCAGCT CTCCGCAGAG TGATGCATT TTTTGGAACT TCTTGCAGCT TCGCATTATGCA TCGACTATTT TCTGCCGTA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA AATGAAGACT CTATGGAGAG AAATGAAGA GAGAATACTC GACTATCTT CTATGGAGAG AAATGAAGA GAGAATACTC GACAATACAC GACAATACAC GACAATACAC GACAATACAC GACAATACAC GACAATACAC CAATACGAC GACAATACAC CAATACAC CAATACCAC CA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CCCAGACCCG CGAGCTTCCC GTTACCGGA GTCTACCGAG GTCTACCACAG GTGTTCACCG GTGTTCACCG CATATCAAGC CTTGACAAACC TTTGACAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCAAT GACCATCAGA GAGAAGAAGAG CGGTGCATTC ACTATGATAG CTTCCACTT ATTCCACTA ATTCCACTA AATTCTAGTA AATTGATAA CACAGTGAT TAACTTGGTA TAACTTGGTA	ATAATGTTA TAACCGTGTTA TAACCGTGTTA CAGGGCCG CCTCGGGCCC CCTCGGGCCC CCTCGGGCAC CTCCACACGG TCGTGGCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA AAGAGCTCTT CAACATCTGC TCAAGAACC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC TCACTGCACTG	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAAGAGTG GAAGGCATT TAGAATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTAC CCTTCACTA ACATCAGTGG ACACTGGAG CCAGTTTCT TCCTAAGCTG GAGCACTAC GCTACCTGGA GACCACTGGAAAAC CTTAACTGG GACCACTGGAAAAC CCTTAACTTG TCCTAACTG GACCACTGGAAAAAC CTTACCTTG CTACCTGGAAAAAC CCTTACCTTT CCTAACCTG CTACCTTG CTACCTTG CTACCTTG CTACCTTG CTACCTTT CTCCAAACT CTCCAACT CCTACCTTT CCTAACCTT CCTAACCTT CCTAACCTT CCTAACCTT CTCCAACT CTCAACT CTCCAACT CT	CCCACACTCG AACACTGGCA ACACTGGCAC CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC CGACCCTTGG AAGGATTGCA CGGCCCCA TGGTCCTCAG CACCCTGGCT CGAGGACTCA TGGTCCTCAG CACCCTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTA TTGTCCTAT ATTCGTCCTA TGTCCCTGT AAGATGGGAG AATCTTTTC GATGGCATCA GGGAACTTTA GGGAACAGAG GATATACTGT CCAAGCCCCA ACAATTGTGC CTATGCTCCT CATAATGTAG AATGAATTGC AATGAATAA	120 180 240 300 360 480 540 660 720 780 960 1020 1140 1260 1320 1380 1440 1560 1560 1680 1740 1880 1740
50 55 60 65	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATG TTAAGGATG TTAAGGATG AGATTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACG TCTTTCAGGA TCTTTCAGGA AGGTGTCAGA TTTTTCTCAGG AGGTGTCAGA TTTTTCAGGA TTTTACTGGAT TTTTTCAGGA TGAGAGAGAT ACAAAGGCGA TCTTGAGCA TTTTAGTGAT TTTTTAGTAT AGGACAGACT TTTTTTAGTAT ATCATAAAA ACATTAATGT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCTGGGAGC CCCCCCAGCTGTA GCTCTGCAGC CCCCCAGACT TTTTGGAACT GCACTATATA TTTTGGAACT GCACTATGCA TCCACAGATGT TCTGCCGGTA TCAAGAATGCA ACTGATGCA CCAGTGGGA CAAGTATGTA CTCATCTCT CTATGGAGAG AAATGAAGAT AGTGACAAGG GAGAAACCC GTTTGGCTCT GACTATCCC GTTTGGCTCT GACTATCACAGA GTTTAACTGAC AGGAAATAGA GTTGCATTTC CAATGTTTT CAATGTTTC AAGGCTTTCC ACAATGTTTAACTGAT CAATGTTTC CAATGTTTC CAATGTTTC AAGGCCATATA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACCGG GTGACACCAG GTGTTCACCGG GTGATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTT ACAGCCTGA TTGCCCAAT TGACAACA GTGCCATACT TTTCCCCAAT TTTCCCCAAT TTTCCCAAT TACTCCAGA GGAGAAGAG CGTGCATTC ACTCAGAT GGATACACT ATTCCAACTA ATCCAGTAT ACCAGTATT AATCGAGTAT CAAGAGTGAT CAAGAGTGAT TAACTTGGTA TAACTTGGTA TAACTTGGTA TAACTTGGTAT ACATTGGTAT ACATTGGTAT ACATTGGTAT TAACTTGGTAT ACATTGGTAT ACATTGGTAT ACATTGGTAT ACATTGGTAT ACATTGGGATT TAACTTGGTAT ACATTGGGATT	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGCAC CTCGGGCAC TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGGAT TCAACATCGG AAGAGCTCTT CAACATCTGC CAACATCTGC CAACATCTGC CAACATCTGC CAACATCTGC CAACATCTGC CAACATCTGC CAACATCTGAAC AAGGTGGAAC AGGTGAACCAC GTCATGAACAC GTCATGAACAC GTCATGAACAC GTCTTGATTG TGGAGAATGG GAACAGAG GAAATAGAG GAAATAGAG GAAATAGAG GAATTTCTTCC TTTCTTCAATG TTCCTCAATG	CACGGGCATC ATTTGCTTGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGATA GACGTGGAG CCTTCATTG GAAGGCATTT TAGAATGTAT TAGAATGTAT TAGAATGTAT TAGCAAAGC CTTTAATCCA TGGGGACTAC TGCGAGAGA CCTTCATCGTGA CCCAGTTCT TCCTAAGCG GGAACTAT TCCTCACTA ACATCAGTGG CCCAGTTTCT TCCTAAGCTG GAGCACTGG GATACCAGT GACCACTA ACATCAGTGG GATACCACT ACATCAGTGG CCCAGTTTCT TCCTAAGCTG CACCAGCACTA CACCAGCACTA ACTTACCTT ACTTACCT ACTTACCTT ACTTACCTT ACTTACCT A	CCCACACTCG AACACTGGCA ACCACTGGCTCC CAGCCTTAGT GCCGGTCTGC GCACCCTTGG AAGGATTGCA GTGGGGACTTCC CAGACCCCA TGGTCCTCAG CACCCTGGTT CGAGACCTCA TGGTCCTCAG CACCCTGGTT CAAGAGCTTG AATCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTG AACAGCTTG AAGATGGAG TGTCAGCAG GATATACTGT GCAAGCCGCA ACAATTGTG CATAATGTAC AATGAATTGC AATGAATTGC CATAATGTAC AATGAATTGC AACACTTGC CATAATGTAC AATGAATTGC AACACTTGCACACAAAA CCCTTTTGT	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1680 1740 1800 1800 1900
50 55 60 65 70	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC AATCCAGCC AATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTTCTGGGT TTTTACTGGAT TTCTTCCAGG AGGTGTCAGA ACAAAGGCGA TCTTGAGAT ACAAAGGCGA TTTTGAGAT TGGGACAGACT TTTGTAGTAT AATCATGAAT AATCATCAAT AATCATCAAT AATCATCAAT AATCATCAAT AATCATCACTA AATTCATCACTA AATCATCACTA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCCAGAGT TCTCCGCAGAG AGACCTAATA ATTITGGAACT GCAGAGAAACCT TCTGCCGGTA TCAGCAGTTT TCTGCCGGTA TCAGCAGTTT TCTGCCGGTA AGACTATGGA ACTGAGCT CCCAGTGGGA ACTGAGCCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATAACTA GGAAAATCAC ATTAACTGAT GGAAAATCAC ATTAACTGAT GGAAAATTAG GTTGCCATTTG CAATGTGTTA AGGCCATATA AGGCCATATA AGGCCATATA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCACCGGAG GTCACACAC GTGTTCACGGA CTTGGAATTAT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCCATAT GACCATCAGA GCGTACAGA CCGTGCATAC ATTCCAGATA GACCATCAGA CGGTACAGA CGGTACAGA CGGTACAGA CGGTACAGA CAGATGAGAT ACCAGTATG AATTCCAGTAT ATTCCAGTATG GAGATACAAT AATTCGATAT CAAGAGTGAT TAACTTGGTA ACTAGGATT AACTGGGATT AACTGGGATT AACTGGGATT AGTAGTTTAT	ATAATGTTA TAACGGTGTC GAGTGAGGGCG CCTGGGGGCG CCTCCGGGCA TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTTCAGAA TTGAAGGAT TCAACATCTC CTACATGGA AAGAGCTCTT CAACATCTGC TCAAGAAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC GTGAAGCAGT TCACTGACA AGGTGGAAC AGGTGGAAC TGGACATGG ACTTGACAAG TCATTGACAAC TCGACATGGC ACTTGACAAG TCGACATGGC TCAATGGCAAC TCGACATGGC ACTTGACAAC TCGACATGGC GTGTTGTTTG TGGAGAATGG GAAATAGAG GAAATAGAG GATTTCTTTC TGTTTCTTCA TTCCTCAATT TCCTCAATT	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGATGA AAAGAGATGA AAAGAGATGA AGACGATGAGGAGAGA CCTGCATGGAGGATT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTGC AGATAATGGG GGGAACTATG TCCTCCACTA ACATCAGTGG AGCCTGCAG GCCAGCTTTT TCCTAAGCTG GAGCGACTGG GGTACCTGCAG GCTACCTGTG GCCACTTTACTT TCCTAAGCTG GATCCACTT TCCTAAGCTG GATCCACTT TCCTAAGCTG AGCTTCCTTT TCCTAAGCTG AGCTACCTGTG CCTACCTTTACTT TCCTAAGCTG ACTTACCTT TGCCAGAGAA ACTTTACTTC AAGTTACATT	CCCACACTCG AACACTGGCA CGGTGGCTCC CAGCCTTAGT GCCGGTCTGC GCAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACCCTGGCT CACCCTGGCT CACCCTGGCT ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTT AAGATGGCAGG AATCTTTTC GCAGCACCC GATGGCATCA GGGAACAGG AATCTTTTC GCAGCACCC GATGCATCA GCTAATGTGC CATATGTGC CATATGTGC CATATGTGC CATATGTAG AATGAATTGC ACCTGAGAAA AATCTTTC CATAGATAG AATGAATTGC ACCTAGAAAA CTCCTTTAG CTGCTCCTCA	120 180 240 300 360 420 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1680 1740 1680 1740 1860 1980 2040
50 55 60 65 70	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC AATCCAGCC AATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTTCTGGGT TTTTACTGGAT TTCTTCCAGG AGGTGTCAGA ACAAAGGCGA TCTTGAGAT ACAAAGGCGA TTTTGAGAT TGGGACAGACT TTTGTAGTAT AATCATGAAT AATCATCAAT AATCATCAAT AATCATCAAT AATCATCAAT AATCATCACTA AATTCATCACTA AATCATCACTA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCCAGAGT TCTCCGCAGAG AGACCTAATA ATTITGGAACT GCAGAGAAACCT TCTGCCGGTA TCAGCAGTTT TCTGCCGGTA TCAGCAGTTT TCTGCCGGTA AGACTATGGA ACTGAGCT CCCAGTGGGA ACTGAGCCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATAACTA GGAAAATCAC ATTAACTGAT GGAAAATCAC ATTAACTGAT GGAAAATTAG GTTGCCATTTG CAATGTGTTA AGGCCATATA AGGCCATATA AGGCCATATA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCACCGGAG GTCACACAC GTGTTCACGGA CTTGGAATTAT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCCATAT GACCATCAGA GCGTACAGA CCGTGCATAC ATTCCAGATA GACCATCAGA CGGTACAGA CGGTACAGA CGGTACAGA CGGTACAGA CAGATGAGAT ACCAGTATG AATTCCAGTAT ATTCCAGTATG GAGATACAAT AATTCGATAT CAAGAGTGAT TAACTTGGTA ACTAGGATT AACTGGGATT AACTGGGATT AACTGGGATT AGTAGTTTAT	ATAATGTTA TAACGGTGTC GAGTGAGGGCG CCTGGGGGCG CCTCCGGGCA TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTTCAGAA TTGAAGGAT TCAACATCTC CTACATGGA AAGAGCTCTT CAACATCTGC TCAAGAAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC GTGAAGCAGT TCACTGACA AGGTGGAAC AGGTGGAAC TGGACATGG ACTTGACAAG TCATTGACAAC TCGACATGGC ACTTGACAAG TCGACATGGC TCAATGGCAAC TCGACATGGC ACTTGACAAC TCGACATGGC GTGTTGTTTG TGGAGAATGG GAAATAGAG GAAATAGAG GATTTCTTTC TGTTTCTTCA TTCCTCAATT TCCTCAATT	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGATGA AAAGAGATGA AAAGAGATGA AGACGATGAGGAGAGA CCTGCATGGAGGATT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTGC AGATAATGGG GGGAACTATG TCCTCCACTA ACATCAGTGG AGCCTGCAG GCCAGCTTTT TCCTAAGCTG GAGCGACTGG GGTACCTGCAG GCTACCTGTG GCCACTTTACTT TCCTAAGCTG GATCCACTT TCCTAAGCTG GATCCACTT TCCTAAGCTG AGCTTCCTTT TCCTAAGCTG AGCTACCTGTG CCTACCTTTACTT TCCTAAGCTG ACTTACCTT TGCCAGAGAA ACTTTACTTC AAGTTACATT	CCCACACTCG AACACTGGCA ACCACTGGCTCC CAGCCTTAGT GCCGGTCTGC GCACCCTTGG AAGGATTGCA GTGGGGACTTCC CAGACCCCA TGGTCCTCAG CACCCTGGTT CGAGACCTCA TGGTCCTCAG CACCCTGGTT CAAGAGCTTG AATCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTG AACAGCTTG AAGATGGAG TGTCAGCAG GATATACTGT GCAAGCCGCA ACAATTGTG CATAATGTAC AATGAATTGC AATGAATTGC CATAATGTAC AATGAATTGC AACACTTGC CATAATGTAC AATGAATTGC AACACTTGCACACAAAA CCCTTTTGT	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1680 1740 1800 1800 1900
50 55 60 65 70	TGTTTATTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCCT GTAACGGATC GTAACGGATC TTAAGGCTA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA GCGCCAATCCAGG TCCTGTGGCT TTTACTGGAT TTCTTCAGG TCCTGTGGCT TTTACTGGAT ACAAAGGCGA TCTTCAGCAG TGAGAGAGAAT ACAAAGGCA TCTTGAGCAA TATCCTGAAT ACAATCATAAAA ACATTAATGT ACTTCACTCA AACAAATGCA	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT TCTGCAGTA TCAGAGAC TCACTATGCA TCACTATGCA TCAGAGAACCT TCTGCCGGTA TCAGAGATGCA TCAGAGATGCA TCAGAGATGCA TCAGAGATGCA TCAGTGTTT CTATGAGCCT CCAGTGGGA AAATGAAGAG GAGATACTC GTTTGCCTT GACAATACC GTTTGCATTG CAATACCA ATTAACTGAT CGAATATGA TCAGTGTTT TCAGTGTTT TCAGTTTACTGATTG CATTGCATTTA TGGTGTTTCAATTGCATTTA TGGTGTTTCAATTGCATTTA TGGTGTTTCAAAGCCATAAA AGCCATAAAA ATTTTTTTGTG	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCC CCAGACCCG CCAGACCCG GTCACCACA GTCTACCGGA GTCTACCGGA GTGTTCACCG GTGTACAGGA GTGTTCACCG GTGTAATCAAGC CTTGACAAACC TTTGACAAAC GTCTCATATT AGAGCCTGGA GTCCATATT TCTCTTGGAG GCATACTAT GACCATCAGA GACCATCAGA GACCATCAGA GACCATCAGA GACCATCAGA GACCATCAGA GATACAATC ACCATGGATG ATTCCAACTA ATTCCAACTA AATTCCAACTA AATTCGAATA CAAGAGTGAT TAACTTGGTA ACATGGGATT TAACTTGGTA ACATGGGATT TAACTTGGTA ACATGGGATT TAACTTGGTA ACATGGGATT TAACTTGTATA TGTGTTTTGAA	ATAATGTTA TAACCGTGTTA TAACCGTGTTC GAGTGAGGCG CCTCGGGCCC CCTCGGGCCC CCTCGGGCAC GTCCACACGG TCGTGGCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA TTCAACATGGA AAGAGCTCTT CAACATCTGC TCAAGAAGCC CAAGTGGAAC AAGGTGGAAC ACTGGCACT TCATGACATCTGC GTGAAGATGTTAACTGTTTG TGGACATCTGCCACC GTGTTGTTTG TGGACATCTGTTTGTTTG TGGACATCTGCACAC GTGTTGTTTG TGGACATCTGCACAC GTGTTGTTTG TGGACATCTGCACAC GTGTTGTTTG TGGACATCTGCACAC GTGTTGTTTC TGGACATCTCTCATGACAC GTATTCTTCA GTAGTAACTT TCCTCAATGT TCTTTAATGT TCTTTAATGT TCTTTAATGT	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCTGGGGGAG CCGGGGCAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAAGAGATG AAAAGAGATT TAGACTTATT TAGACTTATT TAGACTTATT TAGCAAAAGC CTTTAATCCA TGGGACTAC TCTCACTGA ACACCAGTGAACATG CCAGGTCTCACTGA CCAGGTCTCCACTGA CCAGGTCTCCTCACTGA CCAGGTCTCCTCACTGA CCAGGTCTCCTCACTGA CCAGGTCTCCTCACTGA ACACCAGTGAACTC GCAGACTAC TCCTAACCTG GAGCACTGC GAGCACTGC CCAGTTTCT TCCTAACCTG CCAGACTAC TGCCAGAGAA ACCTTACCTT	CCCACACTCG AACACTGGCA AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGGT AAGGATTGCA CTGGTCCTAG CACCCTGGT CAGACCCCA TGGTCCTCAG CACCCTGGTT CAGAGAGTTG CAACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA AGATGGAG ATTCTTTTC GATGGCATCA GGGAACTAG AATATATTTC GCAAGCCCC ACAATTGTCC GTATGCATCA CCCATAGAAAA CTCCTTTTGC ACCTTTTGC CATAATGTAC CACTAGAAAA CTCCTTTTCC ATAGGATCA ATAGGTTACA ATAGGTTACA	120 180 240 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1500 1680 1740 1860 1920 1920 1980 2040
50 55 60 65 70	TGTTTATTTC GATACGCACC CCTCTGCCTC GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGATC TTAAGGATG ATAATCTGGT AGATTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAACC TGAAATTGGG TACTCATTGG TTTTCATCAGG TCTTTCAGCA TGAGAGAGAT TTTTCAGGAA TGAGAGAGAT TTTTGAGAA TGAGAGAGACT TTTTGAGAA ACAAATGAA ACAAAATGCA ATTTCACCCA AACAAATGCA	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG GCTGGGAGAG GCTCGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCTCGCAGAG AGACCTAATA TCTGCAGTT TCTGCAGT TCAGAGAT TCTGCAGTA ACTGATT TCTGCAGTA ACTGATCT CCAGTGGA AACTGAGCCT CCAGTGGA AATGAGAGT CTCATCTTT CTATGGAGAG AAATAAGA ATTAACTGAT ATTAACTGAT CTATGCATAGC GTTTGGCTCT GACAATACAC ATTAACTGAT CTATTGCATTT CAGGAATATAA TTTTTTTTT AAGCCATATA ATTTTTTTT CTTTTTTTTTT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCCC CGAGCTCCC CGAGCTTCCC TGTACCGGAG GTCACACCAG GTGTTCACCGG GTGATTACCGGAG GTGTTCACGG GTGATTAT CAGCCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGAG TCTCCATATT AGAGCCTGAA TTTCCCAAT ACTCAGAT ACTCAGAT ACTCAGTAT ACAGTAGT AATTCCAATT AATTCCAATT AATTCGAAT AATTCGATT AATTGGTA AATTGGTA AACTTGGTA ACATTGGTA ACATTGGTA ACATTGGTA ACATTGGTA ACATTGGTA ACATTGGTA ACATTGGTA ACATTGGTA ACATTGGTA ACATGGATT TGTGTTTTAA TCCACCAAAAA	ATAATGTTA TAACCGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGCAC CCTCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA TTGAAGGAT TCAACATGGA AAGAGCTCTT CAACATGGA AAGAGCTCTT CAACATCTG CAACATCTGACAC GTGAAGCAC GTGAAGCAC GTGAAGCAC GTGAAGCAC GTGTTGTTTG TGGGAAATAGGG GAAGGAATGG GAAGTGGAAC GTGTTGTTTG TGGGAAATAGGG GAAGTAATTTG GTGTTTTCTTTAATAT AGCTAATTTG TCTTAATAT AGCTAATTTG	CACGGGCATC ATTIGCTIGC CGGGTCTIGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGATG GAAGGATA GACGTGGAG GAACAATG TAGAATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATCTAT TCCCACTA ACATCAGTGG GGGACTAG CCCAGTTCT TCCTAAGCC GGTACCTGGAGCACTG GAGCACTG GAGCACTG GATACCAGTG GATACCAGTG AACTTACTTA TCTCACATA CATCAGTGG AACTTACTTA TCTTAACTTA TCTTCACATA CATTACTTA TCTTAACTTA CATTACTTA TTTTTACTT ATTTTAGTC AAGTAATTTC TTTTTTAATT TTTTTTAATT	CCCACACTCG AACACTGGAA CAGCCTTAGT GCCGGTCTGC CAGCCTTAGT GCCGGTCTGC GAGCCTTAGT CAGACCCCA TGGTCCTCAG CACCCTGGT CAGACCCCA TGGTCCTCAG CACCCTGGTT CAGAGACTCA TGGTCCTCAG CACCCTGGTT CAACAGCTTG AATCGTCCTT GAGGAGTAG ATTCGTCCTT AGAGTGGAG TGTCAGCAG TGTCAGCAG GATATACTGT GCAAGCCGCA ACAATTGTGC GTATGCTACT CATAATGTAG AATGAATTGC ACCTTAGAAAA CTCCTTTTGT CTTAGAAAAA CTCCTTTTGT CATAATGTAG AATGAATTGC ACCTAGAAAAA CTCCTTTTGT CTGCTCCTCA AATAGGTTACA CAAGACCTTT	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1320 1380 1450 1560 1680 1740 1880 1740 1880 1980 2040 2160 2160 2160
50 55 60 65 70	TGTTTATTTC GATACGACC CCTCTGCCTC GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATG TTAAGGATG ATTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGCCAATCC GGAATTACGAT TTTACTGGAT TTTACTGGAT TTTACTGGAT TTTTCTCCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTGAGCAA ACAATAACG ATTCATTGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ATTCCTCCAG AAAACTGGAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCATGCATC GCCACGTGT CTCCGCAGAG AGACCTAATA TITTGGAACT GCACTATCA GCACTATCA GCACTATCA GCACTATCA TCTCGCAGAG ACACTATCA TCACCTGTTT TCTGCCGGTA TCAGAGAATGGA ACACTGATCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATGAAGAT AGTGACACGC GTTTGGCTCT GACAATACAC ATTAACTGAT CGAATACTAC TCACTCTTT CAATGTTTT CAATGTTTT CAATGTTTT CAATGTTTA CAATGTTTA CAATGTTTA TGGCCATTTA TAGCCATTTA ATTTTTTTTGG CCCTATCTTTA ATTTTTTTTTT	ACGTCTCCAT GATTCGGGGG ACTCCACCAC ACTCCACCAC CGCTAGGTCG CGCAGCCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCACCGGG GTGTTCACCGG GTGTTCACGG CATATTAACGC TTTGACAAAC TTTGACAAAC TTTGACAAAC CCTTATTTTT AGAGCCTGGA TTTGCCAATTT AGAGCATGGAT ACCCAGTAGT ACCCAGTAGT ACCCAGTAGT ATTCCAGTAT ACTCCAGTATT CAGCATATT ACTCAGTAT ACTCAGTATT CAGCAGTATT ACTCAGTATT CAGCAGTATT ACTCAGTATT ACTCAGTATT ACTCAGTATT ACTTGGTT ACCAGGAT ACTTGGTT AGTAGTTTTT AGTAGTTTTTT AGTAGTTTTTT ACTAGGATT ACTTGGTT ACCAGGAAA CCCTGTTTTT AGTAGCAGAAA CACTGTTTTT AGTAGTTTTT AGTAGTTTTT AGTAGTTTTT AGTAGTTTTT ACCAGGAAA CCCTGTTTTT ACTTCAGGAAA CCCTGTTTTT ACTTCAGCAGAAA CCCTGTTTTT ACTTCAGCAGAAA CCCTGTTTTT ACTTCACGAAAA CCCTGTTTTT ACTTCACACAAAA CCCTGTTTTT ACTTCACACAAAAA CCCTGTTTTT ACTTCACAAAAAAAAAA	ATAATGTTA TAACGGTGTC GAGTGAGGGCG GAGTGAGGGCG CCTCGGGGCA TCGTGGCCA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGATTTCAACATCTG CAACATCTGC TCAAGAAGC TCAAGAGC TCAAGAAGC TCATGACAC TCACTGC TCACTGC TCACTGC TTGTTCTTC TGGAGAACT TTCCTCAATG TCTTTAATAT AGCTAATTTG TCTTTAATAT TGGAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGATG AAAGAGATG AAAGGAAAA ACGGTGAAA CCTGTCATTG GAAGCATTT TAGATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTAC TCCTCACTA ACATCAGTGG ACGCACTGG CCAGTTTTC TCCTAAGCT GAGCGACTGG GATACCACT GCTACCTTT TCCTCACACT CCAGAGAGA ACCTACCACT ACTTACTT TCTTACTT TCTTTTTTAAT TCAAGTCCGT TTTTTTAAT CCAAGTCCGT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA GTGTCCTCAG CACCCTGGTT CGAGACCTTGG CACCCTGGTT CGAGACTTG CACCCTGGTT CAACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA AGATGGCAC ATTCGTCCTTT GGTGACTTTT GGTGACTTTT GGTGAACTTTT GGAACAGGA GATATACTGT CCAACACTGCT CATAGTGTAC CTAGTAGTAC CTAGTAGTAC CTAGTAGTAC CTAGTAGTAC CTAGTAGTAC ACAATTGTAC ACTAGAATA AATGATTAC ACTAGAAAA ATCCCTTTTAG CTCCTCCA ATAGGTTACA CACAGACTTTAC CTCCTCCA ATAGGTTACA CAAGACTTTT CTTCACCTCA ATAGGTTACA CAAGACTTTT CTTCACCTCCA ATAGGTTACA CAAGACTTTT CTTCACCTCCA CAAGACTTTT CTCTCCTCCA CAACACTCT CTCTCCTCCA CAACCTCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCA CAACCTCT CTCTCTCA CAACCT CTCTCTCT	120 180 240 300 360 480 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1620 1740 1860 1980 1980 2040 2160 2160 2220
50 55 60 65 70	TGTTTATTTC GATACGACC CCTCTGCCTC GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATG TTAAGGATG ATTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGCCAATCC GGAATTACGAT TTTACTGGAT TTTACTGGAT TTTACTGGAT TTTTCTCCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTGAGCAA ACAATAACG ATTCATTGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ACATTAATGA ATTCCTCCAG AAAACTGGAT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCATGCATC GCCACGTGT CTCCGCAGAG AGACCTAATA TITTGGAACT GCACTATCA GCACTATCA GCACTATCA GCACTATCA TCTCGCAGAG ACACTATCA TCACCTGTTT TCTGCCGGTA TCAGAGAATGGA ACACTGATCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATGGAGAG AAATGAAGAT AGTGACACGC GTTTGGCTCT GACAATACAC ATTAACTGAT CGAATACTAC TCACTCTTT CAATGTTTT CAATGTTTT CAATGTTTT CAATGTTTA CAATGTTTA CAATGTTTA TGGCCATTTA TAGCCATTTA ATTTTTTTTGG CCCTATCTTTA ATTTTTTTTTT	ACGTCTCCAT GATTCGGGGG ACTCCACCAC ACTCCACCAC CGCTAGGTCG CGCAGCCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCCC CGAGCTTCACCGGG GTGTTCACCGG GTGTTCACGG CATATTAACGC TTTGACAAAC TTTGACAAAC TTTGACAAAC CCTTATTTTT AGAGCCTGGA TTTGCCAATTT AGAGCATGGAT ACCCAGTAGT ACCCAGTAGT ACCCAGTAGT ATTCCAGTAT ACTCCAGTATT CAGCATATT ACTCAGTAT ACTCAGTATT CAGCAGTATT ACTCAGTATT CAGCAGTATT ACTCAGTATT ACTCAGTATT ACTCAGTATT ACTTGGTT ACCAGGAT ACTTGGTT AGTAGTTTTT AGTAGTTTTTT AGTAGTTTTTT ACTAGGATT ACTTGGTT ACCAGGAAA CCCTGTTTTT AGTAGCAGAAA CACTGTTTTT AGTAGTTTTT AGTAGTTTTT AGTAGTTTTT AGTAGTTTTT ACCAGGAAA CCCTGTTTTT ACTTCAGGAAA CCCTGTTTTT ACTTCAGCAGAAA CCCTGTTTTT ACTTCAGCAGAAA CCCTGTTTTT ACTTCACGAAAA CCCTGTTTTT ACTTCACACAAAA CCCTGTTTTT ACTTCACACAAAAA CCCTGTTTTT ACTTCACAAAAAAAAAA	ATAATGTTA TAACGGTGTC GAGTGAGGGCG GAGTGAGGGCG CCTCGGGGCA TCGTGGCCA AAGGAGGATC CTACCATTT ATCATATGCT CTCTCAGAA TTGAAGATTTCAACATCTG CAACATCTGC TCAAGAAGC TCAAGAGC TCAAGAAGC TCATGACAC TCACTGC TCACTGC TCACTGC TTGTTCTTC TGGAGAACT TTCCTCAATG TCTTTAATAT AGCTAATTTG TCTTTAATAT TGGAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT TTGAAGGTCCT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAGAGATG AAAGAGATG AAAGGAAAA ACGGTGAAA CCTGTCATTG GAAGCATTT TAGATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTAC TCCTCACTA ACATCAGTGG ACGCACTGG CCAGTTTTC TCCTAAGCT GAGCGACTGG GATACCACT GCTACCTTT TCCTCACACT CCAGAGAGA ACCTACCACT ACTTACTT TCTTACTT TCTTTTTTAAT TCAAGTCCGT TTTTTTAAT CCAAGTCCGT	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA GTGTCCTCAG CACCCTGGTT CGAGACCTTGG CACCCTGGTT CGAGACTTG CACCCTGGTT CAACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA AGATGGCAC ATTCGTCCTTT GGTGACTTTT GGTGACTTTT GGTGAACTTTT GGAACAGGA GATATACTGT CCAACACTGCT CATAGTGTAC CTAGTAGTAC CTAGTAGTAC CTAGTAGTAC CTAGTAGTAC CTAGTAGTAC ACAATTGTAC ACTAGAATA AATGATTAC ACTAGAAAA ATCCCTTTTAG CTCCTCCA ATAGGTTACA CACAGACTTTAC CTCCTCCA ATAGGTTACA CAAGACTTTT CTTCACCTCA ATAGGTTACA CAAGACTTTT CTTCACCTCCA ATAGGTTACA CAAGACTTTT CTTCACCTCCA CAAGACTTTT CTCTCCTCCA CAACACTCT CTCTCCTCCA CAACCTCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCCA CAACCTCT CTCTCCTCA CAACCTCT CTCTCTCA CAACCT CTCTCTCT	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1320 1380 1450 1560 1680 1740 1880 1740 1880 1980 2040 2160 2160 2160
50 55 60 65 70	TGTTTATTTC GATACGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCC AATCCAGCC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA GGGCCAATCC GGAATTACGG TCTTTCTGAG GGGCCAATCC GGAATTACGG TCTTTCAGGA AGAGAGGAT TTTCTTCAGG AGGTGTCAGA TGAGAGAGAT TTTCTTGAGT TTTTTGAGTAT AATCATAAAAT AATCATGAT AATCATCAAT AATCATCAAT AATCATCAA AACAAATGCA AAAACTGGAA AAAACTGGAA AAAACTGGAA AAAACTGGAA AAAACTGGAA AAAACTGGAA AAAACTGGAA AAAACTGGAA AAAACTGGAA AAAACTGGAT AATCATGTTT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGT GCCCCAGAGT AGACCTAATA ATTTTGGAACT GCAGAGAC TCACGGGA AGACCTAATA TCTGCCGGTA TCAGAGAC TCACGGT TCTGCCGGTA TCAGAGATACT TCTGCCGGTA TCAGAGATGGCT TCCAGTGTTT TCTGCCGGTA TCAGAGATAGCT CCCAGTGGGA AAATAGAGAT AGTGACAAGG GAGATACCTC GACAATACCAC ATTAACTGAT GGAAAATAGA GTTGCTCTTT CAGGCTTTT CAGGCTCT GACAATACAC ATTAACTGAT AGTACATATA AGTGTTTA AGGCCATTTG CAATGTGTTA AGGCCATATACT ATTTTTTGTG CCTCCCAT TCTCCCCAT TCTTCCCGAT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCGCCCC CGAGCTTCC CGAGCTCC CGAGCTTCC CGAGCTCC CGAGCTTCACCGGAG GTCACACAC CATATCAAGC CATATCAAGC TTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGCCCATATT TCTCTTGGAG CCCTATATTTT AGAGCCTGA TTTGCCAATA ACCATCAGAA CGGTGCATTC ATCCACTAGAA CGGTACAGAA CGGTACATA ACCATCAGTAT CAACAGAAT AACTTGGTA ACACAGAAT AACTTGGTA TAACTTGGAT TAACTTGGAT TCACACAGAAA ACACTGGTTTTT GGTCACAGCCT GTCACAGCCT TTTTTTGAA CCACAGAAAA CCACTTTTTT GTCACAGCCT TTTTTTGAA CCACAGAAAA CCACTTTTTT GTCACAGCCT GTCACAGCCT TTTCACACCAGAAAA CCACTTTTTT GTCACAGCCCT GTCACAGCCCT GTCACAGCCCT TTTCACAGCCCT TTTCACACCAGAAAA CCACTTTTTT GTCACAGCCCT GTCACAGCCCT GTCACAGCCCT GTCACAGCCCT GTCACAGCCCT GTCACAGCCCT GTCACAGCCT GTCACAGCCT GTCACAGCCT GTCACAGCCT GTCACAGCCT GTCACAGCCT TTTTTCACACCAGAAAA CCCCTTTTTT GTCACAGCCT GTCACAGCCT TTTTCACACCAGCACA CACTCTTTTT GTCACAGCCT GTCACAGCCT TTTTCACACCAGCACA CACTCTTTTT GTCACAGCCT GTCACAGCCT GTCACAGCCT TTTTTCACACCAGCACA CACTCTTTTT GTCACAGCCT GTCACAGCCT TTTTTCACACCAGCCT GTCACAGCCT TTTTTCACACAGCCT GTCACAGCCT TTTTTCACACCAGCACA CACTCTTTTTCACACCAGCACA CACTCTTTTTCACACCAGCACA CACTCTTTTTCACACCACAC	ATAATGTTA TAACGGTGTC GAGTGAGGGCG CCTCCGGGCAG CCTCCGGCAG AGGAGGATCTCCG CCTACCAGGA AAGGAGGATC CTACCATTT ATCATATGCT CTTCAGAA TTGAAGATCTTC CAACATCTG CAACATCTG CAAGAGCC TCAAGAAGC CAAGTGGAAC AAGGTGGAAC AAGTGGAAC AAGTGGAAC TCAAGAAGC GTGAAGCAGT TCACTGACA TCACTGACA AAGTGGAAC TCACTGACAG AACTTGCTCT TCACTGACAG CTGAACATCTG TCATTGACAAC TCGACTTGCTTTT TCACTGAAGA GAAATAAGA GAAATAAGA GATTTCTTCA GTACTACTT TTCCTCAAT TCCTCAATT TCCTCAATT TCCTCAATT TCCTCAATT TCGTTTCTTC GAGCATACTC GAGCATACTC GAGCATACTC	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG CCCCAGGT CCAGGGGCTA CAGGACAATG AAAGGACATA AAAGGACATA AAAGGACATA AAAGGACATA AAAGGACATA AAAGGACATA AAAGGACATA AAAGGACATA AAAGGACATT TAGAATGTAT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTGC AGGTAATCGG GGGAACTATG GCGACTGCA ACATCAGTGG AGCCCTGCAG CCCAGTTTTCT TCCTAAGCTG GACCCTGCAG CCCAGTTTTCT TCCTAAGCTG GACCCTGCAG AAACTATC CCCAGTAACCACT TCCTAAGCTG AACTTTCCTT TCCTAAGCTG AACTTTCCTT TCCTAAGCTG AACTTTTTTTATCTT TAGAAAATTTC TTTTTTAATCT TTTTTTAATCT TCCAAGTCCT TGGAAAATTTC TTTTTTAATCTT TAGAAAATTTC TTTTTTTAATCT TCCAAGTCCT TGGAAGACTTTA	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GCAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACCCTGGCT CACCCTGCT CACCCTGCT AAGACTCCT AATCGTCCTA ATTCGTCCTA ATTCGTCCTT AAGATGGAG TGTCAGCAGG AATCTTTTT GGGAACACGAG AATCTTTTT GGGAACACTCA GGTGAATTAA GGGAACACTCA CATATGTGC CATATGTGC CATATGTGC CATATGTAC AATGAATTAC CTCATTATGTAC AATGAATTAC CATAGATTAC CATAGATTAC CATAGATTAC CATAGATTAC CATAGATTAC CATAGATTAC CATAGATTAC CATAGATTAC CATAGATTAC CATAGACTTTA TGTTAAGGTTAC CAAGACCTTCA ATAGGTTACA CAAGACCTTCA TGTTAAGGTTACA CAAGACCTTGA GAAGACCTTGA GAAGACCTTGA GAAGACCTGA	120 180 240 300 360 420 660 720 780 840 900 1020 1140 1200 1140 1320 1440 1500 1680 1740 1860 1920 1980 2040 2100 2220 2280
50 55 60 65 70	TGTTTATTC GATACGACC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGAT TTAACGGAT ATAATCTGGT AGATTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA TGATCATTGG TACTCTTGGG TACTCTTGGG TACTCTTGGGT TTTTCCTGGGT TTTTCCTGGAT TTCTTCCAGG AGGTGTCCAGA TCTTCAGGAAT TCTTCAGGAAT TCTTCAGGAAT TCTTCAGGAAT TCTTCAGGAAT TCTTCAGGAAT TCTTCAGGAAT TCTTCAGAAT AGGAGAGACT TTTGTAGTAT AATCATTAAAA ACATAAATGAA ACATAAATGCA TTTCCTGCAG AAAACTGGAT ATTCCTTTCTGAGTAT ACTTCACTTAAT TTCCTTCAGGAAAATGCAA TTTCCTGCAG AAAAATGCAA TTTCCTGCAG AAAACTGGAT ATTTCCTTTCTTCTGTTTCTTCTTCTTCTGCAG AAAAATGCAA TTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCACGTGTA GCTCTGCAGCT CTCCGCAGAG TGATGCATTA TTTTGGAACT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTGCAGTT TCTAGAGATGGA TCAAGAATAGA TCAAGTATGT CTATGAGAGA AAATGAAGA AAATGAAAGA GAGAATACTC GACTATTCCTGATTAAT TCTTCCTCAT CACACTTTT CTATGCTTT TCTGCATTTCCTAT TCTTCCTAT TCTTCCTATT TCTTCCTAT TCTCCTAT TCTCCTAT CACCATTTCC	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCC CCAGACCCG CCAGACCCG CTACCCAC GTGTACCGCG GTCACACCA GTGTTCACCGG GTCACACCAG GTGTTCACCG GTGTTCACCG GTGTTCACGG GTGTTCACGG GTGTTCACGG GTGTTCACAG GTCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGAT GACCATCAGA GGGAGAGAGAG GGGAGAGAGAG GGGTCATC ACCATGGAT GACCATCAGA ATTCCAACT ATTCCACT ATTCCACT ATTCCACT TAACTTGGTA ACATGGGAT TAACTTGGTA ACATGGGATT TAACTTGGTA ACATGGGATT TGTGTTTTGAA TCCACAGAAA CACTGTTTTT TGTTTTTGAA TCCACAGAAA CACTGTTTTTT GTCACAGCCT CTTTCCACAT	ATAATGTTA TAACCGTGTTA TAACCGTGTTA CAGGGCCG CCTCGGGCCC CCTCGGGCCC CCTCGGGCAC CTCCACACGG TCCTGCGCAC TCACACTTT ATCATATGCT CTCTTCAGAA ATGAAGATTTC CAACATCTGC TCAAGAGACTCTT CAACATCTGC TCAAGAGACTCTT TCAACATCTGC TCAAGAAGCC TCAAGTGGAAC AGGTGGAAC TGGACCTGGC ACTTGACAAC GTGTTGTTTG TGGAGAATAGA GAATTCTTTG TGTTTCTTCAATGT TCTTCAATGT TCTTCAATGT TCTTCAATGT TCTTCAATGT TCTTCAATGT TCTTTAATT TCCTCAATGT TCTTTAATTT TCTTCAATTT TCCTCAATTT TCCTCAATTT TCCTCAATTT TCCTCAATTT TCTTTAATTT TCAAGGTCCT TTTTTTTTTT	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAAGAGTG GAAGGCATTT TAGAATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TACCAAAGCC CTTTAATCCA TAGGGAATACGA GGGAACTAT TCCTCACTA ACATCAGTGG GCGACTGC GCTACCTGGAG ACCCTGCAGAGAA ACCCTACCTT ATTACTTAATCCA TGCCAGAGAA TCCTTAACTTG TCCTAACTTG TCCCAGAGAA TCCCTTACTT ATTACTTC ATTACTTC ATTACTTC ATTACTTC ATTACTTC AGATAACTTC TTTTTTAAAT CCAAGTCCGT TGCCAGAGAA TCCTTACTTG TTTTTTAAAT CCAAGTCCGT TGGCATTAACTTC TTTTTTAAAT CCAAGTCCGT TGGCATTAACT TTTTTTAAAT CCAAGTCCGT TGGCCATTAC TTGGCTTGCCT TGGCATTAC TTGGCTTGCT TTGTCACTTG TGGCATTAC TTGTCTCACTTG TGGCATTAC TTGTCACTTG TGCCACTTC TTGTCACTTC TTGTCACT TTGTCACC TTGTCACT TTGTCACC TTGTCACT TTGT	CCCACACTCG AACACTGGCA AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC CAGCCCTTAGT GCAGCCCTAGT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTA TGTCCCTGT AAGATGGCAG AATCTTTTC GATGGCAGC AATCTTTTC GATGGCATCA GGGAACTCTA CGGAACACGCG AATCTTTTC CATAGCAGC GATATACTGT CCATAATGTAG AACAATTGTGC CTATAGCTAC CATAATGTAG ACCTAGAAAA CCCTAGAAAA CCCTTTCCT ATTAGGTAA CCTAGCCCA ATAGGTTAC CAAGACCTTT GTTAAGGTAA CAAGACCTGA GAGACCTGA GTCAGGCGAC	120 180 240 360 480 540 660 720 780 960 1080 1140 1260 1380 1440 1560 1560 1680 1740 1880 1740 1890 2040 2100 2100 2220 2340
50 55 60 65 70	TGTTTATTTC GATACGACC CCTCTGCCTC GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATT GTAACGATT ATATTGGAT GCATCAGCTT ATATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG TTTACTGGAT TTTACTGGAT TTTACTGGAT TTTACTGGAT TTTACTGAG AGGGTCAGAC TTTACTGAG TGGAGAGAC TTTTACTGAAT GGGACAGACT TTTTACTGAAT GGGACAGACT TTTTACTGAAT ACATTAATGA ACATTAATGA ACAAATGCA ATTTCATCTA AACAAATGCA ATTTCTCTGAG AAACTGGAT ATTTCTTCAGG AAACTGGAT ATTCTTCAGGA AACAATGCA TTTCTCTGCAG AAACTGGAT ATTTCTTCAGGAT ATTTCTTCTGCAG AAACTGGAT ATTTCTTCAGGAT ATTTCTTCTGCAG AAACTGGAT TTTCTGCAGT ATTTCTTCTGCAGT ATTTCTTCTGCAGT ATTTCTTCTTCAGCAT TTTCTGCAGT ATTTCTTCTGCAGT ATTTCTTCTTCAGCAT ATTTCTTCTTCAGCAT TTTCTGCAGT ATTTCTTCTTCAGCAT ATTTCTTCTTCTGCAGT ATTTCTTCTTCTGCAGT ATTTCTTCTTCTTCTTCTTCTGCAGT ATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCTGGGAGC CCCCCCAGCTGTA GCTCTGCAGC CCCCCAGACT TCTCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCCACAGTGTT TCTGCCGGTA TCAAGAATGCA TCAAGAATGCA ACTGATGCA CACAGTGGGA CAAGTAGTA CTCATCTCT CTATGGAGAG AAATGAAGAG AAATGAAGAG GAGAATACTCT GACTAATCACT GACTATTGC GACTATTGC GACTATTGC GACTATTGC GACTATTGC GACTATTGC ACTATCTTT CACGCTTTA AGGCATTATA ATTTTTTTGTG CCCTATCTTTA TCCTCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCACCCATTGTC AGGGTCTTGTTC AGGGTCTTGTTC AGGGTCTTGTTC AGGGTCTTGTTTC AGGGTCTTGTTC AGGGTCTTGTT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CCGCGCCC CCGAGCCTC CCGAGCCCC CGAGCTTCCC CTTACCGGAG GTCTACACCAG GTGTTCACCGG GTGTTCACCG CATATTAACG GTGTTTCACAGAC CTTGACAAAC CTTGACAAAC CTTTGACAAAC CTTTGCCAATTT TCTCTTGGAG CCTTATTTT AGAGCCTGAA TTTCCCAATT GACCATCAGA GGAGAAGAAC CGTTGATTAC ACATGATAC ACATGATAC ATTCCAATTA ACACTATTA ACACTATTAC AATTCGAATA CAAGAGTGAT TAACTTGGTA ACATGGAT TAACTTGGTA ACATGGATT AGTAGTTTTAA TCCACAGAAA CACTGTTTTT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CCTTTTTAA CACTGGTTTTTA TCTCACAGAAA CACTGTTTTT CTTTCCACAT GCCTTATAGA	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGCGC CCTCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATCTTC ATCATATGCT CTCTCAGAA TTGAAGGATTTT ATCATATGCT TCAACATGGA AAGAGCTCTT CAACATCTGC CAACATCTGC CAAGTGGAAC AAGGTGGAAC AGGTGGAAC AGGTGGAAC ACTGGACATGG AACTGGCAC GTGATGTTTT TGAAGAATTTG GGAGAATGG GAATTTTTTTT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGAAAA GACGTGGAG GAACGATT TAGATGTAT AGAGTGTAT TAGATGTAT TAGATCAGTGG GGGACTGG GGGACTAG CCCAGGAGAA ACCTTAAGTCG GATACCAGT GATACCAGT GATACCAGT GATACCAGT GATACCAGT GCTACCAGT TCCTAAGTC TCTTAAGT TGTTACT TTTTTTAGT TAGATTAC TTTTTTTAAAT CCAAGTCCGT TGTGCATTAG CTGCGTGGCT CCCCATGGCT CCCCATGCT CCCCATGCT CCCCATGCT CCCATGCT CCCCATGCT CCCATGCT CCCCATGCT CCCATGCT CCCCATGCT	CCCACACTCG AACACTGGCA ACACTGGCTCC CAGCCTTAGT GCCGGTCTGC GCACCCTTGGTGCAG GCACCCTTGG AAGGATTGCA GTGGGGACTTC CAGACCCCA TGGTCCTCAG CACCCTGGTT CAGAGACTCA TGGTCCTCAG CACCCTGGTT CAACAGCTTG AATCGTCCTTA GTGTCCCTGT AAGATGGAG TGTCAGCAG TGTCAGCAG GATATACTGT CAACAGCTCA ACAATTGTC GCTAACAGAG GATATACTGT CATAATGTAC ACATTGTCC CATAATGTAC ACATTGTAC ACATTGTAC ACATTGTAC ACATTGTAC ACATTGTAC CATAATGTAC CATAATGTAC ACATTGTAC ACATTGTAC ACATTGTAC ACAGACTTTT CTTAAGGTAA CAAGACTTTT GTTAAGGTAA GAAGACCTGA ACAATTATAC GTCAGGCAC GACATATAGT GTTAAGGTAA GAAGACCTGA GACATATAGT GACACAGGAC GACATATAGT GACACAGGAC GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT	120 180 240 300 360 420 660 720 780 840 900 1020 1140 1200 1140 1320 1440 1500 1680 1740 1860 1920 1980 2040 2100 2220 2280
50 55 60 65 70	TGTTTATTTC GATACGACC CCTCTGCCTC GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGATT GTAACGATT ATATTGGAT GCATCAGCTT ATATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG TTTACTGGAT TTTACTGGAT TTTACTGGAT TTTACTGGAT TTTACTGAG AGGGTCAGAC TTTACTGAG TGGAGAGAC TTTTACTGAAT GGGACAGACT TTTTACTGAAT GGGACAGACT TTTTACTGAAT ACATTAATGA ACATTAATGA ACAAATGCA ATTTCATCTA AACAAATGCA ATTTCTCTGAG AAACTGGAT ATTTCTTCAGG AAACTGGAT ATTCTTCAGGA AACAATGCA TTTCTCTGCAG AAACTGGAT ATTTCTTCAGGAT ATTTCTTCTGCAG AAACTGGAT ATTTCTTCAGGAT ATTTCTTCTGCAG AAACTGGAT TTTCTGCAGT ATTTCTTCTGCAGT ATTTCTTCTGCAGT ATTTCTTCTTCAGCAT TTTCTGCAGT ATTTCTTCTGCAGT ATTTCTTCTTCAGCAT ATTTCTTCTTCAGCAT TTTCTGCAGT ATTTCTTCTTCAGCAT ATTTCTTCTTCTGCAGT ATTTCTTCTTCTGCAGT ATTTCTTCTTCTTCTTCTTCTGCAGT ATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCTGGGAGC CCCCCCAGCTGTA GCTCTGCAGC CCCCCAGACT TCTCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCCACAGTGTT TCTGCCGGTA TCAAGAATGCA TCAAGAATGCA ACTGATGCA CACAGTGGGA CAAGTAGTA CTCATCTCT CTATGGAGAG AAATGAAGAG AAATGAAGAG GAGAATACTCT GACTAATCACT GACTATTGC GACTATTGC GACTATTGC GACTATTGC GACTATTGC GACTATTGC ACTATCTTT CACGCTTTA AGGCATTATA ATTTTTTTGTG CCCTATCTTTA TCCTCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCACCCATTGTC AGGGTCTTGTTC AGGGTCTTGTTC AGGGTCTTGTTC AGGGTCTTGTTTC AGGGTCTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTTC AGGGTTCTTGTTC AGGGTTCTTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTC AGGGTTCTTGTTC AGGGTTTTGTTC AGGGTTCTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTCTTTC AGGGTTTTTC AGGGTTTTGTTC AGGGTTTTTC AGGGTTTTCTTC AGGGTTTTCTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGGTTTTGTTC AGGTTTTGTTC AGGTTTTGTTTT	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CCGCGCCC CCGAGCCTC CCGAGCCCC CGAGCTTCCC CTTACCGGAG GTCTACACCAG GTGTTCACCGG GTGTTCACCG CATATTAACG GTGTTTCACAGAC CTTGACAAAC CTTGACAAAC CTTTGACAAAC CTTTGCCAATTT TCTCTTGGAG CCTTATTTT AGAGCCTGAA TTTCCCAATT GACCATCAGA GGAGAAGAAC CGTTGATTAC ACATGATAC ACATGATAC ATTCCAATTA ACACTATTA ACACTATTAC AATTCGAATA CAAGAGTGAT TAACTTGGTA ACATGGAT TAACTTGGTA ACATGGATT AGTAGTTTTAA TCCACAGAAA CACTGTTTTT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CTTTCCACAT CCTTTTTAA CACTGGTTTTTA TCTCACAGAAA CACTGTTTTT CTTTCCACAT GCCTTATAGA	ATAATGTTA TAACGGTGTC GAGTGAGGCG GAGTGAGGCG CCTCGGGCGC CCTCGGGCAC GTCCACACGG TCGTGGCCGA AAGGAGGATCTTC ATCATATGCT CTCTCAGAA TTGAAGGATTTT ATCATATGCT TCAACATGGA AAGAGCTCTT CAACATCTGC CAACATCTGC CAAGTGGAAC AAGGTGGAAC AGGTGGAAC AGGTGGAAC ACTGGACATGG AACTGGCAC GTGATGTTTT TGAAGAATATTG GAAGAATATTG GAAGAATATTG GAAGAATATTG GTGTTTTTTT TGAAGGTCTTT TTCCTCAATG TCTTTAATAT AGCTAATTTG GTGTTTTTTT TGAAGGTCCT GAGCATACTC TTTGTTATAT TTCAAGTTTTTTT TGAAGGTCCT TTTTTTTTTT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAGGAAAA GACGTGGAG GAACGATT TAGATGTAT AGAGTGTAT TAGATGTAT TAGATCAGTGG GGGACTGG GGGACTAG CCCAGGAGAA ACCTTAAGTCG GATACCAGT GATACCAGT GATACCAGT GATACCAGT GATACCAGT GCTACCAGT TCCTAAGTC TCTTAAGT TGTTACT TTTTTTAGT TAGATTAC TTTTTTTAAAT CCAAGTCCGT TGTGCATTAG CTGCGTGGCT CCCCATGGCT CCCCATGCT CCCCATGCT CCCCATGCT CCCATGCT CCCCATGCT CCCATGCT CCCCATGCT CCCATGCT CCCCATGCT	CCCACACTCG AACACTGGCA AACACTGGCA CGCTGGCTCGC CAGCCTTAGT GCCGGTCTGC CAGCCCTTAGT GCAGCCCTAGT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTA TGTCCCTGT AAGATGGCAG AATCTTTTC GATGGCAGC AATCTTTTC GATGGCATCA GGGAACTCTA CGGAACACGCG AATCTTTTC CATAGCAGC GATATACTGT CCATAATGTAG AACAATTGTGC CTATAGCTAC CATAATGTAG ACCTAGAAAA CCCTAGAAAA CCCTTTCCT ATTAGGTAA CCTAGCCCA ATAGGTTAC CAAGACCTTT GTTAAGGTAA CAAGACCTGA GAGACCTGA GTCAGGCGAC	120 180 240 360 480 540 660 720 780 960 1080 1140 1260 1380 1440 1560 1560 1680 1740 1880 1740 1890 2040 2100 2100 2220 2340
50 55 60 65 70 75	TGTTTATTTC GATACGCACC CCTCTGCCTC GAATCTTCGG GTCTTCCTGC AATCCAGCC CCGGGACCGC GATCTGCCT GTAACGGTG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAA CATCATTGG TACTCTTGAG GCGCAATCCTGGATTCATTGGAT TCTTCAGGA TCTTCATGGT TTTATCTGGAT TCTTCAGGA AGGTGTCAGA TACAGCAA ACATTAGAT ACATCATAAT AATCATCAAA ACATTAATGA ACATTAATGA ACATTCATCA AACAAATGCA AAAACTGGAT ATTCCTGCA TTCCTGCA TTTCCTGCA AAAACTGGAT AATCTGTAT AATCTGTAT AATCTGTAT AATCTGTAT AATCATCAA AAAACTGGAT AATCTGTTTCTCAGGAA AAAACTGGAT AATCTGTTTCTCAGAA AAAACTGGAT AATCTGTTTCTACAAGAACTGGAT AATCTGTTTCTACAAGAACTGGAT AATCTGTTTCTACAAGAACTGGAT AAGATCTCAAGAACTGGAT AGGTACTCAG	CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA ATTTTGGAACT TCTGCCGGTA TCAAGAATGG AACTGATT TCTGCCGGTA ACTGATGT TCAGCAGTGT CCACTGTTT TCTGCCGGTA ACTGAGCCT CCAGTGGTA CAAGAATGG AACTGATGTT CTATGAGAGA AAGTATGAGAGA AAGTATGACGC GACAATACCC GTTTGGCTCT GACAATACAC ATTAACTGAT CAGATGTTTA CGGAAAATAGA GTTACTTTA CAGCATTTTA CAGCATTTTA CAGCATTTTA CAGCATTTTA CATTTTTTTTTG CCTTTTA TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCTGAT AGGCCTTTTTA AGGCCTTTTTA CAGCGTCTTTTA CAGCGTCTTTTTCTTGAT CACCATTGTC AGGGTCTTTTTA TCTTCCCCAT TCTTCCTCCAT TAAATGGTTTT AGGCCTTTTTA TAAATGGTTTT AGGCTCTTTTTAAATGGTTTT TCTTCCTGAT CACCATTGTC AGGGTCTTTTT TAAATGGTTTT TAAATGGTTTT TAAATGGTTTT TTAAATGGTTTT TTAAATGGTTT TTAAATGGTTTT TTAAATGGTTTT TTAAATGGTTTT TTAAATGGTTTT TTAAATGGTTTTAAATGGTTTT TTAAATGGTTTT TTAAATGGTTTT TTAAATGGTTTT TTAAATGGTTTT T	ACGTCTCCAT GATTCGGGGG ACTCCACCAT ACTCCACCAT CGCTAGGTCG CGCAGCCCC CGAGCTTCC CGAGCTCC CGAGCTTCC CGAGCTTCACCGGAG GTCACACAG GTCACACAG GTCACACAG GTCACACAG GTCACACAG GTCACACAG CCTATTTT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCAAT TTTCCCAAT ACCAGTAGA CGGTACATC ACCATCAGA GGAGAAGAG GGAGAAGAG ACCATCAGA ACCATCAGA ACCATCAGA TATCCAGTAT ACACGGAT AATCCAGTAT CAACTTGTT AGACTTGTTT AGACTTGTTT AGACTTGTTT ACACGAAA CACTTGTTT TGTTTTTGAA TCACAGAAA CACTTTTT GTCACAGCC CTTTCCCACT TTTCCCACT TTTCCCACT TTTCCCACT TTTCCCACT TTTCCCACT TTTCCACT TTTCCCACT TTTCCACT TTTCCACT TTTCCACT TTTCCACT TTTCCACT TTTTCCACT TTTCCACT TTTTCCACT TTTCCACT TTTTCCACT TTTTCCACT TTTCCACT TTTTCCACT TTTCCACT TTTTCCACT TTTCCACT TTTTCCACT TTTTCCACT TTTTTCCACT TTTTCCACT TTTTTCCACT TTTTCCACT TTTTTCACCACT TTTTTCACCACT TTTTTCACCACT TTTTTTCACC TTTTTTTT	ATAATGTTA TAACGGTGTC GAGTGAGGGCG CCTGGGGGCG CCTCCGGGCA TCGTGGCCGA AAGGAGGATCTCCG TCTCACACGG TCGTGGCCGA AAGGAGGATC CTCTTCAGAA TTGAAGGAT TCAACATCTGC TCAAGAAGC TCAAGAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC AAGGTGGAAC AAGGTGGAAC AGGTGGAAC GTGAAGCAGT TCACTGACA TCAAGAAGT TCACTGAAGT TCACTGAATTTG TGTTTCTTCA TCGTTACTAC TCTTTAATAT TGGTTTTCTT TGAAGGTCCT GAGCATACTC CAGTGAACAC TCATTGTTAC TCTTTGTAC TCTTTGTAC TCTTTGTAC TCATTGTACC CAGTGAACACT	CACGGGCATC ATTIGCTIGC CGGGTCTTGGG CCTGGGGGAG CCGCGAGAGG TGCCCAGGT TGCCCCAGGT CAGGGGCTA CGGAACAATG AAAGAGGTG AAAGAGATG AAAGAGATG AAAGAGATG GAAGGCATTT TAGTCTGTAT TAGATGTAT TAGATGTAT TACCAAAGCC TCTTAATCCA TGGGGACTAC TCCTCACTA ACATCAGTGG AGCTACTTG CCCAGTTTAT TCCTAAGCTG GAGCACTAC TCCTACTTT TCCTAAGCTG GAGCACTAC TTTATTTAGTCC AAGTTACTAT TCTTAACCACT TCCTACCTTT ACTTACTAT TCTTAAGCTG CAGAGAA ACCCTGCAGGAC TTTTTTAATCC AAGTTACATT CCTACCTTT CTTATTTAGTC AAGTTACTT TCTTAGTCC TGGCTGCCT TTTTTTAAT CCAAGTCCGT TTTTTTAAT CCAAGTCCTT TTTTTTAAT CCAAGTCCGT TTTGCTTCT TCCCCCATGGCT TTTGCTTCT TTTTTTAAT TCCAAGTCCGT TTTGCTTCT TCCCCCATGGCT TTTGCTTCT TTTTTTTA	CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA GTGTCCTCAG CACCCTGGT CACCCTGGT CACCCTGGT ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA CTGCTCTTTG GTGTCCTTTTG GTGTCCTTTTG GTGTCCTTTTG GTGTCCTTTTG GTGTCCTTTTG GTGTCCTTTTG GTGTCCTTTTG CAACAGCTTT AAGATGGAG AATCTTTTC CAACAGCTTC CATAGTTAAT GCAACACTCA ACAATTGTGC CATAGTTAC ATTGGTTACTTA ATTGGTTACT CTCTCTCA ATTGGTTAC CTCTCTCA ATTGGTTAC CTCTCTCA ATTGGTTAC CTCTCTCA ATTGGTTAC GTCAGCCGCA ACAATTTTC CTCTCCTCA ATTGGTTAC CTCTCCTCA ATTGGTTAC GTCAGCCGTA GACATATAGT GTTAAGGTTAC GACATATAGT TAGAAGTCTTA TAGAAGTGTTA TAGAAGTGTTA TAGAAGTGTTA TAGAAGTGTTA	120 180 240 300 360 420 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1860 1920 2040 2160 2220 2280 22400 2460
50 55 60 65 70	TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGAT ATAACGGAT ATAACGGAT ATAATCTGGT ATAATAAAAT TGAGGGCAAC TGAAATTGGA GATCTCATTGG TACTCATTGG TACTCATTGG TCCTTTGAG GGGCAATT TTTCTTCAGG TCCTGTGGCT TTTACTGGAT TTCTTCAGG AGGTGTCAGA TGAGAGAGAT TTTCTTGAGCAA TATCATTGGAT ACAAAGGCGA TTTCTTGAGCAA TATCCTGAAT ACAAAGACTGA ACAATAATGT ACTTCACTCA AACAAATGCA TTTCCTGCAG AAAACTGGAA TTTCCTGCAG AAAACTGGAA TTTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTGCAG AAAACTGGAT TTCCTTCACTAA ACAAATTCCTTTCTCACAGACTTTCCTCACAGACTTCTTCTCTCACAGACTCTTCTCTCTC	CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG GCACGCGTGAGCC CCCCCCAGGG AGACCTAATA TTTTGGAACT TCTGCAGGA TCACTGCTT TCTGCCGGTA TCACAGTGTT TCTGCCGGTA TCAGAGACCT TCAGAGACCT TCTGCAGGA AACTGTT TCTGCGGTA TCAGAGATGCA TCAGTGTGT CCAGTGGGA AATGAGACT CTATGAGAGA AATGAAGAG AAATGAAGA GGAGATACTC GACAATACCT GACAATACT GACAATACT TCAGGTTT TCTGCATTG CAATGTTA TGCACTTCT TCATGATTCA TCACTCT TCATGATTCA TCATCATTA TCACTCT CACATTTTC CACCATTGTC AGGGTCTTTA TCTTCCTCCAT TCACCATTGTC AGGGTCTTTT TCTTCCTGAT TCACCATTGTT TCACATTGTT TCACATTGTT TCACCATTGTT TCACATTGTT TCACATTGTT TCACATTGTT TCACCATTGTT TCACATTGTT TCACCATTGTT TCACATTGTT TCATATTTA	ACGTCTCCAT GATTCGGGGG ACTCCACCAT CGCTAGGTCG CTCGCCGCC CCAGACCCG CTGACCCGG GTCACCCAG GTCTACCGGG GTCACACCAG GTGTTCACCGG GTGTTCACCGG GTGTTCACCGG GTGTTCACGG GTGTTCACGG GTGTTCACGG GTGTTCACGG GTGCAATT TCTCTTGGAG GCCATATT TTCTCTTGGAG CCTTATTTT AGAGCCTGGAT GACCATCAGA GACCATCAGA GACCATCAGAT GACCATCAGAT GACCATCAGAT GATTCCAACT ATTCCAACTA AATTCGATAT TAACTTGGTA ACATGGGTT TAACTTGGTA ACATGGGTT TGTCACAGCCT CTTTCCACAT GCCTTATAGAA CACTGTTTTT GTCACAGCCT CTTTCCACAT TGTCACACCT CTTTCCACAT TGTATAGAAT TGTATAGAAT TGAAACCTCT TTGAAACCTCT TTGACAACCTCT TTGACAACCTCT TTGACAACCTCT TTGACAACCTCT TTGACAACCCTCT TTGACAACCTCT TTTCACAACCTCT TTTCACAACCTCT TTTCACAACCTCT TTTCACAACCTCT TTTCACAACCTCT TTTCACAACCTCT TTTCACAACCTC	ATAATGTTA TAACCGTGTTA TAACCGTGTTC GAGTGAGGCG CCTCGGGCCC CCTCGGGCCC CCTCGGGCCC CCTCGGCCC CTCCGGCCC CTCCGGCCC CTCCGGCCC CTCCGGCCC CTCCCACCGG TCGTGGCCGA AAGGAGGATC TCACATTTT ATCATATGCT TCAACATGGA AAGGGCTCTT CAACATCTGC CAAGTGGAAC TCAAGGAGC TCAAGGAGCC GTGAAGCAGC TCACTGACAC GTGTTGTTTG TGACAACAC GTGTTGTTTG TGAGAATGG GAAATAGAG GAATTCCTTCAATG TGTTTCTTCAATG TCTTTAATT TCCTCAATG TCTTTAATT TCCTCAATG TCTTTAATT TGAGGTCCT TTTTTTTTTT	CACGGGCATC ATTIGCTIGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG AAAAGAGGTG AAAAGAGATG GAAGGCATT TAGAATGTAT TCCTAAGTAG AGACAATTC TCCTAAGTAG AGACAATTC TCCTAAGCTG GAAGAACACT GCTACATTA TCCTAACTTG TGCCAGAGAA ACCTTACTTT TTTTTAAAT TCCATAGTAG TGCCAGAGAA CCTTACCTT TTTTTTAAAT TCCAAGTAG TTTTTTTTTT	CCCACACTCG AACACTGGCA ACACTGGCTCC CAGCCTTAGT GCCGGTCTGC GCACCCTTGGTGCAG GCACCCTTGG AAGGATTGCA GTGGGGACTTC CAGACCCCA TGGTCCTCAG CACCCTGGTT CAGAGACTCA TGGTCCTCAG CACCCTGGTT CAACAGCTTG AATCGTCCTTA GTGTCCCTGT AAGATGGAG TGTCAGCAG TGTCAGCAG GATATACTGT CAACAGCTCA ACAATTGTC GCTAACAGAG GATATACTGT CATAATGTAC ACATTGTCC CATAATGTAC ACATTGTAC ACATTGTAC ACATTGTAC ACATTGTAC ACATTGTAC CATAATGTAC CATAATGTAC ACATTGTAC ACATTGTAC ACATTGTAC ACAGACTTTT CTTAAGGTAA CAAGACTTTT GTTAAGGTAA GAAGACCTGA ACAATTATAC GTCAGGCAC GACATATAGT GTTAAGGTAA GAAGACCTGA GACATATAGT GACACAGGAC GACATATAGT GACACAGGAC GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT GACACAGAG GACATATAGT	120 180 240 300 360 480 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1500 1680 1680 1680 1680 1680 1920 1980 2040 2160 2210 2220 2234 2400

	CTCAACCATA	CTC -				m. m	2010
				CATATTGATT			2640
				CAACCCCCAG			2700
				TCATCTGTAT			2760
5				CAGCTCAGTG			2820
)				CAAGGGATCT			2880
				CAGTTTCATC			2940
	GCAGTCTGTG	GAAAAATTGT	CTTCCACAAA	ACTGGTCCCT	GGTGCCAAAA	ATGTTGGGGA	3000
	CCACTGCTCT	AGAGAGAGGT	CATGATATCA	TACCAACCAA	ATGGAAATGA	CAAATGTTTT	3060
				TITITITIT			3120
10 -				GCAGGTGCTC			3180
•				CTACTATGGG			
							3240
				TTTATCTAAG			3300
				GACATTGTAT			3360
1.5				TCTCTTTTCA			3420
15	TTCTAAAAGT	TTGATGCATT	GGAAAAATTT	CCTTGAGGCA	TTTAGCAACA	CATAGAAAAT	3480
	GGGCTTTGAT	TCTTTTCCAA	AACTTTTAGC	CATAGGGTCT	TTTATAGACA	GGGATAGTAA	3540
				GAATGATAAA			3600
				TGTTCTTTTC			3660
				CATTCTAAGG			3720
20							
20				TCTAGGAAAA			3780
				TTCCTATGAG			3840
	CCATCAACAC	ATTTTATACT	TTGCATCTCC	AAATTTATTG	TGGCGAGACT	TGTCCATTGT	3900
	GAAAGTTAGA	GAACATTATG	TTTGTATCAT	TTCTTTCATA	AAACCTCAAG	AGCATTTTTA	3960
	AGCCCTTTTC	ATCAGACCCA	GTGAAAACTA	AGGATAGATG	TTTAAAAAACT	GGAGGTCTCC	4020
25				TTTAAGTAAT			4080
				ACATCTGCAC			4140
				AAGAGTGCCA			4200
				TAATTGATCG			4260
20				CAAAAAGATC			4320
30	GATATTTGCA	TAATTGGCTG	CAATTATTTA	ATGTTTAATT	GGGTTGATCA	AATGAGATTC	4380
	AGCAATTCAC	AAGTGCATTA	ATATAAACAG	AACTGGTGGC	ACTTAAAATG	ATAATGATTA	4440
	ACTTATATTG	CATGTTCTCT	TCCTTTCACT	TTTTTCAGTT	TCTACATTTC	AGACCGAGCT	4500
				AACCAAGATT			4560
				ATTTGCTGTT			4620
35							
55				CCAAAAGAAG			4680
				TTTATAACAC			4740
				AGAAACAAGT			4800
	GAATCAGGTT	TTTTCTACCT	GGTAAACATT	CTCTATTCTT	TTCTCAAAAG	ATTGCTGTAA	4860
	GAAAAAATGT	AAGAC					
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45	(MKDCSNGCSA EWSSEFGWEK	 ECTGEGGSKE PHIKPLQNLS	 VVGTFKAKDL LHPGSSALHY	 IVTPATILKE AVELFEGLKA	 KPDPNNLVFG FRGVDNKIRL	TVFTDHMLTV FQPNLNMDRM	
45	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP	 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE	 IVTPATILKE AVELFEGLKA WVPYSTSASL	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK	120 180
	(MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV	 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN	120 180 240
	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG	 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
45 50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL	UVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240
	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY	 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT	UVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT	 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTH EDHQITEVGT LTMDDLTTAL DIQYGREESD	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO:	 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTH EDHQITEVGT LTMDDLTTAL DIQYGREESD	UVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA see id Accession	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession Lence: 121.	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE 1 #: NM_005	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	 KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI	TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300
50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQOVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding sequ	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA see id Accession	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequal	ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accession Lence: 121. 11	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 .1194 21	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300 360
50	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accessionence: 121. 11	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LOQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 .1194 21 TCGGTGGCCG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 I TTGTGCGCGCT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG	TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300 360
50 55	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequence ACAGAGGGCG CCCAGCTGGA	ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession ence: 121. 11 GGTCGCGCGC GGGGAACTAG	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LHPGSSALHY LQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE 1 #: NM_005 11194 21 TCGGTGGCCG TCTGCTCCAG	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 TTGTGCGCGT GTGGCAAGCT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA	TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC	120 180 240 300 360
50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequ 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG	ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession ence: 121. 11 GGTCGCGGG GGGGAACTAG ACTGGTACCA	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE 1 #: NM_005: 11194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTTC	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TTGTGCGCAAGCT TACGACTATG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGAA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC	120 180 240 300 360 60 120 180
50 55	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYD GCQVLWLYD GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG CGCTCCACGA	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accessionence: 121. 11	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LOQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AGTTGGTGCC	TVFTDHMLTV FOPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG	120 180 240 300 360 60 120 180 240
50 55	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG ACTTGGGTCC	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession Lence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA ACTCGTACCA GCACCCGGGA GCACCCGGGA	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 1194 21 1 CGGTGGCCG TCTGCTCCAG TCACTATTCC ACCCAGCCCT	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTIATG AAGAAATTCG CAGCTTTGGT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA ACTGCTGGCC CTCCTGGAAC	TVFTDHMLTV TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GCCGCCCTGG GCGGCCCTGG	120 180 240 300 360 60 120 180
50 55	 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG ACTTGGGTCC	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession Lence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA ACTCGTACCA GCACCCGGGA GCACCCGGGA	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 1194 21 1 CGGTGGCCG TCTGCTCCAG TCACTATTCC ACCCAGCCCT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA ACTGCTGGCC CTCCTGGAAC	TVFTDHMLTV TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GCCGCCCTGG GCGGCCCTGG	120 180 240 300 360 60 120 180 240
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequ 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG CGCTCCACGA ACTTGGGTCC GGGTGCCCTG	ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec ici Accession ience: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA CGCCCAGCGA GCAGCGGGG GCGGCGGGG	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LHPGSSALHY LOQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE #: NM_005: 1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCCT GGAATCCCAG	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTIATG AAGAAATTCG CAGCTTTGGT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGAG AAGCTTGGAG AAGCTTGGAG AAGCTTGGAA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTA CGCGAACTAC	120 180 240 300 360 60 120 180 240 300
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding sequil ACAGAGGGCG CCCAGCTGGA ATTGGACCGCG CGCTCCACGA ACTTTGGGTCC GGGTGCGCTCG GCCTCCCTCA	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA see id Accessionence: 121. 11 GGTCGCGGGG GGGAACTAG ACTCGTACCA CGCCAGCAGAC GCAGCAGAC GCAGCAGAC TCCGCCGGAACAC TCCGCCGTGA	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE 1 #: NM_005: 1194 21 TCGGTGGCCG TCTGCTCCAG TCTCTCAG TCACTATTC GGACATCTGG ACCAGCCT GGAATCCCAG CTGCATGTGG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGTTCT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGTGGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGGA ACCACCAGGA	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTCG GTGGCCGGTA GCCGAACTAC GCCGACTAC GCCGCTGAGG	120 180 240 300 360 60 120 180 240 300 360 420
50 55	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQOVLWLYG GWEFKVSERY LASRILSKLT Seq ID NO: Nucleic Accoding sequity according sequity according acc	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession lence: 121. 11 GGTCGCGCGC GGGGAACTAG ACTCGTACCA CGCCCAGCGA GCAGCCGGGA GCAGCCGGGA GCAGCAGGA GCAGCCGGGA GCAGCCGCGGA GCAGCCGGGA GCAGCCGCGGA GCAGCCGGGA GCAGCCGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGGA GCAGCCGGA GCAGCCGGGA GCAGCCGGA GCAGCCGGA GCAGCCGGA GCAGCCGGA GCAGCCGGA GCAGCCGGA GCAGCCGCGA GCAGCCGGA GCAGCCGCGCA GCAGCA GCAGCCGCGCGCA GCAGCCGCGCA GCAGCAGA GCAGCCGCGCA GCAGCCGCGCA GCAGCAGA GCAGCCGCGCA GCAGCAGA GCAGCCGCGCGCA GCAGCAGA GCAGCCCGCGCA GCAGCAGA GCAGCCCGCGCA GCAGCCGCGCA GCAGCCCGCGCA GCAGCCGCGCA GCAGCCGCGCA GCAGCCCGCGCA GCC	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE 1 #: NM_005 1194 21 1 CGGTGGCCG TCTGCTCCAG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCCT GGAATCCCAG CTGCTTGGC TGCCTTGGC TGCCTTGGC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CASCTTTGGT GACTACTGGA AGCGGCTTCT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGA ACGTGGGCC CTCCTGGAAC AAGCTTGGGA CCACCCAGGA GATACTCGCC	TVFTDHMLTV TVFTDHMLTV TOPPLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCTCGG GCGCCCTGG GCGCCCTGG GCGGACTAC GCCGCTGGAG CAAGGAGTTC CAAGGAGTTC	120 180 240 300 360 60 120 180 240 300 360 420 480
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequil ACAGAGGGCG CCCAGCTGGA ATGGACCGCG CGCTCCACGA ACTTGGGTCC GGGTGCGCTG GCCTCCCTCA AGAGCGGTGA GCCACCCCCG	ECTGEGGSKE PHIKPLQNLS PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA see id Accession Lence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCAGCCGGGA GCAGCCGGGA GCAGCGGGA GCAGCCGGGA GCAGCCGGGA GCGACCGGTGA ACTCCCCCTGCA ACTACACTCC	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LOWER PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUBER TEGNOTE TCGGTGGCCG TCGGTCCAG TCACTATTC GACATCTGG ACCCAGCCCT GGAATCCCAG TGCCGTTGGC CTGCATGTGG CCGAGCTCGAA	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT GTGCAAGCT TACCACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCTG GCCCCCCGG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA AGTTGGTGCC CTCCTGGAAC AAGCTTGGA CCACCCAGGA AGATACTCGCC TAGCGCCCAT	TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGC GTGGCCGCTGCC GCAGCCAAC GCCGCCTTGC GCCGCCTGCAC GCCGCCTGCAC CCCCTGCAC CCCTGCAC CCCTGCAC CCCTGCAC CCCTGCAC CCCTGCAC CCCCTGCAC CCCCTGCAC CCCCTGCAC CCCCTGCAC CCCCTGCAC CCCCTGCAC CCCCTGCAC CCCCTGCAC CCCCCTGT CCTCCCCTGT	120 180 240 300 360 60 120 180 240 300 360 420 480 540
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGGG CCCACCTGGA ACTTGGGCC GGGTGGCTG GCCTCCCTCA AGAGCGGTGG GCTCCCCCC TTGTTGGGCG TTGTTGGGCG TTGTTGGGCGT	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA see id Accessionence: 121. 11	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE 1 #: NM_005: 1194 21 TCGGTGGCCG TCTGCTCCAG TCTACTATTC GGAATCTGG ACCAGCCTT GGAATCCAG CTGCATTGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CCAGCCTTGGC CCAGGCTCGAC CCAGCCTGCC CCAGGCTCGCACCTGCC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGCAAGCT TACGACTATG AAGAATTCG CAGCTTTGGT GACTACTGAA AGCGCCTCGG GCCCCCCGG GCCCCCCGGCCAACC TCCCAGGTCTG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGTGGGAA AGGTTGGGA CCACCAGGA CCACCAGGA GATACTCGCC TAGCGCCCAAG AGAGCCCAAG	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGGTA GCCGGTACTAC GCCGCTGGAG CAAGGAGTTC CTTCCCCTGT CGACTCCCAG	120 180 240 300 360 60 120 180 240 300 420 480 540 600
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGGG CCCAGCTGGA ATTGGACGGC GGCTCCACGA ACTTGGGTCC GGCTCCCTCA AGAGCGGTGA GCCACCCCG GGTGAAGAAA	ECTGEGGSKE ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accessionence: 121. 11 GGTCGCGGG GGGAACTAG ACTCGTACCA CGCCAGGAA CGCAGCAGAA GCAGCAGAA GCACCAGCAGAA GTGACCTGCT ACTACACTCC ACTACACTCC ACCCCAGGAA TCGACGTGAC	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 1194 21 TCGGTGGCCG TCACTATTCC GGACATCTCAG ACCCAGCCT GGAATCCCAG CTGCATGGG CGCGTTGGC CGAGCTTGGC CGAGCTTGGA CCAGGCCTGC ACGAGCTGGA ACCAGGCCTGC AGTAAAGAAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCGG GCCGCAACC TCCAGGTCTG AGGCAACCT TCCAGGTCTG AGGCAGTCTT AGGCAGTCTT AGGCAGTCTT AGGCAGTCTT AGGCAGTCTT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AGCTTGGGAC CTCCTGGAAC CACCTCAGGAC GATACTCGC TAGGCCCAT TAGGCCCAAG TGAGTACGCG TGAGTACGCA	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTA CGCGACTAC GCCGCTGGGC CAAGGCAAC CTCCCTGT CCCTTCCCCTGT CGACTCCCAG GAAGCCAAC	120 180 240 300 360 60 120 180 240 300 480 540 600 660
50556065	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GWGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequing ACAGAGGGGG CCCAGCTGGA ATGGACCGCG ACTTGGGTC GGGTGCGTG GCCTCCCTCA AGAGCGGTGA GCCACCCCG TTGTTGGGCG TGTTTGGGCG GGTGAAGAAA ATCATCGCGG	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession lence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA ACTCGTACCA GCAGCAGGA GCAGCCGGGA GCAGCAGGAC TCCGCCGTGA GTGACCTGCT ACTACACTCC AGCCCAAGGAC TCGGCCCAAGGAC TCGGCCCAAGGAC TCGGCCCAAGGAC TCGGCCCAAGGAC TCGGCCGAGAC TCGGCCAAGGAC TCGGCCCAAGGAC TCGGCCCAAGGAC TCGGTGAC TGGGTGCAGAC TGGGTGCAGAC	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE 1 #: NM_005 1194 21 1 CGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCCT GGACATCCGG CTGCTCGAG CTGCATGGG CGCGTTGGC CGAGCTGGC CGAGCTGGA CCAGGCCTGGC CGAGCTGGAA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAATTCG CAGCTTTGGT GACTATTGGT GACTATTGGT GACTATTGGT GACTATTGGT CAGCTCTGG GCCGCCAGCT TCCAGGTCTG AGGCAGTCTT CCCCGCATGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTA ACGGGGGAGCA ACGGGGGGGAC CTCCTGGAAC CACCCAGGA GATACTCGCC TAGCGCCCAT AGAGCCCAGG TGAGTACGG	TVFTDHMLTV TVFTDHMLTV TOPPLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GCGCCCTGG GCGCCTGG CAGGCACTAC GCGAACTAC GCCGACTGAG CAAGGAGTTC CTTCCCCTGT CGACTCCCAGG GAAGCCAAC	120 180 240 300 360 60 120 180 240 300 360 420 540 600 720
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequil ACAGAGGGCG CCCAGCTGGA ATGGACCGCG ACTCCACCG ACTCCACCG GCTCCACCG ACTCCACCG ACGCTCCACCG TTGTTGGGCG GTGAAGAAA ATCATCGCG CACCACCAAC	ECTGEGGSKE PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec ici Accession Acticacacacacacacacacacacacacacacacacacac	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LOWER PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE TEST NM_005 1194 21 TCGGTGGCCG TCACTACTTCG GGAATCCAG TCACTATTCG GGAATCCAG GGAATCCAG CTGCATGGG TGCCGTTGGC CGAGCTCGAA CCAGGCCTGC AGTAAAGAAG CCAGGCCTGC AGTAAAGAAG CCTTCTGGAT TGCTGCCCCT	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT GCGCCCTCGG GCCGCAACC TCCAGGTCTG AGCAGTCTT CCCCGCATGA TTTCCTCCAG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGAA ACGGCGGGAA CTACCCAGGAA CACCCAGGAA CACCCAGGA AGATACTCGC TAGGCCCCAT AGAGCCCAAG ATCTCTTCCA AAAGCTGCTT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGC GTGGCCGCCTGCGC GCAGCCAAC GCCGCCTGGAG CCAGCCATC CCCTGCTGGAG CCAGCACTAC CCCAGCACTAC CCCAGCACTAC CCAAGAAGAG	120 180 240 300 360 60 120 180 240 300 480 540 600 660
50556065	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequil ACAGAGGGCG CCCAGCTGGA ATGGACCGCG ACTCCACCG ACTCCACCG GCTCCACCG ACTCCACCG ACGCTCCACCG TTGTTGGGCG GTGAAGAAA ATCATCGCG CACCACCAAC	ECTGEGGSKE PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS PHIKPLQNLS EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec ici Accession Acticacacacacacacacacacacacacacacacacacac	VVGTFKAKDL LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LOWER PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE TEST NM_005 1194 21 TCGGTGGCCG TCACTACTTCG GGAATCCAG TCACTATTCG GGAATCCAG GGAATCCAG CTGCATGGG TGCCGTTGGC CGAGCTCGAA CCAGGCCTGC AGTAAAGAAG CCAGGCCTGC AGTAAAGAAG CCTTCTGGAT TGCTGCCCCT	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAATTCG CAGCTTTGGT GACTATTGGT GACTATTGGT GACTATTGGT GACTATTGGT CAGCTCTGG GCCGCCAGCT TCCAGGTCTG AGGCAGTCTT CCCCGCATGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGAA ACGGCGGGAA CTACCCAGGAA CACCCAGGAA CACCCAGGA AGATACTCGC TAGGCCCCAT AGAGCCCAAG ATCTCTTCCA AAAGCTGCTT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGC GTGGCCGCCTGCGC GCAGCCAAC GCCGCCTGGAG CCAGCCATC CCCTGCTGGAG CCAGCACTAC CCCAGCACTAC CCCAGCACTAC CCAAGAAGAG	120 180 240 300 360 60 120 180 240 300 360 420 540 600 720
50556065	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq I ACAGAGGGCG CCCCACCTGA ATGGACCGCA GCTCCACCA AGAGCGGTGGGCTC GCCTCCCTCA AGAGCGGTGGGCTG GCTCCCTCA AGACCACCAGA ATCATCGCGG GCTGAAGAAA ATCATCGCGG CACCACCAGCACCACCAGCAAC GCTCCAAGAGACGCTCCAAGAG	ECTGEGGSKE ETGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accessionence: 121. 11 GGTCGCGGC GGGGAACTAG ACTCGTACAC GCAGCAGAA GGACCAGGA GTACCACTGA TCGACGTGAC TCGACGTGAC TCGACGTAC TCGACGTAC TCGACGTAC TCGACGTAC TCGACGTAC TCGACGTAC GGATGCCCC GACACAACTA GGATGCCCCC	VVGTFKAKDL LHPGSSALHY LQDLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005: 1194 21 TCGGTGGCCG TCAGTCGCCAG TCACTATTC GGAATCCCAG CCTGCATGGC TGCCATGGC TGCCGTTGGC CGAGCTCGA CCAGCCTT GGAATCCCAG CCTTCTGGAT TGCTCCAG CCTTCTGGAT TGCTCTGGAT TGCTCTGGAT TGCTCAGAT TGCTGGCCCTT AAAAGAAG CCTTCTAGAT TGCTGCCCCT AAAAGAGGCTCAA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA GCCCCTCGG GCCCCTCGG GCCCCTCGG TCCAGGTCTT AGGCAGTCT AGGCAGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGTTGGGAC CTCCTGGAAC CACCCAGGA GATACTCGCC TAGCCCCAT TGAGCCCAAG TGAGTACGCA AAGCTTCTTCCA AAAGCTCCTTCCA AAAGCTCCTTCCA AAAGCTCCTT	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV TOPNINDEM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGAATTCTAC GCCGCCTGG GGAACTAC GCCGCTGGG CAAGGAGTTC CTTCCCCTGT CGACTCCCAGG GAAGCCAGC CATCTCCCATC CATCTCCATC CCCAAGAAGGGT CCAAGAAGGGT CCAAGAAAGGAT	120 180 240 300 360 60 120 180 240 300 420 480 540 660 720 780 840
50556065	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGCG CCCAGCTGGA ACTGGACAGCGCG GGCTCCACCGA ACTTGGGTCC GGGTGCGCTGA AGAGCGGTGA TTGTTGGGCG GCTCCCCCCA TTGTTGGGCG GGTGAAGAAA ATCATCGCGG CACCAGCAACC CGCTCCAAGAA ATCATCGCAG GCTCCAAGAA ATCATCGCAG GCTCCAAGAA ATCATCGCAG GCTCCAAGAA GGTCAAAGAAAG GATAAGGAAG	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTAL DIQYGREESD 120 DNA sec id Accession lence: 121. 11 GGTCGCGGG GGGGAACTAG ACTCGTACCA CGCCCAGGGA GCAGCCGGGA GCAGCCGGGA GCAGCGGA GTGACCTGCT ACTACACTCC AGCCCAAGAT TCGACGTGAC TCGCGTGCAGA AGCACAACTA AGGATGCCCC ATGAAGAGAT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 1194 21 TCGGTGGCCG TCACTCCAG TCACTCTCCAG ACCCAGCCTT GGACATCCAG CCTGCTTGGC CGAGTTGGC CGAGTTGGC CGGATTCGAG CCAGGCTTGG CGAGTTGGC CGAGCTTGGC CGAGCTTGGC CGAGCTTGGC CGAGCTTGGC CGAGCTTGGC CGAGCTTGGC TGCAGGCTTGC ACTAAAGAAG CCTTCTGGAT TGCTGCCCTT TGTGAGCCTC TGTGAGCCTCC TGTGAGCCTCC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AACAAATTCG CAGCTTTGGT GCGCCTCGG GCCGCAACC TCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTACAGAGAG CTACAGAGAG CTACAGAGAG CCACCTGTAG CCACCTGTAG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGA AAGTTGGTGCC CTCCTGGAAC CAACCAGGA GATACTCGCC TAGCGCCCAT AGAGCCCAAG TGAGTACGCG ATCTCTTCCA AAAGCTCCAGG AAAGTTACGCG AAAGTGAGGC AAAGTGAGGG	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GCGGCCCTGGGG CCAGCGGACTAC GCCGCTGGGG CCAGCGGACTAC CCCGAGGACTAC CCCGAGGACTAC CCCAGTC CATCTCCATC CCAAGAAGGG GGGAAAGGAT TGCCCAGTC	120 180 240 300 360 60 120 180 240 300 420 480 540 660 720 780 840 900
5055606570	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GWGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequing ACAGAGGGGG CCCAGCTGGA ACTGGACCGCG GCGTCCACGA ACTTGGGTCC GGGTGCGCTG GCCTCCACGA ACTTGGGTCC GGCTGCAGCA ACTTGTTGGGCG GGTGAAGAA ATCATCGCGG CACCAGCAAC GCTCCAAAGA GGTAAGGAAC GCTCCAAAGA GGTAAGGAAC TGCAGGAAC GCTCCAAAGA TGCAGGAGAAC TGCAGGAGAAC TGCAGGAGAAC TGCAGGAGAAC	ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession Lence: 121. 11 GGTCGCGGGC GGGGACTAG ACTCGTACCA ACTCGTACCA GCACCAGGA GCACCAGGA GCACCAGGA TCGCCGTGA GTGACCTGC ACTACACTC ACGCCAGAA TCGACGTGA ACTACACTC AGCCCAGAA AGCACAACTA GGATGCCCCC ATGAAGAAT AACCCATCCA	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE 1 #: NM_005 1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTTC GACATCTGG ACCCAGCCCT GGAATCCAG CTGCATGGG CGAGCTGGA CCAGGCTGGC CGAGCTGGC CGAGCTGGA CCTAGGTGGC CGAGCTGGA CCTAGGAGCTGGC TGTGAGAGAG CTTTTGGAT TGCTGCCCCT TATGATACT TTATGATACT	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG GACTATGGT GACTACTGGA AGCGGCTTCT GCGCCCTCGG GCCGCAACC TCCAGGTCTG ACGCAGTCTT CCCCGCATGA TTTCCTCCAG TTTCCTCCAG CTAGAGAAGAG CCACCTGTAG GAGAATTCGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTA ACGGGGGAA ACGGGGGAA ACGTGGGAA CCACCAGGA CCACCAGGA CCACCAGGA GATACTCGCC TAGCGCCCAT AGAGCCCAG TGAGTACGG TGAGTACGG ATCTCTTCCA AAGCTCCTGAA AAGCTCCTGAA AAGCTCCTGAA AAGCTCCAGG AAAGCTCCAGG AAAGCTCCAGA AAAGCTCCAGA AAAGCTCCAGA AAAGCTCCAGA	TVFTDHMLTV TVFTDHMLTV TOPPILIMERM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GCAGCCTGA GCAGCCTGA CCCGCTGTGC CAAGCAGTC CAAGCAGTC CAAGCAGTC CATCTCCATC CCAAGAAGGG GGGAAAGGGT GGGAAAGGGT TGCCCAGTC CCAAGAAGGG GGGAAAGGAGT TGCCCAGTC GTACCACACC	120 180 240 300 360 60 120 180 240 480 420 480 600 660 720 780 840 900 960
5055606570	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GGCTCLSCTGA ACTGGA ACTTGGGC CCCACCTGGA ACTTGGGCC GGTGACCCCC TTGTTGGCG GGTGAAGAAA ATCATCGCG CACCAGCAGC GCTCCAAGAGAGAGGCTGA ACTCCAGAACTCCAAGAACTCCAGCACCCCC TTGTTGGCG TCCCAAGAACTCCAGCAACTCCAAGAACTCCAAGAACTCCAGCAACTCCAAGAACTCCAGCAGCAACTCCAAGAACTCCAGCAACTACCTGGAGCCCACCACACACA	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA see id Accession lence: 121. 11 GGTGCGGGGACTAG ACTCGTACCA GGGAGAGAC TCCGCCGTGA GTGACTGCT ACTACACTC AGCCAAGAT TCGACGTGAC TGCGTGAGAT AGCACAACTA GGATGCCCC ATGAGAGACC ATGAGAGACC GCAAGAGACC GCAAGAGACC ACCAACCA GGATGCCCC ATGAGAGACC AGCACCATCA GGATGCCCC ATGAGAGACC GCAAGAGACC GCAAGAGACC GCAAGAGACC GCAAGAGACC ATGAGAGACC GCAAGAGACC AGCACCATCCA GCAAGAGACC	VVGTFKAKDL LHPGSSALHY LQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE 1 #: NM_005: 1194 21 TCGGTGGCCG TCTGCTCCAG TCTACTCCAG TCACTATTC GGAATCCAG CTGCATGTGGC CTGCATGTGGC CTGCATGGA CCAGCCTT TGGATCCAG CTTCTGGA CCAGCCTGC AGTAAAGAG CCTTCTTGGA CCTTCTGGAT TGCTGCCCT AAAAGAGGCT TGTGAGCCTC TTTATGATACT GAATGATCAA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGCAAGCT TACGACTATG AAGAATTCG CAGCTTTGGT GCCCCTCGG GCCCCTCGG GCCCCTCGG TCCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG GAGAATTGGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGTGGGACAA ACGTGGGCCCT TAGCGCCCT TAGCGCCCAT AGAGTCCCAGA TGAGTACGCC ATCTCTTCCA AAAGCTTCTTCA AAAGCTGGTT AAGCTCCAGG AAAGTGAGGC CCAAGAAGAA TGTGGGCCCT TAGCGCCCT TAGCGCCCAGG ATCTCTTCCA AAAGCTGGTT AAGCTCCAGG AAAGTGAGGC CCCAAGAAGAA TCTTGGCCCT	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV TOPPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCACC GGATTTCTAC GCCGCCTGG GTGGCCGGTA GCAGCTAC CATCCCATG CAAGCACT CCATCCCATG GAAGCAGT CCATCCCATC	120 180 240 300 360 60 120 180 240 420 480 540 600 660 720 840 900 960 1020
50556065	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq I ACAGAGGGGG CCCAGCTGGA ACTTGGGTCC GGGTGCAGTG GCCTCCCTCA AGAGCGGTGAAGAGAAA ATCATGGGG CACCAGCAAC GGTTCAAGA GTAAGGAAG GATAAGGAAG GATAAGGAAG GATACCGGCCCCCCCCCC	ECTGEGGSKE ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL LTMDDLTTAL DIQYGREESD 120 DNA secid Accessionence: 121. 11 GGTCGCGGG GGGAACTAG ACTCGTACCA CGCCAGGAA GCAGCAGAA TCGACGGAA GTGACTGTACACTCC AGCCCAAGAT TCGACGTGAC AGCACAACTA GGATGCCCC ATGAAGAGAT AACCCATCCA GCAAGAGACT TGGCCGCGTGACT ACTACACTCC ATGAAGAGAT AACCCATCCA ACCCAAGAGACT TGGCCAGCTGACTGCCCATGAAGAGACT TGGCCAGCTGACTGACAGAGACACTA CGAAGAGACT TGGCCAGCTG	VVGTFKAKDL LHPGSSALHY LQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 .1194 21 TCGGTGGCCG TCACTATTCC GGACATCCAG ACCCAGCCT GGAATCCCAG CCTGCTTGGC CGAGCTGGC AGTAAGAAG CCTTCTGGAT TGCTGCCCT TAAAGAGGCT TGTGAGCCT TGTAGACT TTTTGATACT TGATGATCAA CATCTAGGTT TGTAGACCT TGTAGACCT TGTAGACCT TGTAGACCT TGTAGACCT TGTAGACCT TGAATGATCAA CATCTAGGGTT TGAATGATCAA CATCTAGGGTT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GCCCCTCGG GCCGCAACC TCCAGGTTCT CCCGCATGA TTTCCTCCAG CTAGGAGAGTTT CCCCGATGA CTAGGAGAGGAG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGTGGGA CCACCCAGGA CCACCCAGGA GATACTCGCC TAGGCCCAA TGAGTACGC AAGCTTGTCA AAGCTGCTT AAGCTCCTT AAGCTCCTT AAGCTCCAGG AAAGTAGCT TAGGCCCAAG TGAGTACGC TTCTTCCA AAAGCTGCTT TAGGCTCCAGG AAAGTAGAGC CCAAGAAAGAA TCTTGGCCCT TGATCCTAGT	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGTTA CGCGACTTA CGCGACTTA CGCGACTTA CGCGACTTC CTTCCCTGT CATCTCCATC CATCTCCATC CAAGAAGGG GGAAAGGAT TGCCCAGTC CAAGAAGGG GGGAAAGGAT TGCCCAGTC CAAGAAGGG CGAGCACAC CAAGACAGC CAAGGACGAC CAAGGACGAC CAAGGACGAC CAAGGACGAC CAAGGACGAC CAAGGACCACC	120 180 240 300 360 60 120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1080
5055606570	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQOVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGGG ACAGAGGGGGG ACTGGAGA ACTTGGGTGC GGGTGGAGTGA GCCACCCCG TTGTTGGGG GGTGAAGAAA ATCATCGCGG CACCAGCAAC GCTCCAACA GCTCCAACA GCTCCAGAAC GCTCCAGAAC GCTCCAGAAC GCTCCAGAAC GCTCCAGAAC GCTCCAGAAC GCTCCAGCAAC GCTCCAGAGCAC GCTCCAGCAC GGTAGCAGCCCA TACCTGGAGG GTACCGGCCCA GAATACTTAC	ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accessionence: 121. 11 GGTCGCGGG GGGAACTAG ACTCGTACCA CCCAGCGA GCAGCAGAGAC TCCGCCGTGA GTGACCTACTACACTC AGCACAACTA GGATGCCCC AGCACAACTA GGATGCCCC AGCACAACTA GGATGCCCC ATGAAGAGAT AACCCATCA GCAAGAGACT TGCGTGCCC ATGAAGAGAT AACCCATCA GCAAGAGACT TGCGCCAGCTG ATGAACTACA CTCA GCAAGAACTA AACCCATCCA GCAAGAACTA AACCCATCCA GCAAGACGCTG ATGAACTGGC	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE 1 #: NM_005 1194 21 TCGGTGGCCG TCACTACTGG ACCCAGCCCT GGAATCCCAG CTGCTTGGC CGGCTTGGC CGGCTTGGC CGGCTTGGC CGGCTTCTGGT TGCCGTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCATGTGG TGCTGCCCTT AAAAGAGGC TTGTGACCTC TTATGATACT GGAATCATACT GGAATCATACT GGAATCATACT GGAATCATAGGTT GGAAGCCGAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GGCCCCTCGG GCCGCAACC TCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGA CCTACCTGTAG GAGAATTGGA CCACCTGTAG GAGAATTGGA CCACCTGTAG GAGAATTGGA CAGGTTTGCAAGTAAG AAGAGGATGGT TCCAAAGTAA GAGAGGATGG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGA ACGTGGGAC CCACCAGGA CCACCAGGA GATACTCGCC TAGCGCCAT AGAGCCCAAG ATGCTTCCAA AAGCTCCTGA ATGCTCCTGAAC AAAGCTCCTAG CCAAGAAGAA TCTTGGCC TGATCCTAGT TGATCCTAGT TGATCCTAGT TGATCCTAGT	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV TOPNINMDRM PSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAGCCAAC GGATTTCTAC GCCGCCTGGG GCGCCCTGG GCGCCCTGG GCGCCCTGG GCGCACTAC CCAGACTAC CCAGACTAC CCAGACTAC CCAGACTAC CAAGAAGGG GGAAAGGAGT TCCCAGTC CAAGAAGGG GGGAAAGGAT TGCCCAGTCC GTACCACGC GAGGACCAC AAGGCCACC AAGGCCACC AAGGCACCC AAGGCACC AAGGCACCC AAGGCACC AAGGCACCC AAGGCACC AAGGCACCC AAGGCACC AAGGCACCC AAGGCACCC AAGGCACCC AAGCCACC AAG	120 180 240 300 360 60 120 180 240 300 360 420 780 840 600 780 840 900 960 1020 1080
5055606570	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGGG CCCAGCTGGA ATGGACCGCG ACTCCACGA ACTTGGGTCC GGGTGCAGCA AGAGCGGTGA GCACCCCCG TTGTTGGGCG GGTGAAGAA ATCATCGCGG CACCAGCAAC GCTCCAAGA GATAAGGAAG GATAAGGAAG TGCCAGCCCA TGCCAGCCAAC GGATACCGCCC GAATACTTAC GAATGCCAGC	ECTGEGGSKE PHIKPLQNLS PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD id Accession lence: 121. 11 GGTCGCGGC GGGGAACTAG ACTCGTACCA ACTCGTACCA GCAGCAGGA GCAGCCGGGA GCAGCAGGA GTGACCTGC ACTACACTC AGCCCAGGA AGCACACTA GGATGCCCC ATGAAGAGAC ATGAAGAGAT TCGCCAGCGA GCAGCAGCAC ATGAAGAGAT AACCCATCCA GCAAGAGAC GCAGCAGCTG AGCAGCAGCTG AGCAGAGAC ATGAAGAGAT AACCCATCCA GCAAGAGAC GCAAGAGAC ATGAAGAGAT AACCCATCCA GCAAGAGAC ATGAACTGC GCAAGAGAC GCAAGACACTT	UVGTFKAKDL LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY LHPGSSALHY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE L#: NM_005 L1194 21 TCGGTGGCCG TCGCTCCAG TCACTATTTC GACATCTGG ACCAGCCCT GGAATCCAG CCTGCTTGGC CGAGCCTGGA CCAGGCCTGGA CCAGGCCTGGA CCAGGCCTGGA TGCCGTTGGC TGCAGTGGC TGCAGTGGC TGCAGTGGC TGCAGTGGC TGCAGTGGC TGTGAGCCTC TGTGAGCCTC TTATGATACT GAATGATCAA CTCTAGGGTT GGAAGCCTAG GGAAGCCTAG GCAGAAAAGAG GCAGAAAAGAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGCAAGCT TACGACTATG AAGAAATTCG CAGCTCTGG GCCCCTCGG GCCCCTCGG GCCCCTCGG TCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG CAGAGAGAG CCACAGTAG CTAGAGAGAG CGACAGTAG CAGAGAGAG CATTCAGAGTAG CATTCAGAGT CATTCAGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCCTGGGCA ACGGGGGA AGTTGGTGCC CTCCTGGAAC CTACCCAGGA CCACCAGGA TGAGTACGCC ATCTCTCCA AAAGCTCCAG ATCTCTCCA AAAGCTGCTT AAGCTCCAGG AAAGTAAGGC CCCAAGGAGAA TCTTGGCCCT TGATCCTAGGAGAGAA TCTTGGCCCT TGATCCTAGTACCTAGTACCCAGGAAGAA TCTTGGCCCT TGATCCTAGTACCTAGTACCTAGTACCTAGTACCTAGTACCTAGTA	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FSLGVKKPTK LPAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTGA CGCGACTAC GCCGCTGGG GAAGCCAAC CACGCTGGG GAAGCCATC CCAGACTAC GCAACTAC GCGAACTAC GCCGACTGG GAAGCCAGT CGACCATC CCAGGAGGGTC CATCTCCATC CCAAGAAGGG GGAAAGGAT TGCCCAGTC GAGGAAGGAG GGAAAGGAC CAAGGCCACA CAAGGCCACA AAGGCCACA CAAGGCCACA CAAGGCCACA CAAGGCCACA CAAGGCCACA CAAGGCCACAAA	120 180 240 360 360 120 180 240 480 540 660 660 720 780 840 900 1020 1080 1140
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505560657075	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYG GWEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGCG CCCAGCTGGA ACTGGACA ACTGGCGCG GGTTCCACGA ACTTGGGTCC AGAGCGGTGAAGAAA ATCATCGCGG CACCAGCAACA GCTCCAAGAA GTAAGGAAG GTACCGCCC GAATACTTAC GAATGCCAGC AGCCTGCACACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC GAATACTGCAGC AGCCTGACCA AGCATACTTAC GAATGCCAGC AGCCTGACCA AGTAACTTGT	ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession lence: 121. 11 GGTCGCGGC GGGGAACTAG ACTCGTACCA ACCCCAGCGA GCAGCCGGA GCAGCCGGA GTGACCTGC ACTACACTCC AGCCCAAGAT TCGACGTGAC TCGACGTGAC AGGACAACTA AGGACAACTA AGGATGCCCC ATGAAGAGAC GCAAGAGAC GCAAGAGACA GCAAGAGACA TGACCTGCC ATGAAGACA TGACCACCC ATGAAGAGAC TGACCAGCTG AGCACAACTT ACATITITGTT ACATITITGTT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 1194 21 TCGGTGGCCG TCACTCCAG TCACTCTCCAG ACCCAGCCTT GGACATCTAG CCAGCCTT GGACATCTAGG TGCCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTCTGGAT TGCTGCCCTT AAAAGAAGA CCTTCTGGAT TGTGAGCCTC TATGATACT GAATGATCAA CAGGCTTGC GAATGATCAA AAAAGACACA TTCTAGGTT GGAAGCCGAG GCAGAAAAGA AAAAGACACA TACAGCAGGA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG GACTTTGGT GGCCTCGG GCCGCAACC TCCAGGTTCT CCCCGCATGA TTTCCTCCAG CTAGAGAGA CCTCTCCAG GCAGATCTT CCCCGCATGA GAGAATTCGA CAGCTTTGCT GAGAGAGA CCACCTGTAG GAGAATTCGA CAGTTCCCGGT TCCAAAGTAA GAGAGATGG ATTGAGTACC AGTTTTCTTT CACTCTGGAC	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCOTGAGCAA ACGGCGGGA AAGTTGGTGCC CTCCTGGAC CACCCAGGA GATACTCGCC TAGCSCCCAT AGAGCCCAAG TGAGTACGCG ATCTCTTCCA AAAGCTGCTT AAGCTCCAGG ATCTCTTCCA CAAGAAGAA TCTTGGCCC CTAGGCCCAT CGATCATGGCC CCAAGAAGAA TCTTGCCCT TGATCCTAGT CTACGGAGAA TCAGTAGGT CTACGAGGAA TCAGTAGGT CTACGAGGAA TCAGTAGGT CTACGAGGAA TCAGTAGCT CTACGAGGAA TCAGTAGGT CTACGAGGAA TCAGTAGGT CTACGAGT TGATCTCCC AGTAGATTGC CAGTAGATTGC CAGTAGATTAGC CAGTAGATTGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGAT	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAGCCAGC GGATTTCTAC GCCGCCCTGGG GCGCCCTGGGG CCAGGCACTAC GCGGACTAC CCCGAGCCAGC CAAGGAGTTC CTTCCCCTGT CGACCAGAG GGGAAAGGGG GGAAAGGGG GGGAAGGAT TGCCCAGTC CTACCACAGC GAGGGACGAC AAGGCACCA AAGGCACCT TACACCAAAA TCTCCCCTTT AGAATCGATT	120 180 240 360 360 120 180 240 480 540 660 660 720 780 840 900 1020 1080 1140
5055606570	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYG GWEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGCG CCCAGCTGGA ACTGGACA ACTGGCGCG GGTTCCACGA ACTTGGGTCC AGAGCGGTGAAGAAA ATCATCGCGG CACCAGCAACA GCTCCAAGAA GTAAGGAAG GTACCGCCC GAATACTTAC GAATGCCAGC AGCCTGCACACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC ACCAGCACAC GAATACTGCAGC AGCCTGACCA AGCATACTTAC GAATGCCAGC AGCCTGACCA AGTAACTTGT	ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA sec id Accession lence: 121. 11 GGTCGCGGC GGGGAACTAG ACTCGTACCA ACCCCAGCGA GCAGCCGGA GCAGCCGGA GTGACCTGC ACTACACTCC AGCCCAAGAT TCGACGTGAC TCGACGTGAC AGGACAACTA AGGACAACTA AGGATGCCCC ATGAAGAGAC GCAAGAGAC GCAAGAGACA GCAAGAGACA TGACCTGCC ATGAAGACA TGACCACCC ATGAAGAGAC TGACCAGCTG AGCACAACTT ACATITITGTT ACATITITGTT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence 1 #: NM_005 1194 21 TCGGTGGCCG TCACTCCAG TCACTCTCCAG ACCCAGCCTT GGACATCTAG CCAGCCTT GGACATCTAGG TGCCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTCTGGAT TGCTGCCCTT AAAAGAAGA CCTTCTGGAT TGTGAGCCTC TATGATACT GAATGATCAA CAGGCTTGC GAATGATCAA AAAAGACACA TTCTAGGTT GGAAGCCGAG GCAGAAAAGA AAAAGACACA TACAGCAGGA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA GCCGCCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG GAGAATTCG CAGCATCT AGGCAGTCT TCCAGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG GAGAATTCG CAAAGTAA GAGAATTCG AGGAATTCGGA TCCAAAGTAA GAGAGATGAG ATTGAGTAC AGTTTTCTTT	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCOTGAGCAA ACGGCGGGA AAGTTGGTGCC CTCCTGGAC CACCCAGGA GATACTCGCC TAGCSCCCAT AGAGCCCAAG TGAGTACGCG ATCTCTTCCA AAAGCTGCTT AAGCTCCAGG ATCTCTTCCA CAAGAAGAA TCTTGGCCC CTAGGCCCAT CGATCATGGCC CCAAGAAGAA TCTTGCCCT TGATCCTAGT CTACGGAGAA TCAGTAGGT CTACGAGGAA TCAGTAGGT CTACGAGGAA TCAGTAGGT CTACGAGGAA TCAGTAGCT CTACGAGGAA TCAGTAGGT CTACGAGGAA TCAGTAGGT CTACGAGT TGATCTCCC AGTAGATTGC CAGTAGATTGC CAGTAGATTAGC CAGTAGATTGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGATTAGC CAGTAGAT	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAGCCAGC GGATTTCTAC GCCGCCCTGGG GCGCCCTGGGG CCAGGCACTAC GCGGACTAC CCCAGTC CATCTCCATC CCAAGAAGGG GGAAAGGAT TGCCCAGTC CATCTCCATC CCAAGAAGGG GGGAAAGGAT TGCCCAGTC GTACCACACAC AAGGCACCA AAGCCACCTT AGAATCGATT	120 180 240 300 360 60 120 180 240 300 420 480 540 660 720 840 900 900 900 1020 1080 1140 1200 1200
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505560657075	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GCQCVLWLYG GUGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequil ACAGAGGGCG CCCAGCTGGA ACTIGGGCG CGCTCCACCA AGAGCGGGG GCTCCACCA AGAGCGGTGA GCTTGGGGCG GCTCCACAGA ATCATCGCGG GCTCCACAGA ATCATCGCGG GTAAAGAAA ATCATCGCGG GATAAGGAAG GCTCCAAAGA GCACACCCC GAATACTTGG GAATACTAGC GAATGCCAGC AGTAACTGGCAG CGATACCAGC CGATTGCCAGCCA AGTAACTTGT GCAGCCAGC AGCAGCAGC AGCAGCAGC CGATTGCCAGCCA AGTAACTTGT CCACCCAGC AGCAGCAGC CGATTGCCAGCCAGC AGCAGCAGC AGCAGCAGC CCTCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCC CCCCTCTCCCCC CCCCTCTCCCCC CCCCTCTCCCCC CCCCTCTCCCCC CCCCTCTCCCCC CCCCTCTCCCCC CCCCTCCCCCC	ECTGEGGSKE ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accessionence: 121. 11 GGTCGCGGGC GGGGAACTAG GCAGCAGGA ACTCGTCACCTCACC	VVGTFKAKDL LHPGSSALHY LOQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS TUENCE 1 #: NM_005: 1194 21 TCGGTGGCCG TCTGGTCGCG GCATATTC GGACATCTGG ACCCAGCCT GGAATCCCAG CTGCATGGC CTGCATGGC TGCCTTGGAT CCAGCCTGC AGTAAAGAAG CCTTCTAGAT TGCTGCCCT TAAAGAGGCT TGTAGCCTC TTATGATACT GAATGATCAA CTCTAGGGT GGAAGCCGAG CTGCAAAGAAA CAACCAGCAGAAAAAAAAAA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GCCCCCCGCATGA TTCCCCGCATGA CTACAGGAGAGAG CCACCTGTAG GAGAATTCG CAACCTGTAG GAGAATTCG CAACCTGTAG GAGAATTCG CAACCTGTAG GAGAATTCG CAACCTGTAG GAGAATTCG CAACCTGTAG GAGAATTCG CATCTGGAC CTACAGGAGAG CATCTGGAC AGTTTTCTTT CACTCTGGAC AGTTTTCTTT CACTCTGGAC AGTTTTCTTG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPKGETI SDILYKGETI GTGTGGAGTG GCGTGAGCAA ACGTGGGAC ACGTTGGGAC CCACCAGGA AGGTTGGTGCC TAGGCCCAT AGAGCCCAAG TGAGTACGCC TAGAGCCCAAG TGAGTACGCC TAGAGCCCAAG TGAGTACGCC TAGAGCCCAAG TGAGTACGCC TAGAGCCCAAG TGAGTACGCC TGATCCTAGT AAGCTCCAGG AAAGTGAGGC CCAAGAAGAA TCTTTGCCCT TGATCCTAGT TTGATCTCCC AGTAGATTGCA AAACTTTGGC AAACTTTGGA AAACTTTGGAC AAACTTTGGAC AAACTTTGGAC AAACTTTGGA AAACTTGGA AAACTTTGGA AAACTTTGGA AAACTTTGGA AAACTTTGGA AAACTTTGGA AAACTTTGGA AAACTTTGGA AAAACTTTGGA AAACTTGGA AAACTTTGGA AAACTTGGA AAACTTTGGA A	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FOPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGAATTCTAC GCCGCCTCG GTGCCGGTAC GCGACTAC GCCGCTGGG GAAGCCAAC CTTCCCCTGT CGACTCCCAG GAAGCAGTC CCAAGAAGGG GGAAAGGAT TGCCCAGT GTACCACAGC GAGGACCAAC CTACCCAGC CAAGCAAC CAAGCAAC CTACCCAGC CTACCACAGC CAAGGACGAG CCAAGCCAAC CTACCCAGC CTACCCAGC CTACCCAGC CTACCCAGC CTACCCAGC CTACCCAGC CTACCCAGT CTCCCCTTT AGAATCGATT TCCCCCTTT ACCCAGCTCT TTCTCAGCAG	120 180 240 300 360 60 120 180 240 420 480 540 600 660 720 900 1020 1020 1120 1200 1250 1380 1440
505560657075	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQVLWLYG GWGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding sequity ACAGAGGGCG CCCAGCTGGA ATGGACGGC GGTTCCACGA ACTTGGGTC GGCTCCACCA AGAGGGGTGAAGAAA ATCATCGCGG CACCAGCAAG GCTCCAAGA GATAAGGAAG GATAAGGAAG GATACCAGCAC AGACCACCAC AGACCCCCC GAATACTAG GAATACTAGC GAATGCCAGC AGCCTGAACA AGTAACTTGT GCAGCCACA AGTAACTTGT GCAGCCAGCAC AGCTTGACCAC AGCTTGACCAC AGCTTGACCAC AGCTTGACCAC AGCTTGACCAC AGCTTGACCC CCCCC CCAGCTGACCAC AGCTTGACCAC AGCTTGACCAC AGCTTGACCAC AGCTTGACCAC CCCCCCC CCCCCCCCCC	ECTGEGGSKE ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL LTMDDLTTAL LTMDDLTTAL LTMDLTTAL LTMDLTTAL LTMDLTTAL LTMDLTTAL LTMDLTTAL LTMDLTTAL LTMDLTTAL LTMDLTTAL LTMDLTAL LT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVRMFG WTIVLS Quence 1 #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCT GGAATCCCAG CCTGCTTGGC CGGATTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGC TGCTTGGAT TGCTGCCCT TATGATACT TGATGCCTC GAATGATCAA AAAAGAGGCT GGAAACCAA TACAGCAGGA TACAGCAGA TACAGCAGA TACAGCAGGA TACAGCAGA TACAGCAGGA TACAGCAGA TA	IVTPATILKE AVELPEGLKA WYPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT AAGCATACTGGA AGCGGTTCT GCGCCTCGG GCCGCAACC TCCAGGTCTG TCCAGGTCTG AGGCATCATGG CTACAGGTCT CCCCCATGA CTACAGGATCT CCCCCATGA GAGAATTCGA CTACAGGAGA CGTTCCCGGGT TCCAAGTAA GAGAGATTCGA CGATCTTGGC AGTTTTCTTC CACTCTGGAC GCATTCTTGG TGGTTCTTGG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGA ACGTTGGGCC CTCCTGGACC CACCCAGGA GATACTCGC ATACTTCCA AAAGCTGCTT AAGCTCCTT AAGCTCCTGT AAGCTCCTGT AAGCTCCTGT AAGCTCCTGT TAGCTCCAGGA TCATTCTCCA AAAGTGGCT CTACCGAGAA TCTTGGCCCT TGATCCTAGT CTACGAGAAA TCTTGGCCCT TGATCTTCCC AGTAGATTGC AAACTTTGAC AAACTTTGAC CTACGTAGTT CTACCGAGAAA CCCTTTTGCC AGTAGATTGC AAACTTTGAC CTCCCAAAGAA CCCTTTTGC CTCCCAAAGAA CCCTTTTGC CTCCCCAAAGA	TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV TVFTDHMLTV FOPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGTTA CGCGACTAC CAAGAAGGA CAAGAAGGA CAAGAAGGA GAAGCCAGTC CATCTCCATC CATCTCCATC CATCTCCATC CATCTCCATC CAAGAAGGG GGGAACAGC CAAGACGG GGGACAGC CAAGACGG CAAGACCAGC CAAGACACAC TTCCCCTTT AGACAACA AAGGCCACT AGACCAACA TCTCCCCTTT AGAATCGATT ACCCAGCTCT TTCTCAGCAA AAAGGCTGAC	120 180 240 300 360 60 120 180 240 300 420 480 960 960 900 960 1020 1080 1140 1250 1320 1320 1320 1340 1500
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5	CCCACTCTCA	ATGCTGTGAC	TCAGAACATT	TAAGAGAACT	TCGTCTGTAA	GTAATTTGTC	1980
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	TGTCTCATTC	TGCCTCTGTT	ATGCAATGGG	TTCTACAGCA	CCCTTTCCCG	CAGGTTAGAA	2100
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10	TTTTCTCS SC	TOWNCTOWN	CCCIGCCCAG	GIGITITICIG	AGGGGCCCTI	GAGGCCAAIC	2220
10				AGGGAGAACT			2280
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	CACCAGCCTG	CAATGAATCA	GATGTCTGTC	ACAGAATCTG	GGCCTCTCTG	AAGTTTTCTG	2460
	GAGAGCTGTT	GGGACTCATC	CAGTGCTCCA	CAACGTGGAC	TTGCCTCCTG	GTGTGTTTTA	2520
15	AAGGATCCTC	CAGGAGCTCT	COTTACOCAN	TCATCATGAT	CC y department	dulabelalabelah	2580
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	ATCGCAGGCG	CCTGCCACCA	CGCCTAGCTA	ATTTCTGTAT	TTTTAGTAGA	GATGGGGTTT	2760
	CACCACATTG	GCCAGGCTGG	TCTTGACCTC	CTGACCTAGG	TGATCCACTG	CCTCCATGAT	2820
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30				FPPESCPQEG			240
	DKEDEEIVSL	PPVESEAAQS	COPKPIHYDT	ENWTKKKYHS	YLERKRRNDQ	RSRFLALRDE	300
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40				GCCCGAGGCT			120
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				GACCCGCACC			240
				CCCTGAAAAG			300
15	AAAAAAGCCG	GAGAACTGTG	AGAAGCTCGT	CACTCTGCTG	GAGAATTACA	aggagatgta	360
45	CCAACCAGAA	GACGACAACA	ACAGTGACGT	GACCAGCGAC	GACGACATGA	CCCGGAACAG	420
	AACACACTOO	TCACCACCTC	ACTYCACTOCA	TTCTTTCAGT	GGTGACCGGG	ACTIGGGACCG	480
	GAGGGGCAGA	AGCAGAGACA	TGGAGCCACG	AGACCGCTGG	TCCCACACCA	GGAACCCAAG	540
	GAGGGGCAGA AAGCAGGATG	AGCAGAGACA CCTCCGCGGG	TGGAGCCACG ATCTTTCCCT	AGACCGCTGG TCCTGTGGTG	TCCCACACCA GCGAAAACAA	GGAACCCAAG GCTTTGAAAT	540 600
50	GAGGGGCAGA AAGCAGGATG GGACAGAGAG	AGCAGAGACA CCTCCGCGGG GACGACAGGG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC	AGACCGCTGG TCCTGTGGTG TTATGAGTCC	TCCCACACCA GCGAAAACAA CGATCTCAGG	GGAACCCAAG GCTTTGAAAT ATGCTGAATC	540 600 660
50	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT	TCCCACACCA GCGAAAACAA CGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA	540 600 660 720
50	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC	TCCCACACCA GCGAAAACAA CGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA	540 600 660
50	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGCTCTCCCT	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT	TCCCACACCA GCGAAAACAA CGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA	540 600 660 720
50	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG	AGCAGAGACA CCTCCGCGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGCC	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGCTCTCCCT ACTCATCAAG	AGACCECTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA	TCCCACACCA GCGAAAACAA CGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG	540 600 660 720 780 840
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	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGCC AAAACTATGC TCCCACGGG AGAGCAAGGG AAGGACATTT	TGGAGCCACG ATCTTTCCCT ACTCCAGGGA TGCTCTCCCT ACTCATCAAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATCATC CCGGTCACAG GAGGGAGTCA	TCCCACACCA GCGAAAACAA CGATCTCAGG CACACACAA CTTGCTGAAG AGTGCCTACC CACCGGCGGG AAGGATGTGT AGATTCCCCA GTGATCCAGC	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGCGGGTTTA	540 600 660 720 780 840 900 960 1020 1080
	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCA TCAAATCGGGA TGATAACTGG TGATAACTGG TGAAGGGAAT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGCC AAAACTATGC TCCACCGAG TCCACCGAG AAGGAAAGGG AAGGACATTT GCATTTAGGG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGA TGCTCTCCCT ACTCATCAAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGGTCACAG GAGGGAGTCA GTTTAATTCA	TCCCACACCA GCGAAAACAA CGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGCGGGTTTA CCAGAAAGAG	540 600 660 720 780 840 900 960 1020 1080
	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCA TCAAATCGGGA TGATAACTGG TGATAACTGG TGAAGGGAAT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGCC AAAACTATGC TCCACCGAG TCCACCGAG AAGGAAAGGG AAGGACATTT GCATTTAGGG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGA TGCTCTCCCT ACTCATCAAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATCATC CCGGTCACAG GAGGGAGTCA	TCCCACACCA GCGAAAACAA CGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGCGGGTTTA CCAGAAAGAG	540 600 660 720 780 840 900 960 1020 1080
55	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC AAAACTATGC TCCCACGGAG AGAGCAATG AGAGCATTTAGGG AGAAAGAGGC	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACGA GAGGCTTTAG GCTATCATTT	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGGTCACAG GAGGGAGTCA GTTTAATTCA	TCCCACACCA GGAAAACAA CGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGCGGGTTTA AGCGGGTTTA CCAGAAAGAG CGATTCACGA	540 600 660 720 780 840 900 960 1020 1080
	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGA TGAAACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC AAAACTATGC TCCCACGGAG AGAGCAAGGG AGGACATTT GCATTTAGG TGTCCCAGGA TGTCCCAGGA	TGGAGCCACG ATCTTTCCCT ACTCCAGGG TGCTGAGGA TGCTCATCAT ACTCATCAA CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAA GCTATCATTT AGAAGCCCTT	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTAC GTTTAATTCA TGACACAGAT	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACAACAAA CTTGCTGAAG AGTGCCTACC CACCGGGGGA AGGATGTGT AGATTCCCA GTGATCCAG ACCCTTGTTT GCGAAGGGCT AGTGAGATGA	GGAACCCAAG GCTTTGAAAT ATGCTGAAAT CTCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGCGGGTTTA CCAGAAAGAG GGATTCACGA GAAAAGCCAT	540 600 660 720 780 840 900 960 1020 1080 1140
55	GAGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAA AGTTCTTGAA AGTCTTGTGAA AGTCGTGAGG	AGCAGAGACA CCTCCGCGGG GACGACAGGGG GTGGTGGACC TACAGGAAGC ACGCAGGGGC AAAACTATGC TCCCACGGAG AGAGCAAGGG AAGGCAATTT GCATTAGGG AGAAAAGAGGC TGTCCCAGGA AGACATGT AGAAAGAGGC AGAAAGAGGGC AGAAAGAGGGC AGCCTGAGCA AGCCTGAGCA	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAAG CTGAAGCCAA TGATAATGGA AGTCAAGGA AGTCAAGCAA GAGGCTTTAG GCTATCATTTA GAGAGCCTT GCCTCAGCTC	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTCA GTTTAATTCA TCGACACAGAT TGAAACGAT	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACTGC GGATTTGTGA CAGCAGTTC GAATGTCAGA AGCGGGTTTA CCAGAAAGAG GGATTCACGA GAAAGCCAT AGCCAATTGA	540 600 660 720 780 840 900 960 1020 1140 1200 1260
55	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC TTTTGGGGCA TTTTGGGGCA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGCC AAAACTATGC TCCCACGGAG AAAGCAAGGG AAGGACATTT GCATTTAGGG AGAAAGAGGC TGTCCCACGGA AGCCTGAGCA ATGCCATATG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TGGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG GCTATCATTT AGAAGCCCTT TATGTGATGA TGATGATGA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTCA GAGGGAGTCA TGAACAGAT TGAACACAGAT TGACACAGAT GCCCTCTTT GTTGGGAGG	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACAACAAA CTTGCTGAAG AGTGCCTACC CACCGGGGGG AAGGATGTGT AGATTCCCCA GTGATCCAGC ACCCTTGTTT GGGAAGGGCT AGTGAGATGA ACCCATGTTA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGCGGGTTTA CCAGAAAGAG GAATTCACGA GAAAAGCCAT AGCCAATTGA TCATCTCAGA	540 600 660 720 780 900 960 1020 1080 1140 1200 1320 1380
55	GAGGGCAGA AAGCAGATA GGACAGAAAC CTCCACATA TCGAGATAC TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAG TTTTGGGGCA ATTTGTTGAG	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC AAAACTATGC TCCCACGGAG AGGCAAGGG AGGGACATGG AGGACATGG AGAAAGAGG AGGACATTTAGGG AGAAAGAGGC TGTCCCAGGA AGCCTGAGGA ATGCCATATG CACCAGATCA	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGCTCTCCT ACTCATCAG ACTCATCAG AGTCAAGGA AGTCAAGGA AGTCAAGGA AGTCAAGCGA CATTGAACAA GCTATCATTT AGAAGCCCTT GCCTCAGCTC TATGTGATGA TGCATACTAG TGCATACTAG	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTAC TGACACAGAT TGACACAGAT TGAATGTGGT CCCCTCCTTT GTGTGGGAGG AGAGAACCTC	TCCCACACCA GCGAAAACAA GCGATTCAGG CACAACAAA CTTGCTGAAG AGTGCCTACC CACCGGGGGG AAGGATTCCCAC GTGATCCAGC GTGATCCAGC ACCCTGTTT GGGAAGGCCT AGTGAGATGA ACCGAGTCAC TCGTTCAGTG TATGAGTATG	GGAACCCAAG GCTTTGAAAT ATGCTGAACT TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGCGGGTTTA CCAGAAAGAG CCAGAAAGAG GAAAAGCCAT AGCCAATTGA GCGCATTCAGA GTGACCATTAGA GTGAGTCCTT	540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380
55	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCACATG TCGAGGTCTA AGATGAATC CAAATCGGA TGAAACTGG TGAAGGCAT TGAAACTGG TGAAGGCAT TGAAAGGCAT TCATTTTTTTTTT	AGCAGAGACA CCTCCGCGGG GACGACAGGGCC TACAGGAAGC AAAACTATGC TCCCACGGAG AGAGCAAGGGCC AGAGCAAGGGCC TCCCACGAGA AGAGCAAGGG AGAGCAAGGG TGTCCCAGGA AGCCTGAGCA ATGCCATATA GCACTGAGCA ATGCCATACA GTGGCTGTCA	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TGCTGAGGAA TGCTCATCAC ACTCATCAGA AGTCAAGCCAA AGTCAAGCGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG GCTATCATTTA GGAAGCCCTT GCCTCAGCTC TATGTGATGCA TGCATACTAG GTGAAGTTCA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTCA GTTTAATTCA TGACACAGAT TGAATGTGGT CCCCTCCTTT GTGTGGGAG AGAGAACCTC GAAAAGTCAG	TCCCACACCA GCGAAAACAA GCGATTCAGG CACAACAAA CTTGCTGAAG AGTGCCTACC CACCGGGGGA AGGATTCCAG GTGATTCCAG TGATTCCAG TGATTCCAG TGATTCAGC ACCTTGTTT GGGAAGGGCT AGTGAGATGA ACCAGTCAC TCGTTCAGTG TATAGAGTATG GTTGAGGAGG TTTGAGGAGGGGG TTTGAGGAGGGGGGGG	GGAACCCAAG GCTTTGAAAT ATGCTGAAAT CTCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGACAGTTC GAATGTCAGA AGCAGATTAC CGAAAAGAG GGATTCACGA GAAAAGCCAT AGCCAATTGA TCATCTCAGA GTGAGTCCTT AACGTTTTGA	540 600 660 720 780 840 900 1020 1140 1200 1320 1380 1440 1500
55 60	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCGG TGAAACGGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGAG TATCCACAGT TATCAAGGC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC ACACAGGAG AGACATTGC TCCCACGGAG AGGACATTTAGGG AGGAAGACATTTAGGG AGAAAGAGGC TGTCCCAGGA AGCCTGAGCA ATGCCATATG CACCAGATCA GTGGCATATG TGTGCGAGAGA	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG ACTCATCAG AGTCAAGCGA AGTCAAGCGA AGTCAAGCGA AGTCAAGCGA GAGGCTTTAG GCTATCATTTA GCATCATTTA GCCTCAGCTC TATGTGATGA TGCAAAGTCA CTCAAAGTCA CCTTCAATAA	AGACCGCTGG TCCTGTGGTG TTATGAGTG CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GTTTAATTCA TGACACAGAT TGAATGTGGT CCCCTCCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAC GAGTCACAG	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGGCACTTC GAATGTCAGA AGCAGGTTC GAATGTCAGA AGCAGGTTA CCAGAAAGAG GAATTCACA GAAAAGCCAT AGCCAATTGA TCATCTCAGA TCATCTCAGA ATCATCTAGA ATCAGATTTCAAA ATCAGAAAGAT AACGTTTTGA ATCAGAAGAT	540 600 660 720 780 840 900 960 1020 1140 1200 1320 1320 1440 1500
55	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGAG TATCCACAGT TATCACAGT TCATGAGAC TCATGGTAAGAC TCATGCTAGA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC AAAACTATGC TCCCACGGAG AAGGCAAGGG AAGGCAAGGG AAGGACATTT GCATTTAGGG AGAAAGAGGC TGTCCCAGGA ATGCCTGAGCA ATGCCATATG CACCAGATCA TGTGGGTGTCA TGTGGAGAG GGTTATCTTG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GCTATCATTT AGAAGCCTT GCCTCAGCTC TATGTGATGA TGCATACTAG CTTCAATTA CCTTCAATTA CTCAAGTTCA CTTCAATTA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGC AAAATTCATC CCGGTCACAG GAGGGAGTCA GATTAATTCA TGACACAGAT TGAATGTGGT CCCCTCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAC GAGTGCCGCC GAATCAGGAA	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACAACAAA CTTGCTGAAG AGTGCCTACC CACCGGGGGG AAGGATGTGT AGATTCCACA CTTGTTGTTGTGAAGATCCAGC ACCCTTGTTT GGGAAGGGCT AGTGATCAGC TCGTTCAGTG TATGAGTATC TTTGGAGGAG TCTGCTTGAGGAGA TCGTTCAGGAGAAC TCGTTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAAAC TCGTCAGAAAC TCGTCAGAAAC TCGTCAGAAAC TCGTCAGAAAC	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGGAAGAGG CGATTCACGA AGGAATGA AGCAATTGA TCATCTCAGA GTGAGTCCTT AACGTTTTGA ATCGGAAGGAT CCTTCATGCC	540 600 660 720 780 840 900 1020 1140 1200 1260 1320 1380 1440 1500 1560
55 60	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGAG TATCCACAGT TATCACAGT TCATGAGAC TCATGGTAAGAC TCATGCTAGA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC AAAACTATGC TCCCACGGAG AAGGCAAGGG AAGGCAAGGG AAGGACATTT GCATTTAGGG AGAAAGAGGC TGTCCCAGGA ATGCCTGAGCA ATGCCATATG CACCAGATCA TGTGGGTGTCA TGTGGAGAG GGTTATCTTG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GCTATCATTT AGAAGCCTT GCCTCAGCTC TATGTGATGA TGCATACTAG CTTCAATTA CCTTCAATTA CTCAAGTTCA CTTCAATTA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGC AAAATTCATC CCGGTCACAG GAGGGAGTCA GATTAATTCA TGACACAGAT TGAATGTGGT CCCCTCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAC GAGTGCCGCC GAATCAGGAA	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACAACAAA CTTGCTGAAG AGTGCCTACC CACCGGGGGG AAGGATGTGT AGATTCCACA CTTGTTGTTGTGAAGATCCAGC ACCCTTGTTT GGGAAGGGCT AGTGATCAGC TCGTTCAGTG TATGAGTATC TTTGGAGGAG TCTGCTTGAGGAGA TCGTTCAGGAGAAC TCGTTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAGAAC TCGTCAGAAAC TCGTCAGAAAC TCGTCAGAAAC TCGTCAGAAAC TCGTCAGAAAC	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGGAAGAGG CGATTCACGA AGGAATGA AGCAATTGA TCATCTCAGA GTGAGTCCTT AACGTTTTGA ATCGGAAGGAT CCTTCATGCC	540 600 660 720 780 840 900 1020 1140 1200 1260 1320 1380 1440 1500 1560
55 60	GAGGGCAGA AAGCAGATA GGACAGAAAC CTCCACATA TCAGGAAAC TCAGGTCTA AGATGAATCT CAAATCGGA TGATAACTGG TGAAGGGATT AGTTCTTGAA TCAAAAAGGC GAGCGTGAG TTTTTGGGCA ATTTGTTGAG TATCACAGT TCATAAGAG TATCACAGT TATCACAGT TATCACAGT TATCACAGT TATAGGAA TCATAGGAA TAGCCCCACC	AGCAGAGACA CCTCCGCGGG GACGACAGGGCC TACAGGAGGCC TACAGGAGGCC TACAGGAGGCC TCCCACGGAG AGAGCAAGGGAAGGAAGGAGAGAGAGAGAG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGCTCTCCT ACTCATCAG ACTCATCAG AGTCAAGCCA TGATAATGGA AGTCAAGCGA CATTGAACA GCTATCATT AGAAGCCTT GCCTCAGCTC TATGTGATGA TGCATACTAG TGCATACTAG TGCATACTAG TGCATACTAG TGCATACTAG TGCATACTAG TGCATACTAG TTCAGAAAATTAA TTCAGAAAAAT	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCATC CCGGTCACAG GAGGGAGTCACAG GAGTACACG TGAAACGAT TGACACAGAT AGAGGACCTC GAAAAGTCAG GAGTGCCGCC GAATCAGGAA ATATGGCAAA	TCCCACACCA GCGAAAACAA GCGATTCAGG CACAACAAA CTTGCTGAAG AGTGCCTACC CACCGGGGGG AAGGATTCCAGC GTGATCCAGC GGGAAGGGCT AGTGAGTAGA ACCGAGTCAC TCGTTCAGTG TATGAGTATG TTGGAGGGG TTGGAGGGGA TTGGCTGAAG GTTGGAGGGA GGCAAATTCT TGGAGGAAG GACAAATTCT	GGAACCCAAG GCTTTGAAAT ATGCTGAACT TCCAGGACAA AOGATGGCCA CAAGCACCAG GGATTTGGA ACGCAGTTC GAATGTCAGA ACGCAGTTC GAATGTCAGA AGCACCAT ACCAGAAAGAG CCAATTGA ACGCAATTGA ATCGGAAGAT ATCGGAAGAT CCTTCAGA ATCGGAAGAT CCTTCAGAG ACGAGTGCAG ACGAGTGCAG ACGAGTGCAG	540 600 660 720 780 840 900 960 1020 1140 1200 1380 1380 1500 1560 1620 1680
55 60	GAGGGCAGA AAGCAGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAA ACTTCTTGAA ATTTGTTGAG TATCACAGT ATGTAAGGC ATTTGTTGAG ATTTGTTGAG ATGTAAGGC TATCACAGT ATGTAAGGC CAGCCCACAC GGTGTAAG	AGCAGAGACA CCTCCGCGGG GACGACAGGGG GTGGTGGACC TACAGGAAGC ACACAGGACG TCCACAGGAG AGAGCAAGGG AGAGCAAGGG AGAGCAATTT GCATTTAGGG AGAAACATTT GCATTTAGGG AGACATTT GCATTTAGGG AGCCTGAGCA ATGCCATATG CACCAGATCA GTGGCTGTCA TGTGGAGAGA GGTTATCTTG TTTAGTGGG GAAACCTTCC	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCAACG CTGAAGCCAA TGATAATGGA AGTCAACGAA GAGGCTTTAG GCTATCATTTA GCATACTTTA GCATACTTTA GCATACTTA TGCATACTAC TGCATACTAC TTCATACTAC CCTTCAATAA TGGAATGTAA TTCAGAAAAT TTCATAGTTC	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATCATC CCGGTCACAG GTTTAATTCA TCACACAGAT TGAATGGGT CCCCTCCTTT GTGTGGGAGA AGAGAACCT GAAAGTCAG GAGTGCCGC GAATCAGGAA ATATGGCAA ATATGGCAA TGCCCTGATT	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACTTC GAATGTCAGA CAGCAGTTC GAATGTCAGA GCAGATTCACA GAAAGACCAT AGCCAATTCACA TCATCTCAGA TCATCTCAGA TCATCTCAGA TCATCTCAGA TCATCTCAGA TCATCTCAGA TCATCTCAGA TCATCTCAGA TCATCTCAGA ACGTTTTGA ATCGGAAGAT CCTTCATGCC ACGAGTCCTT	540 600 660 720 780 840 900 1020 1080 1140 1260 1320 1320 1440 1500 1560 1680 1740
55 60	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCTG CAAATCGGGA TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGAG TATCACAGT TATCACAGT TAGTCCCACC GGTGTGTAAG TGGGCATGAC TGGGGATGAC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC ACGCAGGGGC AGAGCAAGGACATTAGGG AGAACATTTAGGG AGAAAGAGGC TGTCCCAGGA AGCCTGAGCA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA GTGGCTGTCA TGTGGAGAGA GGTTATCTTG TTTAGTGAGG AGAACGTTCC AAAGATAATG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG GCTATCATTT AGAAGCCTT TATGTGATGA TGCATACTAG GTGAAGTTCA CCTTCAATAA TGGAATGTAA TTCAAAAAAT TTCAAAAAAT AGGAATGTAA AGCGTGAACA	AGACCGCTGG TCCTGTGGTG TTATGAGTGC CAGGAAACCT CGGAGTGCAGG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAGG GTTTAATTCA TGACACAGAT TGAATGTGGT CCCCTCCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAG GATTCAGGA ATATGGCAA ATATGGCAA ATATGGCAA TGAACGTGAT TGAACGTGAT	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACACCACA CTTCCTGAAG AGTGCCTACC CACCGGGGG AAGGATGTGT AGATTCCCCA ACCCTTGTTT GGGAAGGGCT ACTGATCCAGC ACCCAGTCAC TCGTTCAGTG TATGAGTATG TTGGCTGAAC TTGGCTGAAC TCGTCAGAC TCGTCAGAC TCGTCAGAC TCGTCAGAC TCGTCAGAC TCGTCAGAC TCGTCAAC TCGTCAACC TCGTCAACCTGAC TCGTCAACCTG	GGAACCCAAG GCTTTGAAAT TCCAGGACAA ACGATGGCCA CAGGCACTC GGATTTGTGA CACGCAGTTC GAATGTCAGA ACGAGTTA CAGGAAGAG CAGATGTCAGA ACGAGATTA CAGAAAGCCAT AGCCAATTGA TCATCTCAGA TCATCTCAGA TCATCTCAGA ATCGTTTTGA ATCGTTTTGA ATCGGAAGAT CCTTCATGCC ACGAGTGCAG AAATCCACTT AGCCACCTT AGCCGGGGA	540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1800
556065	GAGGGCAGA AAGCAGATGA GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGAG TATCCACAGT TATCCACAGT TATCAAGAGAC TCATGCTAGA TCATGCTAGA AGCCCCACC GGTGTGTAAG ACCTTTAGG	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC TACAGGAGC AAAACTATGC TCCCACGGAG AAGGCAAGGG AAGGAAGGG AGGACATTT GCATTTAGGG AGAAAGAGGC TGTCCCAGGA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA TGTGGAGAA GGTTATCTTG TTTAGTGAGC AAAACCTTCT CAAAGATAATG CACAGCCCAC	TGGAGCCACG ATCTTTCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GCTATCATTT GCCTCAGCTC TATGTGATGA TGCATACTAG CCTTCAATTA CCTTCAATTA TCGAAGTTCA CCTTCAATAA TTCAAAGTTCA TTCATAGTTA AGCCTTAATGA CCCTTAATGA CCCTTAATGA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATTCATC CCGGTCACAG GAGGGAGTCA GATCAAGAT TGAATGTGGT CCCCTCTTT GAGAGAGGAGAACCTC GAAAAGTCAG GAGTGCAGG GAGTGCAGC GAATCAGGAA ATATGGCAAA TTGAACGTGAT TGAACGTGAT TGAACGTGAT TGGACGCC GAATCAGGAA ATATGGCAAA TTGCACGAAA GTTTCAGAAA	TCCCACACCA GCGAAACCAA CGATCTCAGG CACAACCAA CTTGCTGAAG AGTGCCTACC CACCGGGGGG AAGGATGTGT AGATTCCACG ACCCTTGTTT GGGAAGGGCT AGTGATCCAGC ACCCTTGTTT TGGGAGATCAC TCGTTCAGTG TATGAGTATC TTGGCGGGA TGTCAGCG TTGGCGGAAG GCACACAGA TCGCACCACACACACACACACACACACACACACACACACA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAAGCACCAG GGATTTGTGA ACGCAGTTC GAATGTCAGA ACGAAGGACCAG GCAATTCACGA GAAAAGCCAT AGCCAATTGA TCATCTCAGA GTGAGTCCTT AACGTTTTGA ACTGTTTGA ACTGTTTGA ACTGTATGCC ACGAGGAC AAATCCACTT AGCGCGGGA AAGGGAAAAA	540 600 720 780 840 900 960 1080 1140 1200 1320 1380 1440 1560 1560 1620 1680 1740 1800
55 60	GAGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAA AGTTCTTGAG TCAAAAAGGC GAGCGTGAGC TTTTGTGGGCA ATTTGTTGAG TATCACAAGT ATGTAAGGAC CCACC GGTGTGTAAG TGGGGATGAC GGTGTGTAAG TGGGGATGAC TCAGATTTAGG	AGCAGAGACA CCTCCGCGGG GACGACAGGGG GTGGTGGACC TACAGGAAGC ACACAGGAGGC AAAACTATGC TCCCACGGAG AGGACAAGGG AGAGCAAGGG AGAACATTT GCATTAGGG AGAAAGAGGC TGTCCCAGGA AGCCTGAGCA ATGCCATATG CACCAGATCA GTGGCTGTCA TGTGGAGGA GGTTATCTTG GGTAGTATCT TTTAGTGGG GAAACCTTCC AAAGATAATG CCCAGCCCAG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG GCTATCATTT GCCTCAGCTC TATGTGATGA TGCATACTAG TGCATACTAT TGCATACAT CCTTCAATAA TGGAAGTTCA CCTTCAATAA TTCATAGTTCA AGCGTGAACA TTCATAGTTC AGCGTGAACA CCCTTAATGA CCCTTAATCA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATCATC CCGGTCACAG GTTTAATTCA TGAACAGAT TGAACAGAT TGAACGTGA AGAGAACCTC GAAAAGTCAG GAGTGCCGC GAATCAGGAA ATTCGCAAA TGCCTGATT TGAACGTGAA GTTTCAGAAA GTTTCAGAAA	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACTTC GAATGTCAGA ACGAGTTC GAATGTCAGA CGATTCACGA ACGACATTCA ACGACATTCA ACGACCATTCA ACGACCATTCA ATCCCAT ACGCATTTCA ATCGGAAGAT CCTTCATCA ATCGGAAGAT CCTTCATCA ATCGGAAGAT CCTTCATCA ATCGGAAGAT CCTTCATCACA ATCGGAAGAT CCTTCATCACA ATCGGAAGAT CCTTCATCACA ATCGGAAGAT ACGGTGCAG AAATCCACTT AGCGCGGGGA AAATCCACTT AGCGCGGGGGA AAAGAAAAT AAGAACATCA	540 600 720 780 840 900 960 1020 1140 1200 1380 1380 1500 1560 1620 1680 1740 1860 1920
556065	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAGC TTTTGGGCA ATTTGTTGAG TATCACAGT ATGTAAGAC CTATGCAGA TATCACAGT ATGTAAGAC CGTTGTAAG TGGGGATGAC AACCTTTAGG GAAAATCCAT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC ACACAGGACA TCCCACGGAG AGGACATTT GCATTTAGGG AGAAAGAGGC TGTCCCAGGA AGCCTGAGCA ATGCCATATG CACCAGATCA ATGCCATATG TGTGGAGAGA GTGGTTACTTG TTTAGTGAG GAAACCTTCC AAAGATAATG CCCAGCCCG AAAGTAATG CCAGCCTGAGAAACGTCCC AAAGATAATG ACTAGAGGAAACTTCC AAAGATAATG CCCAGCCCGAAACGTCAGAACGTCAGAAACGTTCAGAAGGAAACGTTCAGAAAGGTAGAAACGTGAGAAACGTGAGAAACGTGAGAAACGTGAGAAACGTGAGAAACGTGAGAAACGTAGAAACATAAAACATAAAAAAAA	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCCAGGAC ACTCAACAGCAA TGATAATGGA AGTCAAGCAA GAGGCTTTAG GCTATCATTTAG GCTATCATTTAG GCTATCATTTA GCCTCAGCTC TATGTGATGA TGCATACTAG TGCATACTAG TTCAATAA TTCAATAAA TTCAAGAAAAT TTCATAGTTCA AGCGTGAACA CCCTTAATGA CCCTTAATGA CCCTTAATGA CCCTTAATGA CCCTTAATGA CCCTTAATGA CCCTTAATGA CCCCTTAATGA CCCCTTAATGA CCCCTTAATGA CCCATTTGA CCCATTTCA CCCATTCA CCCATTTCA CCCATTTCA CCCATTCA CCCATTCA CCCATTCA CCCATTCA CCCATTCA CCCATTCA CCCATTCA CCCATTCA CCCATTTCA CCCATTCA CC	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GTTTAATTCA TGACACAGAT TGAATGTGGT CCCCTCCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAG AATTCAGGAA ATATGGCAA ATATGGCAA ATATGGCAA TGACCTGATT TGAACGTGA GTTTCAGAAA CCTTCATAGC AAAACTAGGAA ATATCAGCAA ATATCAGAAA GTTTCATAGC AAACAGGGT	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA AGGAGGTTA CCAGAAAGAG GGATTCAGA GAAAGCCAT AGCCAATTGA TCATCTCAGA ATCGTCATGA ATCGGAAGAT CCTTCATGC ACGGTCCAG AATCCACTT AGCCAGTCCAG AAATCCACTT AGCCGGGGA AAGACATTA AAGGAAAAAA AAGACATCA AGGAAAAACTA AAGGAAAACCTT	540 600 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1500 1620 1620 1620 1740 1800 1800 1920
556065	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATGACTGG TGAAGGGATT AGTTCTTGAA TCAAAAAGGC ATTTTTGGGCA ATTTGTTGAG TATCACAGT TATCACAGT TAGTCACAGT TAGTCAGAG TAGCCCCACC GGTGTGTAAG TCGGGATGAC ACCTTTAGG GTAGAATGT TAGGAATGT TAGGAATGT TAGGAATGT TAGAAAATCCAT TATTCCTGGT TATTCCTGGT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC AAAACTATGC TCCCACGGAG AAGGAAGGG AGGAGAGGG AGGACATTT GCATTTAGGG AGAAAGAGGC ATGCCAGGAC ATGCCATGAG ATGCCATTC TTTAGTGGAGAG GGTTATCTTG TTTAGTGAGGA AGCTTCC AAAGATCAT CCCAGCCAG AAGGTGTTC AAAGATAATG CCCAGCCAG AAGGTGTTG AAGGTGTTG ACCAGGCAAACCTTCC AAAGGTGTTG ACCAGGCAAACCTTCC AAAGGTGTTG ACTAGAGGGA ACGTCCCTTA	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA AGTCAACCAC GCTGAAGCTTAG GCTATCATTT AGAAGCCTT TATGTGATGA TGCATACTAG CTGAAGTTCA TCCATCATAA TGGAAGTTCA TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT TTCATAGTAC CCCTTAATGA ACCCATTTGA AAAGGCGTCA	AGACCGCTGG TCCTGTGGTGG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTCA GAGGAGTCA TGAACAGAT TGAACAGAT GCCCTCCTTT GTTGGGAGG AGAGACCTC GAATCAGGA ATATGGCACA GATTCAGGAA ATATGGCAA TGCCTGTT TGAACGTGAT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACAAGGGT GAAAACTTAC	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACAACCAA CTTCTGAAG ATGCCTACC CACCGGGGGG AAGGATGTGT AGATTCCCCA GTGATCCAGC ACCGTGAGTCAC ACCGTGAGTCAC TCGTTCAGTG TATGAGTATA GTTGAGGGAA TGGTGAGACGA TGGTGAGACGA TGGTGAGACGA TGGTGAGACGA TGGAGAAC TGGAGAAC TGGAGAAC TGGAGAAC TGGAGAAC TGGAGAAC TGTGAGAAC TGTAACGTA ATGTATCCTGA ATGTATCCTGA AAGGTGAACGTG AATAACGTG AATAAGGAGA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA GGATTTGTGA CACGCAGTTC GAATGTCAGA ACGAAGTCAGA ACGAATGTCAGA ACGAATGTCAGA ACGAATTA CCAGAAAGAG GAATTCACGA GTATCACGA GTATCACGA GTATCACGA GTATCACGA ACGCAGTTCT AACGTTTTGA ACGTTTTGA ACGTTTCAT CCTTCATGCC ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAAAAAT AAGAAAACCTT AGGAACATCA AAGAAAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGACCTTTA	540 600 660 720 780 840 900 960 1080 1140 1200 1320 1380 1410 1560 1620 1680 1740 1800 1800 1920 1980
556065	GAGGGCAGA AAGCAGGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCTC CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAG TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGGG TATCACAGT ATGTAGGAC TCATGCTAGA TAGCACAGC GGTGTGTAAG GACCTTTAGG GTAGAATGT GAAAATCCAT TATTCCTGGT GAAAATCCAT TATTCCTGGT CTTTACAGAT	AGCAGAGACA CCTCCGCGGG GACGACAGGGG GTGGTGGACC TACAGGAAGC ACACAGGAGGC AAAACTATGC TCCCACGGAG AGGACAGGGACATTT GCATTTAGGG AGGACATTT GCATTTAGGG AGCCTGAGCA AGCCTGAGCA ATGCCATATG CACCAGATCA GTGGCTGTCA TGTGCAGGA GGTTATCTTC AAAGATAATG GAAACCTTCC AAAGATAATG CACAGGATGA ACCTTACAGGA AGGTGTGTG ACTAGAGGGA ACGTTCCTTA AGGCGATC CAGGCCTGACA AGGTGTCCTTA GCCGGGATG	TGGAGCCACG ATCTITCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCCATCAAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG GCTATCATTT GCCTCAGCTC TATGTGATGA TGCATACATT TGCATACATT TGCATACATT ACTCTCAATCA TCCATCAATCA TCCATCAATCA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATACAACAC AAAATCATC CCGGTCACAG GAGGGAGTCA GTTTAATTCA TGAACACAGAT TGAACACAGAT TGAACACAGAT AGAGAACTCC GAAAAGTCAG GAGTGCAGC GAATCAGGAA ATACAGAAA TGCCTGATT TGAACGTGAA TGCCTGATT TGAACGTGAA CCTTCATAGC AAACAAGGGT GAAACTAGAA CCTTCATAGC AAACAAGGGT GAAACTAGC AAACAAGGGT GAAACTACA	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGGACTTCTCACAC GAATTCTCAC GAATGTCACAC GCATTTCACAC CCACATTCACAC GCAATTCACAC ACGACATTCA ACGACATTCACAC ATCCCACAC ATCCCACAC ATCCCACAC ATCCCACAC ATCCCACAC ATCCCACAC ATCCCACAC ATCCCACAC AACGCCACT ACGCACCCT ACGCACCCC ACGACTCCT ACCCCCCC ACGACACAC AACCCTT ACCCCCCCC AAACCCTC ACGCACCCC AAACCCTC ACGCACCCC AAACCCTC ACGCACCCC AAACCCTC ACGAAAAAT AAGAACATCA ACGAAAAAT	540 600 720 780 840 900 960 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740 1880 1920 1980 2040
55606570	GAGGGCAGA AAGCAGGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCTC CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAG TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGGG TATCACAGT ATGTAGGAC TCATGCTAGA TAGCACAGC GGTGTGTAAG GACCTTTAGG GTAGAATGT GAAAATCCAT TATTCCTGGT GAAAATCCAT TATTCCTGGT CTTTACAGAT	AGCAGAGACA CCTCCGCGGG GACGACAGGGG GTGGTGGACC TACAGGAAGC ACACAGGAGGC AAAACTATGC TCCCACGGAG AGGACAGGGACATTT GCATTTAGGG AGGACATTT GCATTTAGGG AGCCTGAGCA AGCCTGAGCA ATGCCATATG CACCAGATCA GTGGCTGTCA TGTGCAGGA GGTTATCTTC AAAGATAATG GAAACCTTCC AAAGATAATG CACAGGATGA ACCTTACAGGA AGGTGTGTG ACTAGAGGGA ACGTTCCTTA AGGCGATC CAGGCCTGACA AGGTGTCCTTA GCCGGGATG	TGGAGCCACG ATCTITCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCCATCAAG CTGAAGCCAA TGATAATGGA AGTCAAGCGA CATTGAACAA GAGGCTTTAG GCTATCATTT GCCTCAGCTC TATGTGATGA TGCATACATT TGCATACATT TGCATACATT ACTCTCAATCA TCCATCAATCA TCCATCAATCA	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATACAACAC AAAATCATC CCGGTCACAG GAGGGAGTCA GTTTAATTCA TGAACACAGAT TGAACACAGAT TGAACACAGAT AGAGAACTCC GAAAAGTCAG GAGTGCAGC GAATCAGGAA ATACAGAAA TGCCTGATT TGAACGTGAA TGCCTGATT TGAACGTGAA CCTTCATAGC AAACAAGGGT GAAACTAGAA CCTTCATAGC AAACAAGGGT GAAACTAGC AAACAAGGGT GAAACTACA	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA GGATTTGTGA CACGCAGTTC GAATGTCAGA ACGAAGTCAGA ACGAATGTCAGA ACGAATGTCAGA ACGAATTA CCAGAAAGAG GAATTCACGA GTATCACGA GTATCACGA GTATCACGA GTATCACGA ACGCAGTTCT AACGTTTTGA ACGTTTTGA ACGTTTCAT CCTTCATGCC ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAAAAAT AAGAAAACCTT AGGAACATCA AAGAAAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGAACCTT AGGACCTTTA	540 600 720 780 840 900 960 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740 1880 1920 1980 2040
55606570	GAGGGCAGA AAGCAGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC TTTTGGGCA ATTTGTTGAG ATGTAAGAGC ATTTGTTGAG TATCACAGT ATGTAAGAC CGTTGTAAG TGGGGATGAC TATCACAC TGGGGATGAC TATCTTGAG TGGGGATGAC TATCTTGTAG TGGGGATGAC TATCTTGTAG TAGCCCCAC TGTTGTAAG TGGGGATGAC TATTCTTGTGA TATTCTTGTGA TATTCTTGTAGT TATTCTTGTA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGG ACGACAGGGC AAAACTATGC TCCCACGGAG AGGACAGGG AGGACAGGG AGGACATTT GCATTAGGG AGAAAGAGGC ATTCCCAGGA AGCCTGAGCA ATGCCATATG CACCAGATCA TGTGGAGAGA GGTTATCTTG TTTAGTGAGC AAAGATAATG CCCAGCCCAG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT TCGCTGAGGA TGGTCTCCCT TACTCAAG CTGAAGCCAA TGATAATGGA AGTCAAGCAA GAGGCTTTAG GCTTACATTTA GCCTCAGCTC TATGTGATGA TGCATACTAG TGCATACTAG TGCATACTAG TTCAATAA TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT ATCAGAAAT ACCCTTAATGA CCCTTAATGA CCCTTAATGA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGCA TTGAAGGCAG	AGACCGCTGG TCCTGTGGTG TCCTGTGGTGC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATCATC CCGGTCACAG GTTTAATTCA TGACACAGAT TGAATGTGGT CCCCTCCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAG GAATCAGAA ATATGGCAA ATATGGCAA ATATGGCAA CCTTCATATC TGAACGTGA CCTTCATAGC AAACAGGGT AAACAAGGGT AAACAAGGGT AAACAAGGGT AAACAAGGGT AAACAAGGGT AAACAAGGGT AAGCTCAGAG AAGCTCAGAG AGGCTCAGAG	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACTC GAATGTCCAG GCATTTCTGA CAGCAGTTC GAATGTCAGA GCAGTTCAGA GCAATTCAGA GCAATTCAGA TCATCTCAGA TCATCTCAGA ATCGGAAGAT CCTTCATGC AACGTTTTGA ATCGGAAGAT CCTTCATGCA AACGCCTT AGCCAGGGGA AAATCACTT AGCGAGACATT AGCGAGACATT AGCGAGACATT AGCGCGGGA AAGACATT AGCGCGGGA AAGACATT AGGAAAAT TTCATAGTGG ATCAGAAAAT TTCATAGTGG	540 600 720 780 840 900 960 1080 1140 1260 1320 1380 1440 1560 1620 1620 1620 1740 1800 1900 2040 2160
556065	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC GAGCGTGAGC TTTTGGGGCA ATTTGTTGAG TATCACAGT TAGTCACAGT TATTCACAGT TCATTCACAGT TCATTCACAGT TCATTCACAGT GCCATTCACT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGGC AAAACTATGC TCCCACGGAG AGAGCAAGGG TGTTCCCAGGA AGACAGTT GCATTTAGGG AGAAACAGT TGTCCAGGA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA GTGGCTGTCA TGTGGAGAGA GGTTATCTTG CAAACCTTC AAAGATAATG CCCAGCCAG AAGGTGTGTG AAAGATAATG CCCAGCCAG AAGGTGTGTG ACTAGAGGGA CAGTCCCTTA GGCCGGGATG GAAACCTCT GAAACCTCTG GAAACCTCT GAATCTCAGA	TGGAGCCACG ATCTTTCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCT ACTCATCAG TGGTCACAG TGATAATGGA AGTCAAGCGA AGTCAAGCGA GAGGCTTAG GCTATCATT AGAAGCCT TATGTGATGA TGCATACTAG GTGAAGTTCA CCTTCAATAA TGGAATGTAA TTCAAGAAAAT TTCATAGTTC AGCGTGAACA CCCTTAATGA AGCGTTAATGA CCCTTCATTAA ACCCATTTGA AAAGGCGTCA ACAGGCGTCA ACAGGCGTCA ACAGGCGTCA ACAGGCGTCA ACAGGCAGACTTT ACCCATTTGA AAAGGCGTCA ACAGGCAG AGAGTCATAC	AGACCITGG TCCTGTGGTG TCATGAGTCC CAGGAAACCT CAGGAATCCACACACACACACACACACACACACACACACA	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACACCACA CTTGCTGAAG AGGCCTACC CACCGGGGG AAGGATGTGT AGGATCCCACA ACCCTTGTTT GGGAAGGCT ACTTCAGT ACCCAGTCAC TCGTTCAGTG TCTGAGTAA TTGGCTGAAC TGTGAGGAA TCGTCAGAC TGTGAGGAA TCGTCAGTC ACTGAACTTG TCGTCAGTC ACTGACCAGA CGTGAACTTG TCGTCAGTC ACTGACCAGA CGTGAACTTG ATGATGGTA ACTGTGAC ACTGTGACCAGA ACTGTGACCAGA ACTGTGACCAGA ACTGTGACCAGA ACTGTGACCAGA ACTGTGACCAGA ACTGTGACCAGA ACTGTGACCAGA ACTGTGACCACAA ACTGTGACC CCTCTTGAAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA GAGTGTCC GGATTTGTGA CACGCAGTTC GAATGTCAGA ACGAGTTC GAATGTCAGA ACGAGTTC GAATGTCAGA GCAGATTCAGA GCAAATGA GCAATTGA TCATCTCAGA GTGAGTCCTT AACGTTTTGA ATCGGAAGAT CCTTCATGC ACGAGTGCAG AAGACACTT AGCCGGGGA AAGACATTC AGGAGAAAT AAGAAAAT AAGAAAAT AAGAAAAT AAGAAAAT AAGAAAAT ATCAGAAAAT TCATAGTGG GTGATGAGG	540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1860 1920 2040 2160 2160 2220
55606570	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAT AGTTCTTGAA TCAAAAAGGC TTTTGGGGCA ATTTGTTGAG TATCCACAGT TATCCACAGT TCATGCTAGA TAGCCCCACC GGTGTGTAAG GGAGCTTTAGG GTAGCATTCAGA TATCCAGT TAGCACTTCAGG TATCCTGGT CATACGATG CATACCATC CAAAAAGGCC CCACC CCCCCCC CCCCCCC CCCCCCCC	AGCAGAGACA CCTCCGCGGG CACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC AAAACTATGC TCCCACGGAG AAGGAAGGG AGGAGAGGG AGGACAGGG AGGACATTAGGG AGAAAGAGGC TGTCCCAGGA ATGCCTGAGA ATGCCTGAGA ATGCCATATG TTAGTGGG GAAACCTTC TTAGTGAGCA AGGTGTTGC AAAGATATG CCCAGCCAG AAGGTGTTG ACTAGAGGA ACTTCCCTTA GCCGGGATG AAGAACCTTC GGCCGGGATG AAGAACCTTC GATCCCTTA GGCCGGGATG AAGAACCTTC GAATCACATA	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGA AGTCAAGCGA GAGGCTTTAG GCTATCATTT GCCTCAGCTC TATGTGATGA TGCATCATTT TCCAGAGTTCA TTCAGAAGTTCA TTCAGAAATT TTCAGAAATT TTCAGAAATT TTCAGAAATT AGCATGTGAC CCTTCATGA CCCTTTAATGA CCCTTTAATGA CCCTTTAATGA CCCTTTAATGA CCCTTTAATGA CCCTTTAATGA CCTTTAATGA CCTTCATGA AAAGGCGTCA CCTTCATGCA CCTTCATCCA CCTTCATCA CCTTCATCCA CCTTCATCA CCTTCATCA CCTTCATCAT CCTTCATCCA CCTTCATCAT CTTCATCAT	AGACCGCTGG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGGAG AAAATTCATC CCGGTCACAG GAGGGAGTCA GAGGAGTCA TCAACAGAT TCAACAGAT TCAACAGAT TCAACAGAT TCAACAGAT TCAACAGAG AGAGACCTC GAAAAGTCAG GAGTCAGGAA ATATGCGAA TCCCTGTT TCAACGGAA ATATGGCAA ATATGGCAA GTTCAGAAA CCTTCATAGC AAACAAGGT AAACAAGGGT AAACAAGGGT AAACAAGGGT AAACTAGAA CCTATGAAAA CTATGAAAA CTATGAAAA CTATGAAAA CTATGAAAA	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACAACAAA AGTGCCTACC CACGGGGGG AAGGATGCCAC AGTACCAGC AGTACCAGC AGCACTCACA AGTACCAGC AGCACTCACC AGTAGATCAGC ACCTCTTTT GGGAAGGGCT AGTAGATCAGC TCGTCAGTG TATGAGTAAC TCGTCAGTG ATGACAAATTCT GAGCAAAATTCT GAGCAAACTG ATGACTGTA ATGATGTATG ATGACTGTA AAACTGTCAC AAAATTCT CACCCTGA AAAATTCTTCACAGAAACTGTACACAGAAACTGTACACAGAAACTGTACACAGAAACTGTACACACAGAAACTGTACACAGAAACTGTCACACACA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGGACCAC GGATTTGTGA CACGCAGTTC GAATGTCAGA ACGAAGAG CCAGTTCACA ACGAATGCAA ACGAATGAA ACGAATTCACA ACGAATTCACA GTAGTCCAT ACCGTTTCA ACCGTTTCA ACCGTTTCA ACCGTTTCA ACCGTTTCA AACGTTTCA AACGTTTCA AACGTTTCA AACGAACAT ACGCACCT AAAGACAT ACGCACCT ACGAACAAT ACGAACAT ACGCACCT ACCGTTCATCC ACAGTCCAT ACCGTTCATC ACAGTCCT ACCGTTCATC ACCTCTTCATCC ACAGACAAAT TCATACTCG ATCAACGA ATCAACACA ATCAACACA ATCAACACAC CTCATCACGA CCACTAACGA	540 600 720 780 840 900 960 1080 1140 1200 1320 1380 1440 1500 1680 1740 1860 1920 1980 2040 2160 2220 2280
55606570	GAGGGCAGA AAGCAGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAA ATTTCTTGAA ATTTGTTGAG TATCACAGT ATGTAAGGC GAGGGTAAGC CCATTCAGA TTTTCTTGAG TGAGGGATGAC GCTGTGTAAG TGGGGATGAC TATTCCTGGT GAAAATCGT TATTCCTGT TATTCCTGT TCTTTAGGT TCTTTAGGT TCTTTAGGT TCTTTAGGT TCTTTCTGAT TCTTTCTGAT TCTTTCTGA TCATTCTCGA TCATTCTCGA GCCATTCACT CGAAAAGGCG AAATGTTAC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAGGC ACACAGAGGC ACACAGAGGC ACACAGAGGC ACACAGACAG	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT TGCTCACCAG CTGAAGCCAA TGATAATGGA AGTCAAGGA GAGGCTTAG GCTATCATTA GCATACATTA GCATACTAT GCCTCAGCTC TATGTGATGA CCTTCAATAA TGGAATGTAA TTCATAGATTA TTCATAGTTCA CCTTCAATTA TCGAAATTTA AGCGTGAACA CCCTTAATTA ACCCTTTAATGA CCATTTGA AAAGGCGTC TAGAGCACT TAGAGACT TACCATTTGA AAAGGCGTCA TCAATGACA CCTTCAATCA CCTTCAATTA ACCATTTGA AAAGGCGTCA TCAATGACC CCTTCAATCA CCTTCAACC CCTCTAACCC CCTTCAACCC CCTTCAACCC	AGACCGCTGG TCCTGTGGTG TCTGTGGTGCTG CGGGAAACCT CGGGATCACG ATCCAAGAGA ARATCATCA CCGGTCACAG GTTTAATTCA TGACACAGAT TGAATGTGGT CCCCTCTTT GTGTGGGAG AGAGAACCT GAATCAGAA ATATGGCAA ATATGGCAA ATATGGCAA TGCCTGATT TGAACGTGAA CCTTCATAGC AAACAGGT AAACAGGT AAACAGGT AAACAGGT AAACAAGGT AAACAAGGT AAACAAGGT AAACAAGGT AAACAAGGT CATTAACAGA AGGTATGAA CTATGAAA CTATGAAA	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACTTC GAATGTCAGA CAGCAGTTC GAATGTCAGA GCAGATTCAGA GCAATTCAGA GAAAGCCAT TCATCCAGA ACGAGTTTCAGA TCATCTCAGA ATCATCTCAGA ATCATCTCAGA ACGTTTTGA ATCGGAAGAT CCTTCATGCA ACGATTCAGA ACGTTTTGA ATCGGAAGAT ACGTTTTGA ATCGGAAGAT ACGTTTTGA ATCGGAAGAT ACGTTCATGCA AGGAACATT AGCTCTTTAGCC ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCACTAAGGA CCCCTAGGGA	540 600 720 780 840 900 960 1080 1140 1200 1380 1440 1500 1560 1620 1620 1620 1740 1800 1920 1980 2040 2160 2220 2280 2340
55606570	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCTGGA TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC TATCTGGA TATCACAGT TATCACAGT ATGTAAGAC TATCACAGT ATGTAAGAC TATCACAGT ATGTAAGAC TATCACAGT ATGTAAGAC TATCACAGT TATCACAGT TATCACAC TATCACAGT TATCACAC TCATTACAGAT TATTCTTGGA GCAATACCAC CCAAAAGGCG ACCTTACAGA GCCATTCACA AGCTCAGAA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC ACGCAGGGC ACGCAGGGC AGGACAGGG AGGACATTT GCATTTAGGG AGGACATTT GCATTTAGGG AGCCATGAGCA ATGCCATGAG ATGCCATGAGCA ATGCCATGAGCA ATGCCATGAGCA ATGCCATGAGCA ATGCCATGAGCA ATGCCATGAGCA AGGCCGGGATCA AGGCCGGGATCA ACGCCCTTA ACGCCGGGATC ACTCCCTTA AGCCCGGGATC ACTCCCTTA AGCCCGGGATC ACTCCCTTA AGCCCGGGATC ACTCCCTTA AGCCCGGGATC ACTCCCTTA AGCCCGGGATC AAGATCCCTT AAGAACCTTCC GAATCTCAGA AGCCAGAAAT AGCCACATTA AGTCACAGTG	TGGAGCCACG ATCTTTCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT TCGCTGAGGA TGGTCTCCCA CTGAAGCCAA TGATAATGGA AGTCAAGCGA AGTCAAGCGA GAGGCTTTAG GCTATCATTTA GCCTCAGCTC TATGTGATGA TGCATACTAG TTCAAGAAAA TTCAAGAAAA TTCAAGAAAA TTCAAGAAAA TTCAAGAAAA TTCAAGAACA CCCTTAATGA AGCGTGAACA CCCTTAATGA AGCGTGAACA CCTTCATGA AAAGGCGTC TTGAAGGCGC CTTCATGA AAAGGCGTCA CCTTCATCA CCTTCATGA AAAGGCGTC AGAGTCATAC CCTTTAATGA CGCTCTAACCC CATATGAGGCC TAGCAGGGCC	AGACCGCTGG TCCTGTGGTG TCTGTGGTGC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATCATC CCGGTCACAG GTTTAATTCA TGACACAGAT TGAATGGGT GCCCTCCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAG AATCAGGAA ATATGGCAA ATATGGCAA ATATGGCAA ATATGGCAA CCTTCATGAAA CCTTCATAGC AAACTTAG GAAAACTTAC CAAAACTTAG AAACTTAGAAA CCTTCATAGC AAACTTAGC AAACTTAGAAA CCTTCATAGC AAACTTAGC AAACTTAGC AAGCTCAGGG TATAACAAGG TATAACAAGA CTATGAAAAC CGTCTGTTATT CAGTAAACCC	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACCAG GGATTTGTGA CAGCAGTTC GAATGTCAGA AGGAGGTTA CCAGAAAGAG GGATTCAGA GAAAGCCAT AGCCAATTGA TCATCTCAGA ATCGAATGA ATCGAATGA ATCGGAAGAT CCTTCATGC ACGGTCCAG AAATCCACTT AGCCAGTCCAG AAATCCACTT AGCGAGGAAAAT ATCAGTAGAAAAT TTCATAGTAG ATCAGAAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA CAGAGTCTAC	540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1620 1680 1740 1800 1980 2040 2160 2220 2280 2340 2400
5560657075	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGAAGGGAAT AGTTCTTGAA GAGGGATT ATTCTTGAA TCAAAAAGGC ATTTGTGAG TATCACAGT TATCACAGT TAGCCCCACC GGTGTGTAAG TCAGGATGAC TAGCAGAT TAGCAGAT TAGCAGAT TAGCAGAT TAGTAGAATGT CATTCAGAT TCATTAGGAC CATTCACAGT TATTCTGGT CATTCACAGT TATTCTGGT CATTCACAGT TCATTCTCAGAT TCATTCTCAGAT TCATTCTCAGAT TCATTCTCACACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAAC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC AAAACTATGC TCCCACGGAG AGAGCAAGGG AGGACATTAGGG AGAAAGAGGC AGCCATATGC ACCAGATCA ATGCCATATG CACTAGAGA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA AGGCTGTCC AAAGATCATC CAAAGCTTCC AAAGATCATG ACTAGAGGA ACGTCCTTA GCCCGGGATG ACTAGAGGA CAGTCCCTTA GCCCGGGATG ACTAGAGGA ACGTCCTTA GCCAGACCTT AGAGCAAAAT TCACCATTA AGGCAAAAT TTCACAGTG TTCACAGTG	TGGAGCCACG ATCTITCCCT ACTCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG TGGTCACCA TGATAATGA AGTCAAGCAA TGATAATGAA AGTCAACTT AGAAGCCTT TATGTGATGA TGCATACTAG TTCAACTAG TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT TTCATGTGTCA CCCTTCATGA CCCTTCATGA AGAGCCTT ATGTGTCA CCCTTCATGA CCCTTCATGA CCCTTCATGA ACCCTTCATGA CCCTTCATGA ACCCTTCATGA ACCCTTCATGA ACCCTTCATGA ACCCTTCATGCA TTGAAGGCAG ACAGTCATAC CCTTAATGAGGCAG ACAGTCATAC CCTTAACCC CATATGAGGGC TCCACCCTCA	AGACCGCTGG TCCTGTGGTG TCATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTCA GAGGGAGTCA TGAACAGAT TGAACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAG AGAGACCTC GAATCAGGAA ATATGGCAA ATATGGCAA TGCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACATCAG AGGGTATAGG AGGGTATAGG AGGGTATAGG CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CAGAGTTACG GAGAGTTCGT	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACACACACA CTTGCTGAAG AGGCCTACC CACCGGGGGG AAGGATGTGT AGATTCCCCA GTGAAGCACA ACCCTTGTT GGGAAGGCT ACTTCATT GGGAAGGCT ACTTCATGT ATTAGATATG GTTGACTGAA TTGGCTGAA TTGGCTGAAC TCTCCTGA AGTAACTTCT AATTAGGAGGA AAAGTTCT CATCCCTGA AAAGTATCC CTCATGAGACA CCACAGAACTCC CTCTTGAAC CCTCTTGAAC CCTCTTGAAC CACAGAGATTC CAAACTTCAC CAAACTTCAC CAAACTTCAC CAAACTTCAC CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTAGAC CAAACTTCACA CAAACTTAGAC CCTCTTGAAAC CAAACTTAGAC CAAACTTAGAC CATCAGACGGAC CCTCTTGAACA CCTCTGAACCGAC CCTCTTGAACACACAC CCTCTTGAACACACAC CCTCTTGAACACACACAC CCTCTTGAACACACACACACACACACACACACACACACAC	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGGCACCAG GGATTTGTGA CACGCAGTTC GAATGTCAGA ACGAAGGGTTA CCAGAAAGGG GATTCACGA GAAAAGCCAT AGCCAATTGA TCATCTCAGA GTGAGTCCTT AACGTTTTGA ATCGTCTCAGA ATCGGAAGAT ACGAAGATCACTT AGCGCGGGA AAGAGAAAAT AAGAACATCA ACGAAGAAAAT TTCATGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA CCTCTGTGA ACCACTAAGGA CCACTAAGGA CCACACCTCTGA	540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1800 1980 2040 2160 2220 2280 2340 2460
55606570	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGAAGGGAAT AGTTCTTGAA GAGGGATT ATTCTTGAA TCAAAAAGGC ATTTGTGAG TATCACAGT TATCACAGT TAGCCCCACC GGTGTGTAAG TCAGGATGAC TAGCAGAT TAGCAGAT TAGCAGAT TAGCAGAT TAGTAGAATGT CATTCAGAT TCATTAGGAC CATTCACAGT TATTCTGGT CATTCACAGT TATTCTGGT CATTCACAGT TCATTCTCAGAT TCATTCTCAGAT TCATTCTCAGAT TCATTCTCACACT CGAAAAGGCG AAATGTCTAC AGCTCAGAAA CATTCAGAAC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC AAAACTATGC TCCCACGGAG AGAGCAAGGG AGGACATTAGGG AGAAAGAGGC AGCCATATGC ACCAGATCA ATGCCATATG CACTAGAGA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA ATGCCATATG CACCAGATCA AGGCTGTCC AAAGATCATC CAAAGCTTCC AAAGATCATG ACTAGAGGA ACGTCCTTA GCCCGGGATG ACTAGAGGA CAGTCCCTTA GCCCGGGATG ACTAGAGGA ACGTCCTTA GCCAGACCTT AGAGCAAAAT TCACCATTA AGGCAAAAT TTCACAGTG TTCACAGTG	TGGAGCCACG ATCTITCCCT ACTCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG TGGTCACCA TGATAATGA AGTCAAGCAA TGATAATGAA AGTCAACTT AGAAGCCTT TATGTGATGA TGCATACTAG TTCAACTAG TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT TTCATGTGTCA CCCTTCATGA CCCTTCATGA AGAGCCTT ATGTGTCA CCCTTCATGA CCCTTCATGA CCCTTCATGA ACCCTTCATGA CCCTTCATGA ACCCTTCATGA ACCCTTCATGA ACCCTTCATGA ACCCTTCATGCA TTGAAGGCAG ACAGTCATAC CCTTAATGAGGCAG ACAGTCATAC CCTTAACCC CATATGAGGGC TCCACCCTCA	AGACCGCTGG TCCTGTGGTG TCATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTCA GAGGGAGTCA TGAACAGAT TGAACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACACAGAG AGAGACCTC GAATCAGGAA ATATGGCAA ATATGGCAA TGCCTGATT TGAACGTGAA GTTTCAGAAA CCTTCATAGC AAACATCAG AGGGTATAGG AGGGTATAGG AGGGTATAGG CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CTATGAAAAC CAGAGTTACG GAGAGTTCGT	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACACACACA CTTGCTGAAG AGGCCTACC CACCGGGGGG AAGGATGTGT AGATTCCCCA GTGAAGCACA ACCCTTGTT GGGAAGGCT ACTTCATT GGGAAGGCT ACTTCATGT ATTAGATATG GTTGACTGAA TTGGCTGAA TTGGCTGAAC TCTCCTGA AGTAACTTCT AATTAGGAGGA AAAGTTCT CATCCCTGA AAAGTATCC CTCATGAGACA CCACAGAACTCC CTCTTGAAC CCTCTTGAAC CCTCTTGAAC CACAGAGATTC CAAACTTCAC CAAACTTCAC CAAACTTCAC CAAACTTCAC CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTCACA CAAACTTAGAC CAAACTTCACA CAAACTTAGAC CCTCTTGAAAC CAAACTTAGAC CAAACTTAGAC CATCAGACGGAC CCTCTTGAACA CCTCTGAACCGAC CCTCTTGAACACACAC CCTCTTGAACACACAC CCTCTTGAACACACACAC CCTCTTGAACACACACACACACACACACACACACACACAC	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACCAG GGATTTGTGA CAGCAGTTC GAATGTCAGA AGGAGGTTA CCAGAAAGAG GGATTCAGA GAAAGCCAT AGCCAATTGA TCATCTCAGA ATCGAATGA ATCGAATGA ATCGGAAGAT CCTTCATGC ACGGTCCAG AAATCCACTT AGCCAGTCCAG AAATCCACTT AGCGAGGAAAAT ATCAGTAGAAAAT TTCATAGTAG ATCAGAAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA CAGAGTCTAC	540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1620 1680 1740 1800 1980 2040 2160 2220 2280 2340 2460
5560657075	GAGGGCAGA AAGCAGGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCTC CAAATCGGGA TGATAACTGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAA ATTTTTTTGGGCA ATTTTTTGAG TTACACAGT ATGTAAGAC GGTGTGAGC TCATGCTAGA ATTTATAAGAC GGTGTGTAAG TGAGGAATGT GAAAATCCAT TATTCCTGGT CTTTACAGAT TATTCTTGGT CAATTCTTAGA GCCATTCAC GGTGTTAAG GCAATCCAC GGTGTTAAG GAAATCCAT CATTCCTGGT CAATTCCACAG GCAATCAC AGCATTCAC AGCTCAGAAAA AGCTCAGAAAA AGCTCAGAAAA AGCTCAGAAAA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGGC AAAACTATGC TCCACGGAG AGGACAGGG AGGACAGTT GCATTAGGG AGGACATT GCATTAGGG AGCCTGAGCA ATGCCATATG CACCAGATCA TGTGCATATG CACCAGATCA GTGGCTGTCA TGTGGAGGA AGCCTGAGCA AGGCTGTCA AGGCTGTCA AGGCTGTCA CAGGTGTTCA AGGCTGTGG ACTAGAGGGA ACGTTCCTTA GGCCGGGATG ACTAGAGGGA CAGTCCCTTA GGCCGGGATG AAGAACCTCT GAATCTCAG ATTCACAGTG ATTCACAGTG TTCACAGTG TTCACAGTGGT TTCACAGTGGT TTCACAGTGGT TACAGTAGGTT	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT TACTCATCAAG CTGAAGCCAA TGATAATGGA AGTCAACGA CATTGAACAA GAGGCTTTAG GCTATCATTT GCCTCAGCTC TATGTGATGA TGCATACTAG TGCATACTAT TGCATACTAG CTTCAATAA TCGAAGATCAT ACCCATTTGA AAAGGCGTC ACCTTCATGA AAAGGCGTC CCTTCATGA AAAGGCGTC CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGCA TGGAGGACT TCAAGGCAG CCTTCATGCA TTGAAGGCAG CCTTAACCC CATATGAGAG TACCAGGGCC CTCAACCATCA CTCAACC	AGACCGCTGG TCCTGTGGTG TCCTGTGGTG TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATACAACAC AAAATCATC CCGGTCACAG GAGGGAGTCA GTTTAATTCA TGAACACAGAT TGAACACAGAT TGAACGTGAG AGAGAACCTC GAAAAGTCAG GAGTGCOGC GAATCAGGAA ATTCAGCAAA TGCCTGATT TGAACGTGAA CCTTCATAGC AAACAAGGGT GAAAACTTAC AAGCTCAGAA CCTTCATAGC AAACAAGGGT TATAACAAG TGATAACAAG TGATAACAAG CTATGAAA CTATGAAAC CAGGAGTCGT TAGCTTAGT	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGCCA CAGGACTTC GAATGTCAGA CAGCAGTTC GAATGTCAGA CGATTCAGA CGATTCAGA CGATTCAGA CGATTCAGA GCAATTGA TCATCTCAGA ATGCGATTTA ATCGGAAGAT ACGTTTTTGA ATCGGAAGAT CCTTCATGC AAATCCATT AGCGCGGGGA AAATCCACTT AGCGCGGGGA AAATCCACTT AGCGCGGGGA AAATCCACTT AGCGCGGGGA AATCCACTT AGCGCGGGGA ATCAGAGAAAT TCATAGTGG ATCAGAAAAT TCATAGTGG CTGATGAGGA CCTCTGTGGA CCACTAAGGA CCTCTGTGGA CAGAGTCTAG CACACCTCTGA	540 600 720 780 900 960 1080 1140 1260 1380 1440 1500 1560 1680 1740 1800 1920 1980 2040 2160 2220 2340 2460 2520
5560657075	GAGGGCAGA AAGCAGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATACTGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC TTTTGGGCA ATTTGTTGAG TATCCACAGT ATGTAAGAC TATCCACAGT ATGTAAGAC TATCCACAGT TATCCACAGT TATCCACAGT TATCCTGAT TATTCCTGGT CTATACAGAT TCATTCTCGA GCCATTCACT CAAAAAGGC GAAAAGCC AACTTTATCCACAGT TATTCCTGAA TCATTCCTGAA TCATTCCTGAA CATTCACAGAT CATTCACAAAC AGCACAGAAAA	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAGGC AAAACTATGC TCCCACGGAG AGGAGAGCATTT GCATTAGGG AGAAGCATTT GCATTAGGG AGACAGGTC ATTAGGG AGCCTGAGCA ATGCCATGAG AGCCTGAGCA ATGCCATGAG AGCCTGAGCA ATGCCATATG CACAGATCC TATAGTGAGC ATTAGTGAGC ATTAGTGAGC AAAGATAATG CCCAGCCCA AAGGTCCCTTA ACGTCCCTTA AGGCCAGATC GAAACCTTC GAAACCTTC GAAACCTTC GAAACCTTC GAATCTCAGA TCCACATTA AGGCCAAAAT AGTCACAGTG TTCGATGCTA AGTCACAGTG TTCGATGCTA ATGAATTGG AATGAGTGT AAAGATTGG	TGGAGCCACG ATCTITCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT TGCTCACCAG CTGAAGCCAA TGATAATGGA AGTCAAGCACA GAGGCTTAG GCTATCATTA GCTATCATG GCTATCATTA GCTATCATTA GCTATCATTA TGCATACTAT TGCATACTAC CCTTCATTA TCGAACAT TTCATAGTTCA CCTTCATTA TCGAACATT ACCCATTTGA AAAGGCGTCA CCTTCATGA CCTTCATGA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA CCTTCATGA CCTTCATGA CCTTCATGA AAAGGCGTCA CCTTCATGCA CCTTCATCCC CATATGAGGGC TCAACCATCA CCTTCATCCA TGGAACTTAA	AGACCGCTGG TCCTGTGGTG TCTGTGGTGCTGG ATCCAAGAGA ATAATCAACC AAAATCAACC AAAATCATCA GAGGAGAGACT GAGGAGACTA GAGGAGATCA GTTTAATCA TGACACAGAT TGAATGGGA GAGGGAGTCAG GAGGAGACCTC GAAAGCCAGAT TGAATCAGAA ATATGGCAA ATATGGCAA ATATGGCAA ATATGGCAA CCTTCATAGC AAACATGGA GAAACTTAC AAACAGGGT AAACATGAA CCTTCATAGC AAACATGAA ACGTTAGAGA ACGTTAGAGA ACGTTAGAGA ACGTTAGAGA ACGTTAGAGA ACGTTAGAGA ACGTTAGAGA AGGGTATGAGA CTATGAAAAC GAGGATTCGT TAGCTAAGC GAGAGTTCGT TAGCTAAGGA	TCCCACACCA GCGAAACCAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA CAGCACTC GGATTTCTGA CAGCACTTC GAATGTCAGA CGATTCCAGA AGGAGGTTTA CCAGAAAGAG GGATTCACAA GAAAGCCAT AGCCAATTGA ATCCTCAGA ATCCTCAGA ATCCTCAGA ATCCTCAGA ATCCACTT AGCGAGAGAT ACGTTTTGA ATCGGAAGAT ACGTTTCAGCA AAATCCACTT AGCGCGGGA AAAACCTTT AGCACTACTAG ATCATAGTGG GTGATGAGGA CCTCTGTGGA CCACTAAGGA CCTCTGTGGA CAGAGTCTAC ACACCTCTTAC ACACCTCTAC ACACCTCTTAC ACACCTCTTAC ACACCTCTAC ACACCTCTACA ACACC	540 600 720 780 840 900 960 1080 1140 1260 1320 1380 1440 1500 1500 1620 1620 1620 1620 2040 2160 2240 2240 2340 2440 2460 2520
5560657075	GAGGGGCAGA AAGCAGGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGG TGAAGGGAAT AGTTCTTGAA TCAAAAAGGC TTTTGGGGCA ATTTGTTGAG TATCACAGT TATCACAGT TAGCCCACC GGTTGTAAG TCACAGT TATCACAGT TATCACAGT TATCACAGT TATTCTTGAG GTACGAATGT CATTTCTCGG GTACGAATGT CATTTCACAGT TCATTCACAGT AATTCACAGT AATTCACAGT AATTCACAGT AATTCACAGT AATTCACAGT CATTCACAGA CATTCACAAAAGGCG AAATGTCTAC AAATGTCTAC AAGCAAAAGGCA AAATGTCTAC AAGCAAAAGGCA AAGGAAAAGGCA AATTCAGAAA CATTCAGAAA CATTCAGAAA CATTCAGAAA CATTCAGAAA CATTCAGGAA AGACCTTAAT	AGCAGAGACA CCTCCGCGGG GACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC AAAACTATGC TCCCACGGAG AGAGCAAGGG TGTTAGGG AGAAGACATT GCATTTAGGG AGAAGAGGC TGTCCCAGGA AGCCTGAGCA ATGCCATATG CACCAGATCA GTGGCTGTCA TGTGGAGAGA GGTTATCTG GAAACCTTC AAAGATAATG CCCAGCCCAG	TGGAGCCACG ATCTITCCCT ACTCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG TGGTGAGCAA TGATAATGGA AGTCAAGCGA GAGGCTTAG GCTATCATTAG GCTATCATTA GCATACATTA GCATACATTA GCATACTAG CCTTCAATGA TTCAAGAATTA TCGAAGTTA TCGAAGATTA ACCATTTAG ACGGAGACTT ACCCATTTAG AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTAATGA CCTTTAATGA TTGAAGGAG AGAGTCATAC CTTTAATGA TTGAAGGCG TTAACCC CATATGAAGC CTTAATCAA CGTCTAACCC CATATGAGCA TAGCAGGGCC TCAACCATCA TGGAATCTAA AGGAGTCTAA	AGACCGCTGG TCCTGTGGTG TCATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GTTTAATTCA TGACACAGAT TGAATGTGGT CCCCTCCTTT GTGTGGGAGG AGAGAACCTC GAAAAGTCAG AATTCAGGAA ATATGGCAA ATATGGCAA ATATGGCAA ATATGGCAA GTTTCAGAAA GTTTCAGAAA GTTTCAGAAA GTTTCATAGC GAAACTTAC GAAAACTTAC GAAAACTTAC CATAGCTAGAA CCTCTGTTAT TGAACAGGT TATAACAAGA TTAGCTTAGTT TAGCTTAGTT TAGCTTAGTT TAGCTTAGTG TGAGAAAGGA TGCCAGAGAG TGCCAGAGAG	TCCCACACCA GCGAAACCAA GCGAATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA GAGTGTCCAGGACTCAGA CAGCACTTC GAATGTCAGA CAGCACTTC GAATGTCAGA CAGCACTTC GAATGTCAGA GCAATTGA GCAATTGA TCATCTCAGA ATCACTCTTAGA ATCACTTTTGA ATCACTTTTGA ATCACTTTTGA AAATCACTT AGCCGGGGA AAGAGAAATC AAGAAAATC AAGAAAATC ATCACTT AGCTCTGTGA ATCAGAAAT TCATCAGAAGA TCATCTGGGA CCTCTGTGGA CCACTAAGGA CCTCTGTGGA CCACCTCTGA CTCCAAGAAG TTTAATTCTC AAGGGGGCCAG	540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1680 1740 1860 1980 2040 2160 2220 2280 2340 2460 2580 2640
5560657075	GAGGGCAGA AAGCAGATG GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCT CAAATCGGGA TGATACTGGA TGAAGGGAT AGTTCTTGAA TCAAAAAGGC ATTTGTGAG TATCACAGT TATGAGAC TATCACAGT TAGCCCCACC GGTGTGTAAG TCAGATGAC TATCACAGT TATTCTTGG TAAGAATGT TATTCTTGG CTATCTTAGG TATCAGATT TATTCTTGGT CATTTCTTGGT CATTTCTTGGT CATTTCTTGGT CATTTCTTGGT CATTTCTTGGT CATTTCTTGGT CATTTCTTGGT CATTTCTTGGT CATTCTCTGGT CAGAAAGGCG AAATGTCTAC AGCTCAGAGC AGCTCAGAGC AGGAAGGGAA CATTCAGAGC AGGAAGGGAA AGACCTTAAT TAAGAATCGC	AGCAGAGACA CCTCCGCGGG CACGACAGGG GTGGTGGACC TACAGGAAGC ACGCAGGGC AAAACTATGC TCCCACGGAG AAGGAAGGG AGGAGAGGG AGGAAGGGG AGGAAGGGG AGGAAGGGG AGGAAGGGC ATCCCAGGAC ATGCCATATG CACTGAGCA ATGCCATTA GGGTGTCA TTTAGTGAG GGAAACTTT CAAGCAGAC AAGGTGTTC GAACCTTC GAAGCCAG AAGGTGTTG GCCAGGATCA AAGGTGTTG ACGAGACAT TCACCATTA GACCAGATCA TTCACCATTA GAGCAAAAT TCACCATTA GAGCAAAAT TTCACCATTA AGTCACAGT TTCACAGT TTCACAGT TTCACAGT AATGAATTGG TTCACAGT AATGAATTGG AATAAGCGAC AACTATGAAGGG AACTATGAAGGG AACTATGAAGGG AACTATGAAGGG AACTATGAAGCGAC AACTATGAAGGGA AACTATGAATGGG AATAAGCGAC AACTATGAAGGGA AACTATGAAGGGA AACTATGAAGGGA AACTATGAAGGGA AACTATGAAGGGA AACTATGAAGGGAC AACTATGAAGGGAC AACTATGAAGGGAC AACTATGAAGGGAC AACTATGAAGGGAC AACTATGAAGGAC AACTATGAAGGAC AACTATGAAGGAC AACTATGAAGGAC AACTATGAAGAGCAC AACTATGAAGGAC AACTATGAAGGAC AACTATGAAGAGCAC AACTATGAAGAGAC AACTATGAAGAGAC AACTATGAAGAGAC AACTATGAAGACGAC AACTATGAAGAGAC AACTATGAAGACGAC AACTATGAAGAGAC AACTATGAAGAGAC AACTATGAAGACGAC AACTATGAAGACGAC AACTATGAAGAGAC AACTATGAAGACGAC AACTATGAAGACAC AACTATGAAGACACAC AACTATGAACAC AACTATGAAGACAC AACTATGAACAC AACTATGAACACAC AACTATGAACACAC AACTATGAACACAC AACTATGAACACAC AACTATGAACACACACACACAC AACTATGAACACACACACACACACACACACACACACACAC	TGGAGCCACG ATCTTTCCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCCT ACTCATCAG CTGAAGCCAA TGATAATGA AGTCAAGCAA AGTCAACAA GAGGCTTTAG GCTATCATTT AGAAGCCAT TGCTCATTAG TCCATCATTA TGCATACTAG TTCAGAAGTTA TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT TTCAGAAAAT TTCATGTGAC CCTTCATGA ACCTTTAATGA CCCTTCATGA ACCTTTAATGA CCCTTCATGA ACCTTTAATGA CCCTTCATGA ACCTTTAATGA CCCTTCATGA AAAGGCGTCA CCTTCATGA AAAGGCGTCA CCTTCATGA ACAGTCATACCC CATATAGAGGCG TCCACCATTTAACCC CATATAGAGGC TCCACCATTCAACCC CATATAGAGGC TCCACCATCA CTCTTATCCA CTCTTATCCA CTCTTATCCA CTGTTATCCA CTGTTATCCA ACAGTCATCA	AGACCGCTGG TCCTGTGGTG TCATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA AAAATCAACC AAAATTCATC CCGGTCACAG GAGGGAGTCA GAGGAGTCA TGAAAGTGGT GTTTAATTCA TGACACAGAT TGAAAGTCAG AGAGAACCTC GAAAAGTCAG GAGTGCAGA ATATGGGAA ATATGGGAA ATATGGCAA ATATGGCAA ATATGGCAA GTTTCAGAAA CCTTCATAGC GAAACTTAG AAGCTCAGAG TATAACAAGG TATAACAAGG TATAACAAGG CTATGAAAA CTATGAAAC CTATGAAAC GTCTTAATGC AAGCTCAGAG AGGGTATAC AGGGTATACA AGGGTATACTA AGGGTAAACC GTCTTATTT CAGTAAACC GTCTTATTT CAGTAAACC GTCTTATTT CAGTAAACC GAGAGTTCGT TAGCTTAGTG TGAGAAGGGA ACAGGGGAG ACAGAGGGTA ACAGGGAGA ACAGAGGGTA ACAGGGAGA	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACACACACA CTTCTGAAG AGGCCTACC GCGCGGGG AAGGATCCCCA GCGATCCCCA AGTGCTCAGG ACCCTCTTT GCGAAGGCC ACCCTCTTT GCGAAGGCC ACCCTCAGT ATTAGATATG GTTCAGGT ATTAGATATG GTTCAGGAAA TCTCCCTGA ACTAACCTGA AAAGTATCC CAAAACTTG AAAACTTGAAAACCTG AAAACTTGAAAACTTG AAAACTTGAAAACTTC AAAACTTTAAAACAGAA CCCTCTTGAAA CAGAAGATTC CAAAACTTCACAAACAGAACCTC CATAACTTAGAAACAGAACCTCCAAACACCTCAAACAACCTCAAACAAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA GGATTTGTGA CAGGCACTTC GAATGTCAGA AGGACCAG GGATTTCAGA AGGAAGAG CCAGATTCAGA AGGAAGAG GAATTCACGA GAAAAGCCAT AGCCAATTGA TCATCTCAGA GTGAGTCCTT AACGTTTTGA ATCGGAAGAT CCTTCATGCC ACGAGTGCAG AAATCCACTT AGCGCGGGA AAGGAAAAT TCCACTGTGA ATCAGAAAAT TTCATGTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA CCACTAAGGA CCTCTGTGA CCACTAAGGA CCTCTGTGA CCACTAAGGA CCTCTGTGA CCACTAAGGA CCTCTGTAA CTCCAAGAAG TTTATATCTC AAGGGGCAG AACCTCAGAA	540 600 720 780 840 900 960 1020 1140 1200 1320 1380 1410 1560 1620 1680 1740 2040 2160 2220 2280 2340 2460 2520 2580 260 2700
5560657075	GAGGGCAGA AAGCAGGATC GGACAGAGAG ATACCAAAAT CATGGAAAAC CTCCCACATG TCGAGGTCTA AGATGAATCGG TGAAGGGAAT AGTTCTTGAA AGTTCTTGAA ATTTTTTGGGCA ATTTGTTGAG TTACCACAGT ATGTAAGGC TATCCACAGT ATGTAAGGC GAGCGTGAGC TTATCCACAGT ATGTAAGGAC TCATGCTAGA TAGCCACAC GGTGTGTAAG TGGGGATGAC CACTTTAGG GTACGAATGT TATTCCTGGT TCTTTACAGAT TCATTCCTGG TCTTTACAGAT TCATTCCTGGT CTTTACAGAT TCATTCACAG AGATCCTTAAG AGCTCAGAAA CATTCAGAG AGGATGAC AGGAAGGGA ACATTCAGAG AGGATCCTTAAT AGGTCAGAAA CATTCAGAGC AGGAAGGGAA TCACAATGGA AGAATCCCT AAGAATCCC AAGTGTTACT AAGAATCCC AAGTGTTCCT AAGAATCCC AAGTGTTCCT AAGAATCCC AAGTGTTCCT AAGTATCCC	AGCAGAGACA CCTCCGCGGG GACGACAGGG GACGACAGGG GACGACAGGG GACGACAGGGC AAAACTATGC TCCCACGGAG AGGACAGGGC AGGACAGGGC AGGACAGGGC AGGACAGGGC AGGACAGGGC AGGACATTT GCATTTAGGG AGCCTGAGCA ATGCCATATG CACCAGATCA GTGGCTGACA TGTGGAGGA AGCCTGAGCA ATGCCATATG CCCAGGACA AGGCTGACCA AGGCTGACCA AGGCTGACCA AGGCTGACCA AGGCTGACCA AGGCTGACCA AAGGTACTC CAAACCTTC GAAACCTTC GAAACCTTC GAAACCTTC GAAACCTTC GAAACCTT AGGCGGATG ATGCACATT AGGCCAGAAAT AGTCCACATT AGGCCAGAAAT ATTCACATTA ATTCACAGTGG ATTAAGGGT AATGAATTGG GATAAGCGAC GAAATTGG GATAAGGGAAAT GCCAGTAGGGT ATGAATTGG GATAAGCGAC GAACTATGAAG GCAAGAGGGAT GACCAGGGAC GACTATGAAG GCAAGAGGGAT GACGAAGGGAC	TGGAGCCACG ATCTITCCT ACTCCAGGGC TCGCTGAGGA TGGTCTCCT TGCTCATCAG CTGAAGCCAA TGATAATGGA AGTCAAGCAA GAGGCTTAG GCTATCATTA GCATACAG GCTCAGCTC TATGTGATGA CCTCAGCTC TATGTGATGA CCTTCAATAA TTCATAGTTCA CCTTCATTA AGAGGCCTT AGGAGAGTTTA CCCTTAATTA CCCTTAATGA CCTTCATGA CCTTCATGA CCTTCATGA AAAGGCGTC TTGAAGGCAG CCTTCATGA AAAGGCGTC CCATATGAGA CCTTCATGCA TTGAAGGCAG TCAACCAC CCTTAATGAC CCTTAATGAC CCTTAATGAC CCTTAATGAC CCTTAACCA TTGAAGGCAG TAGAACATCA TGGAATCTAA AGAAGATTCAA AGAAGATTCAA AGGAAGTTCAA CTTGTTATCCA TCGAATCTAA CCTTCATCCA TCGAATCTAA CACTCTGTCAT CTGGTGAGTT CTGGTGAGTT CTGGTGAGTT CTGGTGAGTT CTGGTGAGTT CTGGTGAGTT CTGGTGAGTT CTGGTGAGTT CTGGTGAGTT	AGACCGCTGG TCCTGTGGTG TCCTGTGGTGT TTATGAGTCC CAGGAAACCT CGGAGTGCAG ATCCAAGAGA ARAATCAACC AAAATCATC CCGGTCACAG GTTTAATTCA TGACACAGAT TGACACAGAT CCCCTCCTTT GTGTGGGAG AGAGAACTCAG GAATCAGGA ATACCACAGAT TGACACAGAT TGACACAGAT TGACACAGAT TGACCTGAT TGAAAGTCAG GAATACAGAA CCTTCATAGC AAACAAGGGT ATAACAGA AGGTCAGA AGGTCAGA CTATGAAAC CTATGAAAC CTATGAAAC CTATGAAAC TATGAAAC TAGGAAGGGA TAGGAAGGGA TAGGAAGGGA TAGGAAAGGGA TAGGAAAGGGA TAGGAAAGGGA TAAGAAGGATTAG TAAGAAGGAT TAAAACGAATTAGT TAGAAAGGAT TAAGAAGGAT TAAGAAGAT TAAGAAGGAT TAAGAAGGAT TAAGAAGAT TAAGAAGAT TAAGAAGAGAT TAAGAAGAAT TAAGAAGAT TAA	TCCCACACCA GCGAAAACAA GCGATCTCAGG CACAACACAA	GGAACCCAAG GCTTTGAAAT ATGCTGAATC TCCAGGACAA ACGATGGCCA GAGTGTCCAGGACTCAGA CAGCACTTC GAATGTCAGA CAGCACTTC GAATGTCAGA CAGCACTTC GAATGTCAGA GCAATTGA GCAATTGA TCATCTCAGA ATGCAATTGA ATCGTTTTGA ATCGTTTTGA ATCGGAAGAT CCTTCATGC ACGAGTGCAG AAGACACTT AGCCGGGGA AAGACATTCA AGGAAAATC ACTCTGTGA ATCAGAAAAT TTCATAGTGG GTGATGAGGA CCTCTGTGGA CCACTAAGGA CCTCTGTGGA CCACTAAGGA CCTCTGTGGA CCACTAAGGA CCTCTGTGGA CCACTAAGGA CCTCTGTGCA CCACGAGGTCTAC ACACCTCTGA CTCCAAGAAG TTTCATAGTGC TCCAAGAAG TTTCATAGTGC TCCCAAGAAG TTTCATAGTAC CTCCAAGAAG TTTCATAGTAC CTCCAAGAAG TTTCATAGTAC CTCCAAGAAG TTTCATAGTAC CTCCAAGAAG TTTCATAGTAC CTCCAAGAAG TTTATATTCTC AAGGGGGCCAG	540 600 720 780 900 960 1080 1140 1260 1380 1440 1560 1560 1620 1620 1620 1620 1620 2040 2160 2220 2280 2240 2460 2460 2580 2640 2760

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			ACTOTOTOCO				2880
			AGTGTGGGGA				2940
			GGGAGAAGCC				3000
5			CTGACCCTCA				3060
,			GTAAGGACTT				3120
			ATGACCAAGA				3180
			CCCACAGCGA				3240
			ACATGGAAGA				3300
10			GCCTGGGCTT				3360
10			GCCTGGTTGA				3420
			ATCAGAGAGA				3480
			TTCATAGCTC				3540
			TGAAGGGGTG				3600
1.0	GAAGCCACGG	AGGAATCGTG	CTGCAGAGAG	GAATCCTGCT	CTTGCTGGGT	CGGCCATTCG	3660
15			GCTTCATTCA				3720
			TGGAGCAGAG				3780
			AGAGAAGTCA				3840
	CTGTGGAGAA	TCTTTCGTCA	ACCCAGCAGA	ACTTGCAGAT	CACGTAACTG	TTCATAAGAA	3900
20	TGAGCCCTAT	GAGTACGGGT	CCTCCTATAC	TCACACCTCA	TTTCTTACTG	AGCCCCTCAA	3960
20	AGGAGCTATA	CCATTCTATG	AATGCAAGGA	TTGTGGTAAG	TCCTTTATTC	ATAGCACAGT	4020
	CCTCACTAAA	CATAAGGAGC	TTCATCTGGA	AGAAGAAGAA	GAAGATGAAG	CAGCAGCAGC	4080
			AAGTTGAAGC				4140
			AGGCTGCTGA				4200
			TGGAGGCTGC				4260
25			TTGGAGAGGC				4320
			CAGATGGTGC				4380
			AAGAGCCAGA				4440
			GTGAAGATCA				4500
			CCTTCACTTC				4560
30			TTGAGCCTGC				4620
			CAGGTGGTGC				4680
			TCAATGACCG				4740
			TAAAGGTTAG				4800
			CAATCCATGA				4860
35			TCTCTAAACT				4920
55			CTTCAGATGT				4980
							5040
			ATCAGATTGA				
			AATGACACTT				5100
40			TGACAGAACA				5160
40			CAGAGGTACC				5220
			ACAAATTTGA				5280
			TGAACCCTGT				5340
			GAAGCTGTAG				5400
45			CTTTAGCTTC				5460
43			AAGGCTTTAC				5520
			ATGTTTGTTG				5580
			TTTTTTTAAC				5640
			CCCTGTAAAT				5700
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50			GGCTAATAAC				5820
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	CAAGTCAGTT	TGCACCCTAG	GTGCCCAGGA	GCTAGTATCC	TTAGATCTTT	CTATCGCTAA	5940
	CTTAATTCTC	TTCGTTATTT	ATCTGACCCT	CTAACTCCAT	GTCTAACTTG	CATT	
~ ~							
55	Seq ID NO:	123 Protein	n sequence				
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- 4	VQTLGGWVQP	ETRTKEEIIE	LLVLEOYLTI		AKKPENCEKL	VTLLENYKEM	60
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			MOREDDROSR				180
			HSHMTQGHSS				240
			SKSGRARESS				300
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			ECKDOGETFN				480
			RVCKETFLHS				540
			MYECKVCGET				600
			DFTDGRDAFM				660
70			DEKAFTISSN				720
. •							780
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75							960
, 5			LNTNQKIYDQ				1020
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			PKCGESFIHS				1140
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						OBIONEEDAA	
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65							

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5	1	1	}	1	1	1	
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			AGTAGGTGAC				120 180
• •			GOGGCCAAGA				240
10 · ·	CCTGGGCAGG	ACACTCCAGG	GCACAGGAGG	ACAAGGTGCT	GGGGGGTCAT	GAGTGCCAAC	300
			GCGGCCTTGT				360
			GTCCTTACAG				420
			CTACAGAATA TGCTACAACA				480 540
15			GACCAGGCAT				600
			CCTGGCCAGA				660
			CCTGACACTC				720
			TACCCGGGGC				780
20			TGCCAGGGGG TGGGGCTCAG				840
20			TACCTGGACT				900 960
			ATCTCCCTTA			7002100001	200
25		125 Protein		•			
43	Protein Acc	ession #: 1 11	NP_009127 21	ŝi.	4.5	F1	
	i	ī	1	1	41	51 I	
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20			VRLGDHSLQN				120
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			TCTAATTCCA				180
			TATGAATTAC				240
			ATCCTTACTG				300
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			GGAGGAGAGC				420 480
			GTTGTCTTCC				540
			AGGGACCTCA				600
50			TTTGGTCTCT				660
50			AGTCTGGCTT GATGTTTGGA				720
			GATGATAATG				780 840
			TGGCTCTCTC				900
<i>E E</i>			CGGATTTCTA				960
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			GCCTTATGCA				1440
			TCTGCTGTAA AACCAGCATA				1500
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••	TAAATTCAAC	AGGAACAGAC	AAGTTAATGA	CAGGTGTCAT	TAGCCCTGAG	AGGCGGTGCC	1680
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			GAAAGGGGGT				1800
70			AGAGACGGGC				1860
, ,			CCAGATCAAC CAAAAGGGTT				1920 1980
	TTGGGAAAGT	GACAATGCAA	TTTGAATTAG	AAGTGTGCCA	GCTTCAAAAA	CCCGATGTGG	2040
	TGGGTATCAG	GAGGCAGCGG	CTTAAGGGCG	ATGCCTGGGT	TTACAAAAGA	TTAGTGGAAG	2100
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00			TCTCTTTGTA				2460
80	TTGTGAATAT						
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		127 Protein	n sequence NP_055606.1				
0.5	1	11	21	31	41	51	
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					21	0	

	MKDYDELLKY	YELHETIGIG	GFAKVKLACH	ILTGEMVAIK	IMDKNTLGSD	LPRIKTEIEA	60
	LKNLRHQHIC	OLYHVLETAN	KIFMVLEYCP	GGELPDYIIS	ODRLSEEETR	VVFROIVSAV	120
	AYVHSQGYAH						180
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	MEDLISLWQY	DHLTATYI.I.I.	I.AKKARGKPV	RURUSSPSCG	OASATPETDI	KSNNWSLEDV	360
				SOFTKYWTES			420
				NOHKREILTT			480
	KIPVNSTGTD	KLMTGVISPE	RRCRSVELDL	NOAHMEETPK	RKGAKVFGSL	ERGLDKVITV	540
10				PDOLLNEIMS			600
							•••
	QSDFGKV INQ	PERFACATOR	PDVVGIRRQR	LKGDAWVYKR	PARTITIOSCY	•	
	Seq ID NO:	128 DNA sec	ruence				
	Nucleic Aci	d Accession	#: EOS sec	nience			
15		ence: 169-1	••	1			
13						r.	
	1	11	21	31	41	51	
		1					
	GGGATCCTTT	CTGGAATGGA	GGTCTTATGA	GCTGCTATTG	AACACGGCAG	AGCCTGTTGG	60
	TGACCTGCAC	ACAGGAGCCC	TOCAGTOAGT	ACTGATTGAA	ጉጉል ር ጥር ል ልርያር፤	עויטרעייטיוישיי	120
20							
20	GCAAAGTTGA						180
	GCCTCTCCGC	AGCCACTCGC	CACTGAGGAT	GCCGATTCTG	AGAATAGCAG	CTTCTATTAC	240
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				ATTAGCTGCA			600
							660
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20				GTCTCCATCC			720
30	ACACATGAAA	ATCCCAAGGG	TGTGTGGAAC	TGCCACGCAG	ATTTCGGCGG	GCATGGGACC	780
				AACCTCCTAG			840
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~ -	CCATACAATC	TCACCTTGTT	TCTGCATACG	CTGTTGGACC	TGCAAGTATT	CGGGAACTGT	1020
35				CAGGTAACAG			1080
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				CTGGCACCTG			1200
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••							
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50				GGACAACAAT			1920
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	GATCCTGATA	CTCTCGGCCT	TTACTTCCGC	CTCCCTCAGA	GCAGCAGCCT	GTCAAAACAC	2340
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						CTGCTTGGCT	3360
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						TGGGACCTGC	3960
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					21		

5	CTATGCCTTT CCTCACCCTT TGCCCTCTGC ACATTTCCCT GAAGTGCAAT TGAGATCTGG GTGAGTGAGC AGTCCCAATC	GTTTTACAAC TTTGAGAGGA GGTCACGGTG ATCACTAGAA AGCTACTCCT AGATCCCGAG	TGAATCCCAC GGTTGGGTGG ATTTTTTTAG CATGTGAGAA TCCTCCACCC GGCACTGTTT	TTTCTCTGGG AGCATGGGAC GGGTGGGCAC GAGAGGCATG AAACTTCAGA GAGCCTCAGA	ACTCCACTGC ATGGGCCATT ATGACCTAGG AAACCGAAGC AGGTGAAGGA ATCAAAGCAC	TTGGTCACTC TACTGCCTTC TAGAGCCAAT TGAGAGGGTT GATAGTGCAT TTCTGAAGCT	4140 4200 4260 4320 4380 4440 4500
10	Seq ID NO: Protein Acc	ession #: N 11 	P_001287.2 21	31 	41	51 }	
15	MAATASPQPL LSGNLLLLMV STLYTINFYS VPVQTHENPK RPAGQGRALK APLHCCFSPI	LLRYVPRRRM GIFPISCMSL GVWNCHADFG IAAALVVAFF	VEIYLLNLAI DKYLEIVHAQ GHGTIWKLFL VLWPPYNLTL	SNLLFLVTLP PYHRLRTRAK RFQQNLLGFL PLHTLLDLQV	PWGISVAWHW SLLLATIVWA LPLLAMIFFY FGNCEVSQHL	VFGSFLCKMV VSLAVSIPDM SRIGCVLVRL DYALQVTESI	60 120 180 240 300 360
20	GMNDLGERQS Seq ID NO: Nucleic Aci	ENYPHKEDVG	NKSA Tuence		QROBOGEODO	21B1M2DN1	300
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	ACATCCACCT						780
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50	AAGATGAAGA	TAAGGATGAT	ACAGTCTCCA	TCAGGCAGTG	GCTGTTGGAA	AGATTTAAGA	1440
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	.41111						
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55		ession #: 1	_		•		
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					ASHDQDIMLL		120
60					HLVSREECRH		180
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	IQAK						
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65		id Accession		71.1			
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70					CCGAGTGCAA		60
, 0						CCCGTGCAAA	120 180
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						TCAGGGTGCG	300
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80						GGACGAGGAA	720 780
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85						CTACCAGCTG	
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15		133 Proteir					
13	1	ession #: F 11	21	31	41	51	
20	EKAVQGSPKS PRGEAPPPPP PFVPPPPALD EELLEDDEEE	SERPECKSKS SSAPFEAELH PTARPGERPD ELGGPGGVTH LLEDDARALL VCLSAGSDSB	LPPKLRRLYG GAGAAAAAA PEERLGVAGG KEPRRCPVAA	PGGGRLLQGA AAAAWDTLK PGSAPAAGGG TGAVAAAAAA	AAAAAAAAA ISQAPQVSIS TGTEDDEEEL AVATEGGELS	AAAAATATAG RSKSYRENGA LEDEEDEDEE PKEELLLHPE	60 120 180 240 300 360
25	LAMRLDLTEA PHHPALDSAW FGRLFSTMAP	RVQVWFQNRR TAAAAAAAA LTSASTAAAL ILPGTSTGKB	AKWRKREKAG FPSLPPPPGS LRQPTPAVEG	AQTHPPGLPF ASLPPSGAPL	PGPLSATHPL GLSTFLGAAV	SPYLDASPPP FRHPAPISPA	420 480 540
30		134 DNA sec					
30	Nucleic Act	ld Accession 11	#: CAT CI	ister 31	41	51	
	TTTTTTTTTT	TTTTTTTAAA	 GCAGATCATC	TCTCCAAATC	 ATCACTTCTA	 TCAAGCCTAT	60
35		GTGTTATAGC ACACATATTC					120 180
33	ACAGAACTGA	TTCCTGCAGA	ATATCCTGAG	ATACTTATCA	AGCTGTTAAA	GGAGACATCA	240
		TGTATTGCCC					300 360
40	TAGAATAGAA	AAGCACCTTG	AAAACTGTAG	TCTGACTTAA	TAGACACAAA	TATAATGAAA	420
70		ATAAGATCCT TGCACAGGAA			GCAAAAGGCA	CAAGCITCAG	480
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45	Nucleic Act Coding sequent 1	id Accession mence: 199 11	1 #: NM_0067 963 21	31 		1	60
	Nucleic Act Coding sequ 1 GCCGCGGGAG CGGGCTGGAC	id Accession lence: 199 11 AGGAGGCCAT TCAGGAAGCC	#: NM_0067 963 21 GGGCGCGCGC GGAGTCGCAG	31 GGGGCGCTGC GAGGCGGCGC	 TGCTGGCGCT CGTTATCAGG	 GCTGCTGGCT ACCATGCGGC	60 120
45 50	Nucleic Aci Coding sequ 1 GCCGCGGGAG CGGCTGGAC CGACGGTCA	id Accession lence: 199 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG	#: NM_0067 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT	31 GGGGGGCTGC GAGGGGGCGC GGAGAGGACG	TGCTGGCGCT CGTTATCAGG CCGAACTCGG	 GCTGCTGGCT ACCATGCGGC GCGTTGGCCG	120 180
	Nucleic Aci Coding sequ 1 GCCGCGGGAG CGGGCTGGAC CGACGGGTCA TGGCAGGGGA CGCTGGCAC	id Accession pence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGGC	1 #: NM_006* 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT	31 GGGGCGCTGC GAGGCGGCGC GGAGAGGACG CACGTATGCG GAAACCTATA	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC	120 180 240 300
50	Nucleic Aci Coding sequ 1 GCCGCGGGAG CGGGCTGAC CGACGGGTCA TGGCAGGGGA CGCTGGGCAC GGGTGGATGG	id Accession ence: 199 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGCT TCACGGCGGC TCACGGCGGC	H: NM_006* 63 21	31 GGGGCGCTGC GAGGCGGCGC GGAGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC	120 180 240 300 360
	Nucleic Act Coding sequ 1 GCCGCGGGAG CGGCTGGAC CGACGGGTCA TGGCAGGGGA CGCTGGGCAC GGGTGGATCA TACTACACCC CCCTATGACA	id Accession lence: 19 11 AGGAGGCCAT TCAGGAGGC TCACGTCGG GCCTGCGCCT TCACGCGGCT TCACGCTGCG TCCAGTTTGGT TTGCCTTGGT	H: NM_006* 63 21 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	31 GGGGGCTGC GAGGCGGCGC GGAGAGGACG CACGTATGCG GAAACCTATT TCCATGCCAT TATCTGAGCC GCACCTGTCA	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG	120 180 240 300 360 420 480
50	Nucleic Aci Coding sequ I GCCGCGGGAG CGGGCTGAAC CGACGGGTCA TGGCAGGGGA CGCTGGCAC GGGTGATGG TACTACACCC CCCTATGACA CCCATCTGTC	id Accession lence: 199 11	H: NM_006* 63 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG CACATTTGAG	31 GGGGCGCTGC GAGGCGGCGC GAGGAGGACC CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCA TTTGAGAACC	I TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCTCAG CCTTCTGGAG CTTCTGGAG CTCGCTACCT CCTACACTAA GGACAGACTG	CTGCTGGCT GCTGCTGGCT ACCATGGCGG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT	120 180 240 300 360 420
50	Nucleic Aci Coding sequ 1 GCCGCGGGAG GCGCTGGAC CGACGGGTCA TGGCAGGGGA CGCTGGGCAC GGGTGGATGG TACTACACCC CCCATCTGTC CGCTGGGGGT CAGGTGGCCAC CCCATCTGTC CAGGTGGCCCA	id Accession lence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGGC TCACGTTTGG GTTACTTCGT TTGCCTTGGT TCCAGGCCTC ACATCAAACAA TCATAAACAA	#: NM_006* 63 21 GGGGGGGGG GGAGTCGCAG CATCGTGGGT GTGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATGAGGA CTCTATGTGG CTCTATGTGG CTCTATGTGG	31 GGGGGGCTGC GAGGGGGGCG GAGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TTTGAGAACC CTGCCATCTC AACCACCTCT	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA GGACAGACTG TCCTCAAGTA	CTGCTGCTGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CCAGGAAGTT CCAGTTTCCGC	120 180 240 300 360 420 480 540 600
50	Nucleic Aci Coding sequ	id Accession lence: 19 11 AGGAGGCCAT TCACGTCGCG GCCTGCGCT TCACGTCGCG TCACGTTTGG TCCACGTTTGG TTACTTCGT TTCCCTTGGT TCCACGCCTC ACATCAAAGA	#: NM_006* 163 21	31 GGGGCGCTGC GAGGCGGCGC GAGAGGACG CACGTATGCG GAAACCTATA TCCATGCAT TATCTGAGCC TATCTGAGAACC CTGCCATCTC CTGCCATCTC GACCACCTCT GGCAATGCCC	TGCTGGCGCT CGTTATCAGG CCGAACTGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA GGACAGACTG CCCACACCCT TCCTCAAGTA AAGGCGGAA	CAGGAGACTTCCCCCGGAGACCCCCGGAGACCCCCGGAGACCCCCCAGAGACCCCCC	120 180 240 300 360 420 480 540
50 55	Nucleic Aci Coding sequi	id Accession lence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGCCTGC TCACGCTTTGG TTCACTTCGT TTGCCTTGGT TCCAGGCCTC ACATCAAAGA TCAGAGACAT TTGGAGACAT TCAGGACAC GGGGAGTGGG GGGGAGTGGG	#: NM_006* 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGATTCC GCACTGCTTT ATCGAATATC GAAGCTGTT ATCGAATATC GAAGCTGTT CACATTTGAG GGATGAGGCA CTCTATGTGC GGTTTGTGCT CTTGGCCTGT CTTGGCCTGT CTGTGGTCGG	31 GGGGCGCTGC GAGGCGGCGC GAAGAGGACG CACTATAGCG GAAACCTATA TCCATGCCAT TATCTGAGCAC TTTGAGAACC CTGCCATCTC AACCACCTCT GGCAATGCC AACAAGAATG CCCAATCGGC	TGCTGGCGCT TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCTTAG CCTTCGGAG CTCGCTACCT CCTACACTAA CCCACACCCT TCCTCAAGTA AAGGCGGGAA AAGCGGGGAA CCGGTGTCTA CCGGTGTCTA	CAGCATATCS CACCATATION CACCATAGORA CONTROL C	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	Nucleic Aci Coding sequi GCCGCGGGAG GCGCTGGAC CGACGGGCAC TGGCAGGGGA CGCTGGGCAC GCGTGGAC CCCTATGACA CCCATCTGTC GGCTGGGCAC AAGGACATCT TTCGGTGACT GTCGTGACC CCCTCCTGGCC CCCTCCTGGCC	id Accession lence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGGC GCCTGCGCCT TCACGCTCTGGT TCACGCTCGT TCACGTCTGGT TCCAGGTCGGC TCCAGTTTGGT TTGCCTTGGT TCCAGGCCTC ACATCAAAGA TTGGAGACAT CAGGTGGAC CGGGAGTGGAC TTGAGTGGAT CCCTACTCT	#: NM_006* 163 21	31 GGGGCGCTGC GAGGCGGCGC GAGAGGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCC TTTGAGAACC CTGCCATCTC GACACCTCT GCCAATCGC AACCACTCT GCCAATCGC AACAAGAATG CCCAATCGC ATCGGCCAATCGC ATCGGCCAATCGC ATCGGCCAATCGC ATCGGCCAGA	TGCTGGCGCT TGCTGGCGC GGTATATCAGG CCGAACTTGG CCTTCTGGAG CTCGCTACCT CCTACACTAA GGACAGACTG CCCACACCCT TCCTCAAGTA AAGGCGGAA GACTGTGCTA CCGGTGTCTA CCGGTGTCTA TCCCACTCCT TCCCACTCCT TCCCACTCCT TCCCACTCCT TCCCACTCCT TCCCACTCCT	CTGCTGCTGCT ACCATGCGC GCTTGGCCAC GCTCAGCCAC TGATCCCTC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CCAGGAAGTT CCAGGAAGTT CCAGTTCCCC GGATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCAGAC GGGGCCGGTC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	Nucleic Aci Coding sequi I GCCGCGGGAG GCGCTGGAC CGACGGTCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGGT CAGGTGGCCA AAGGACATCT TTCGGTGACT GTCGTGACT AGCCACCACT TGACCACCACT TGAGCCTACCC	id Accession lence: 19 11 AGGAGGCCAT TCACGAGAGCC TCACGTCGCG GCCTGCGCT TCACGTCTGGT TCACGTCTGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCAGGTCGGT TCAGGTCGT TCAGGCCTC ACATCAAAGA TCAGAGACAT TCAGGTGGACC GGGGAGTGGG TTGAGTGGAT TCGCTACTTT TGAGCCCATG	#: NM_006* 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTTGGT CCAGCTGATT CCAGCTGATT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATGAGGCA CTCTATTGAG GGTTTGTGCT CTTGGCTGT CTTGGCTGT CTGTGGTCGG CCAGAAGCTG CTTCCCTCT CAGCCTGGGG	31 GGGGCGCTGC GAGGGGGCGC GAGGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCAC CTGCCATCTC AACCACCTCT AACCACCTCT AACACACCTC AACAAGAATG GGCAATGCCC AACAAGAATG CCCAATCGGC ATGGCCCAGA CTCTGGGCTCA	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT CCTTCGGAG CTCGCTACCT CCTAACTAA AGGCGGGAA AAGGCGGGGAA AAGGCGGGGAA CCGGTGCTTCA CTGCACTCT CTGCACTCT CCTCACCT CCTCAAGCC CCGCGCGCC CCGCCACCCC CCTCAAGCC CCGCCC CCCCCC CCCCC	CAGGCAGATC CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Nucleic Aci Coding sequ	id Accession lence: 19 11 1 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGTCGT TCACGGCTC ACATCAAACA TCATAAACAA TCGAGACAT CAGGTGGAC TCGGGAGTGGG TTGAGTCGAT TCGACCCATG GGTAATAAAC	#: NM_006* 63 21 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGTGGGGTTCCGGTGGGTTCCCGGGTGGT	31 GGGGCGCTGC GAGGGGGCGC GAGGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCAC CTGCCATCTC AACCACCTCT AACCACCTCT AACACACCTC AACAAGAATG GGCAATGCCC AACAAGAATG CCCAATCGGC ATGGCCCAGA CTCTGGGCTCA	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT CCTTCGGAG CTCGCTACCT CCTAACTAA AGGCGGGAA AAGGCGGGGAA AAGGCGGGGAA CCGGTGCTTCA CTGCACTCT CTGCACTCT CCTCACCT CCTCAAGCC CCGCGCGCC CCGCCACCCC CCTCAAGCC CCGCCC CCCCCC CCCCC	CAGGCAGATC CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Nucleic Aci Coding sequi I GCCGCGGGAG GCGCGGGAG CGGCTGGAC CGACGGGTCA TGGCAGGGGA TACTACACCC CCCTATGACA ACCACTCGTC GGCTGGGGA AAGGACATCT TTCGGTGACT AGCCACCACT TGCTCTGGC TGAGCCTACC TGAGCCTACC TGAGCCTACC TGAGCCTACC TGTCTTGTTT Seq ID NO:	id Accession lence: 19 11 AGGAGGCCAT TCACGAGAGCC TCACGTCGCG GCCTGCGCT TCACGTCTGGT TCACGTCTGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCACGTCGGT TCAGGTCGGT TCAGGTCGT TCAGGCCTC ACATCAAAGA TCAGAGACAT TCAGGTGGACC GGGGAGTGGG TTGAGTGGAT TCGCTACTTT TGAGCCCATG	#: NM_006* 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTTGGT TCAGATATC AAGCTGTCT ATCGAATATC GAAGCTGTCT ATCGAATATC GAAGCTGCT ATCGAATATC GATTGAGC GGTTTGTGC CTTGTGCT CTTGGCTTGT CTTGGCTTGT TTTCCCTT CAGCTTGAGCAAAGCT TTTCCCTT CAGCCTGGGAAAGTT CAGCCTCGGGAAAGTT CAGCCTCGGGAAAGTT CAGCCTGGGGAAAGTT CAGCCTGGGGGAAAGTT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGCAGAACATTCCAGT CAGCCTGAACATTCCAGT CAGCCTGCAGAACATTCCAGT CAGCCTGAACATTCCAGAACATTCCAGAACATTCCAGT CAGCCTGAACATTCCAGAACATTCCAGAACATTCCAGAACATTCCAGAACATTCCAGAACATTCAGA	31 GGGGCGCTGC GAGGGGGCGC GAGGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCAC CTGCCATCTC AACCACCTCT AACCACCTCT AACACACCTC AACAAGAATG GGCAATGCCC AACAAGAATG CCCAATCGGC ATGGCCCAGA CTCTGGGCTCA	TGCTGGCGCT TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT CCTTCTGGAG CTCGCTACCT CCTACACTAA AGGCAGACTG GACCGCAACCCT TCCTCAAGTA AAGGCGGGAA ACGCGGGGAA CCGGTGTCTA CTCCACTCCT CCCACACTCCT CCCACACTCCT CCCACACTCCT CCCACACTCCT CCCACACTCCT CCCACACTCCT CAGGGCATTC CAGGGCATTC	CTGCTGCTGCT GCTGCTGGCG GCTTCAGCCA GCTCAGCCA GCTCAGCCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC GGATGCTGC GCATGCCTGC GCATGCTGC CTCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGTC GGTTCTCTTC TTCAAAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50556065	Nucleic Aci Coding sequi I GCCGCGGGAG GCGCGGGAG CGGCTGGAC CGACGGGTCA TGGCAGGGGA TACTACACCC CCCTATGACA ACCACTCGTC GGCTGGGGA AAGGACATCT TTCGGTGACT AGCCACCACT TGCTCTGGC TGAGCCTACC TGAGCCTACC TGAGCCTACC TGAGCCTACC TGTCTTGTTT Seq ID NO:	id Accession lence: 19 11 1 AGGAGGCCAT TCACGAAGCC TCACGTCGCG GCCTGCGCT TCACGTCTGGT TCACGTCTGGT TCACGCTGCT TCACGCTGCGCT TCACGCTGCGCT TCACGTCTGGT TTGCCTTGGT TCCAGGCCTC ACATCAAAGA TCAGAGACAT CAGGTGGACC GGGAGTGGG TTGAGTGGAT TCGAGTCGAT TCGAGTCGAT TCGAGTCGAT TCGAGTCGAT TGAGTCGAT TGAGTCCAT TGAGCCCATG GGTAATAAAC 136 Protein	#: NM_006* 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTTGGT TCAGATATC AAGCTGTCT ATCGAATATC GAAGCTGTCT ATCGAATATC GAAGCTGCT ATCGAATATC GATTGAGC GGTTTGTGC CTTGTGCT CTTGGCTTGT CTTGGCTTGT TTTCCCTT CAGCTTGAGCAAAGCT TTTCCCTT CAGCCTGGGAAAGTT CAGCCTCGGGAAAGTT CAGCCTCGGGAAAGTT CAGCCTGGGGAAAGTT CAGCCTGGGGGAAAGTT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGAACATTCCAGT CAGCCTGGGGGAACATTCCAGT CAGCCTGGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGGAACATTCCAGT CAGCCTGCAGAACATTCCAGT CAGCCTGAACATTCCAGT CAGCCTGCAGAACATTCCAGT CAGCCTGAACATTCCAGAACATTCCAGAACATTCCAGT CAGCCTGAACATTCCAGAACATTCCAGAACATTCCAGAACATTCCAGAACATTCCAGAACATTCAGA	31 GGGGCGCTGC GAGGGGGCGC GAGGAGGACG CACGTATGCG GAAACCTATA TCCATGCCAT TATCTGAGCAC CTGCCATCTC AACCACCTCT AACCACCTCT AACACACCTC AACAAGAATG GGCAATGCCC AACAAGAATG CCCAATCGGC ATGGCCCAGA CTCTGGGCTCA	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT CCTTCGGAG CTCGCTACCT CCTAACTAA AGGCGGGAA AAGGCGGGGAA AAGGCGGGGAA CCGGTGCTTCA CTGCACTCT CTGCACTCT CCTCACCT CCTCAAGCC CCGCGCGCC CCGCCACCCC CCTCAAGCC CCGCCC CCCCCC CCCCC	CAGGCAGATC CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Nucleic Aci Coding sequi GCCGCGGGAG GCGCGGGAG CGACGGGTCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA ACGTCGGCA AAGGACATCT TTCGTGACT GTCGTGACT GTCGTGACT TTCGTGACT CCCTCCTGGC TGAGCCTACC TGTCTTGTT Seq ID NO: Protein Aci	id Accession lence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGGCGG GCCTGCGCGT TCACGGCGGC TCACGCTGGT TCACGGCGGC TCACGCTGGT TCACGCGGCT TCACGGCGGC TCACGCTGGT TCAGGCACT TCACGCGGCT TCACGCCTC TCACGCCTC TCACGCCTC GGGAGTGGA TCAGAGACAT TCGAGTGGACC GGGGAGTGGG TTGAGTCGTT TCACTCATT TCACCCATG GGTAATAAAC 136 Protein cession #: 1 11 LLLARAGLRK	#: NM_006* 163 21 GGGCGCGC GGAGTCGCAG CATCGTTGGT GTGGATTCC CACATGTTCA ATCGAATATC GAAGCTGTT CACATTTGAG GGATGAGGCA CTCTATGAG GGATTAGTGC GGTTTGTGCT CTTGGCTGT CTGGCTGT CTGGCTGT CTGCCTGT CAGCTGGGG ACATTCCAGT A sequence NP_006790 21 PESQEAAPLS	31 GGGGCGCTGC GAGGGGGCGC GAGGAGGACC GAAACCTATA TCCATGCCAT TTTGAGAACC CTGCCATCTC AACCACCTCT AACCACCTCT GGCAATGCCC AACAAGAATG CCCAATCGGC ATGGCCCAGA ATGGCCCAGA TGGCCCAGA TGATGCCTTG CCACTGCCCAA TGATGCCTTG 31 GPCGRRVITS	TGCTGGCGCT TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCTTAG CTGCTACCT CCTACTAA AGGACTGG AAGGACTG GACAGACTG CCCACACCCT TCCTCAAGTA AAGGCGGGAA ACGGGGAA CGGGTGTCTA CTGCACTCCT CTCAGGCATTCC CTCAGGCATTCC CAGGCATTCC CAGGCATTCC CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCCCT CTCAGGCATTC 41 I RIVGGEDAEL	CAGGAGATTCCAGGAGATTCCAGGAGAGTTCCAGGAGAGTTCCAGGAAGTTCCAGGAAGTTCAGGAAGTTCAGGAAGTTCAGGAAGTTCAGCAGAAGTTCAGCAGCAGAAGTTCAGCAGCAGAAGTTCAGCAGCAGAAGTTCAGCAGAAGTTCAGCAGAAGTTCAGCAGAAGTTCAGACAATATCCAGCAGACAGA	120 180 240 300 360 420 540 660 660 720 780 840 900 1020
50556065	Nucleic Aci Coding sequi GCCGCGGGAG GCGCTGGAC CGACGGGTCA TGGCAGGGGAC TGGCAGGGGAC TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGT TACGCGCAC TGCTGAGCA AGGACATCT TTCGGTGACT GTCCTGAGCA AGCACACT TTCGTTGACT AGCCACCACT TTCGTTGACT AGCCACCACT TGTCTTGTTC Seq ID NO: Protein Acc	id Accession lence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGTCGGT TCACGTTGGT TCCAGGCTGT TCCAGGCGT TCACGTTGGT TCCAGGCGT TCACGTCGGT TCCAGGCCT TCACGTCGGT TCACGTCGT TCCAGGCCT TCACGTCGT TCCAGGCCT TCACGTCGT TCACGCCGT TCACGTCGAC CGGGAGTGGG TTGAGTGGAC CGCTACTCTT TGAGCCCATG GGTAATAAAC 136 Protein cession #: 1 LLLARAGLRK LLSHRWALTA	#: NM_006* 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATTGAGCAT CTTATGAG GGTTTTGTGCT CTTGGCCTGT CTTGGCTTGT CTGGCTGT CTGGCTGT CTGTCGGG ACATTCCAGT ASEQUENCE NP_006790 21 PESQEAAPLS AHCPETYSDL	31 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TGCTGGCGCT TGCTGGCGCT TGCTATCAGG GAGGAGCCTTAG GTGACCTTAG CTCGCTACCT CCTACACTAA GAGCAGACTG CCCACACCCT TCCTCAAGTA AAGGCGGAA GACTGTGTCT GTGGCATGCT TCCCACACCCT TCCCACACCCT TCCCACACCCT TCCCACACCCT TCCCACTCCT TCCCACTCCT TCCCACTCCT TCCCACTCCT CAGGGCATTC 41 RIVGGEDAEL GQLTSMPSFW	GCTGCTGGCT GCTGCTGGCG GCTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGCCCGTC TTCAAAA 51 GRWPWQGSLR SLQAYYTKYF	120 180 240 300 360 420 540 660 720 780 960 1020
5055606570	Nucleic Aci Coding sequi GCGCGGGGAG GCGCGGGGAG CGGCCTGGGCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA ACCACTGGTC GGCTGGGGT CAGGTGGCCA AAGGACATCT TTCGGTGACT TTCGTGACT GCCACCACT GTCTTGTT Seq ID NO: Protein Acc MGARGALLLA LWDSHVCGVS VSNIYLSPRY EDEALPSPHT	id Accession lence: 19 11 11 AGGAGGCCAT TCACGGAGGC GCCTGCGC GCCTGCGCT TCACGGCGGC TCACGTTTGG TTGCCTTGGT TCACGGCGGC ACATCAAAGA TCAGAGACAT TCAGGAGCT ACATCAAAGA TCAGAGCAT TCAGGTGGAC TGAGTGGAT TGAGTGAT TGAGTGAT TGAGTGAT TGAGTCAT TGAGTCAT TGAGTCAT LGETAATAAAC 136 Protein cession #: 1 LLLARAGLRK LLSHRWALTA LGENGVALIN LGEVQVALIN	#: NM_006* 163 21 GGGCGCGC GGAGTCGCAG CATCGTTGG TCAGATATTC GAAGCTGTTT CAGATATTGAG GGATGAGGCA CTCTATTGAG CGTTTTTGCT CTTGGCTGT CTTGGCTGT CTGGCTGT CTGGCTGG	31	TGCTGGCGCT TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT CGTGCTACCT CCTACACTAA GGGCAGACTGG GGACAGCT CCTCAAGTA AAGGCGGGAA AAGGCGGGAA ACTGGTTCT CTCACTCT CTCACTCT CTCACTCT CTCAGCCT CTCAGCCT CTCAGCATCT CTCCACTCC TCCCACTCC TCCACTCC TCCCACTCC TCCCACTC TCCCACTCC TCCCCC TCCCCCC	CAGGAAGTTCCAGGAAGTTCCAGGAAGTTCCAGGAAGTTCCAGGAAGTTCCAGGAAGTTCAGGAAGTTCAGAGAAGTTCAGAGAAGTTCAGAGAAGTTCAGCAGAATATCCAGCAGAATATCCAGCAGAAGTTCAAAAA	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020
50556065	Nucleic Aci Coding sequi GCGCGGGGAG GCGCGGGGAG CGGCCTGGGCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA ACCACTGGTC GGCTGGGGT CAGGTGGCCA AAGGACATCT TTCGGTGACT TTCGTGACT GCCACCACT GTCTTGTT Seq ID NO: Protein Acc MGARGALLLA LWDSHVCGVS VSNIYLSPRY EDEALPSPHT	id Accession lence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGCTGGC TCACGTTTGG TTGCTTGGT TTGCTTGGT TTGCTTGGT TTGCTTGGT TCAGGCGCC ACATCAAAGA TCAGAAGCA TCAGAGCCT CAGGCCTC CAGGCCTC ACATCAAAGA TCAGAGCAT TCAGTGGAC TCAGTGGAC TCAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC TGAGTGGAC LAGAGAGAC LAGAGAGAC LAGAGACCCATG GCTACTCT LLLARAGLRK LLSHWALTA LCHSPYDIAL LCHSVVSMGV YQIGVVSMGV	#: NM_006* 163 21 GGGCGCGC GGAGTCGCAG CATCGTTGG TCAGATATTC GAAGCTGTTT CAGATATTGAG GGATGAGGCA CTCTATTGAG CGTTTTTGCT CTTGGCTGT CTTGGCTGT CTGGCTGT CTGGCTGG	31	TGCTGGCGCT TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT CGTGCTACCT CCTACACTAA GGGCAGACTGG GGACAGCT CCTCAAGTA AAGGCGGGAA AAGGCGGGAA ACTGGTTCT CTCACTCT CTCACTCT CTCACTCT CTCAGCCT CTCAGCCT CTCAGCATCT CTCCACTCC TCCCACTCC TCCACTCC TCCCACTCC TCCCACTC TCCCACTCC TCCCCC TCCCCCC	CTGCTGGCTGGCT GCTTGGCGG GCTCAGCCAC GGTTGGCCG GCTCAGCCAC CTGATCCCTCC CCGGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTGCA CACCAATATC CCAGCCAGAC GGGCCGGTC GGTTCTCTTC TTCAAAA 51 GRWFWQGSLR SLQAYYTRYF CWVTGWGYIK	120 180 240 300 360 420 540 660 720 780 840 900 960 1020
5055606570	Nucleic Aci Coding sequi GCCGCGGGAG GCGCCGCGGAG CCGACGGCAC CCGACGGCAC CCCTATGACA CCCATCTGTC GGCTGGGGT CAGGTCGCAC CCCTATGACA AGGACATCT TTCGTGTGCT AGCCACACT TTCGTGACT AGCCACACT CCTTCTTGGC TGTCTTGACA Seq ID NO: Protein Aci LWDSHVCGVS VSNIYLSPRY EDEALPSPHT FLACNKNGLW FFPLLWALPL Seq ID NO: Nucleic Ac	id Accession lence: 19 lence: 19 lence: 19 li	#: NM_006* 163 21 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	31	TGCTGGCGCT TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GGTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTAACTAA AGGCGGGAA AAGGCGGGAA AAGGCGGGAA GACTGTGTA TCCCACTCT GTCAGTACT GTCAGTACT CCCACCCT TCCTCAGTA AGGCGGGAA AGGCGGGAA AGGCGGGAA GACTGTGTA TCCCACTCT GTCAGGCCCT CAGGGCATTC 41 RIVGGEDAEL QULTSMPSFW STFFFENRTD MVCAGNAQGG IQKLMAQSGM	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CCAGGAAGTT CCAGCAGAC GCATTCCGC GCATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGTC GGTTCTCTTC TTCAAAA 51 GRWPWQGSLR SLQAYYTRYF CWVTGWGYIK KDACFGDSGG SQFDPSWPLL	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020
505560657075	Nucleic Aci Coding sequi GCCGCGGGAG GCGCCGCGGAG CCGACGGCAC CCGACGGCAC CCCTATGACA CCCATCTGTC GGCTGGGGT CAGGTCGCAC CCCTATGACA AGGACATCT TTCGTGTGCT AGCCACACT TTCGTGACT AGCCACACT CCTTCTTGGC TGTCTTGACA Seq ID NO: Protein Aci LWDSHVCGVS VSNIYLSPRY EDEALPSPHT FLACNKNGLW FFPLLWALPL Seq ID NO: Nucleic Ac	id Accession lence: 19 lence: 19 lence: 19 li	#: NM_006* 163 21 21 33 33 34 35 35 35 36 36 36 36 36 36 36 36 36 36 36 36 36	31	TGCTGGCGCT TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT CGTGCTACCT CCTACACTAA GGGCAGACTGG GGACAGCT CCTCAAGTA AAGGCGGGAA AAGGCGGGAA ACTGGTTCT CTCACTCT CTCACTCT CTCACTCT CTCAGCCT CTCAGCCT CTCAGCATCT CTCCACTCC TCCCACTCC TCCACTCC TCCCACTCC TCCCACTC TCCCACTCC TCCCCC TCCCCCC	CAGGAAGTTCCAGGAAGTTCCAGGAAGTTCCAGGAAGTTCCAGGAAGTTCCAGGAAGTTCAGGAAGTTCAGAGAAGTTCAGAGAAGTTCAGAGAAGTTCAGCAGAATATCCAGCAGAATATCCAGCAGAAGTTCAAAAA	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020
505560657075	Nucleic Aci Coding sequi GCCGCGGGAG GCGCCGCGGAG CGACGGGTCA TGGCAGGGGAC CGACGGGTCA TGGCAGGGGAC CCCTTATGACA CCCATCTGTC GGCTGGGGTC CAGGTCGCAC CCATCTGTC TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGTTGACT AGCCACACT TTCGTTGACT AGCCACACT TTCGTTGACT AGCCACCACT TGTCTTGTTT Seq ID NO: Protein Acc	id Accession lence: 19 lence: 19 lagaaggccar TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGGC TCACGTTGGT TCCAGGCGGC TCACGTTGGT TCCAGGCGGC TCACGTTGGT TCCAGGCGGC TCACGTCGGT TGACTCGT TGACTCAAAGA TCATAAACAA TCAGAGACT CAGTGGAC CGGGAGTGGG TGAGTGGAC GGTAATAAAC 136 Protein CCCATG LLLARAGLRK LLSHRWALTA LCMSPYDIAL LCMSPYDI	#: NM_006* 163 21 21 23 21 33 33 33 34 34 35 35 36 36 36 36 36 36 36 36 36 36 36 36 36	31	TGCTGGCGCT TGCTGGCGCT TGCTATCAGG GAGGACTTAG GAGGACCTTAG CCTCCTCGGAG CTCGCTACCT CCTACACTAA GGCAGACTCG CCCACACCCT TCCTCAAGTA AAGGCGGAA GACTGTGCT TCCCAAGTA AGGCGGCATCC CAGGCATTC CAGGCATTC 41 RIVGGEDAEL GQLTSMPSFW STFEFENRTD MVCACNAQGG IQKLMAQSGM 41 CTCGGGCTGG	GCTGCTGGCT GCTGCTGGCC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTGGA CACCAATATC CCAGCCAGAC GGGGCCGGTC GGTTCTCTC TTCAAAA 51 GRWPWQGSLR SLQAYYTRYF CWVTGWGYIK KDACFGDSGG SQFDPSWPLL	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020

		CCCACGTATG					240
	CTGACTTCCA	TTGAAACTGA TGCCATCCTT	CTTAGTGAT	CAGGCCTACT	GGATGGTCCA ACACCCCTTA	CTTCGTATCG	300 360
_	AATATCTATC	TGAGCCCTCG	CTACCTGGGG	AATTCACCCT	ATGACATTGC	CTTGGTGAAG	420
5		CTGTCACCTA AGAACCGGAC					480
		CATCTCCCCA					540 600
	ATGTGCAACC	ACCTCTTCCT	CAAGTACAGT	TTCCGCAAGG	ACATCTTTGG	AGACATGGTT	660
10	TGTGCTGGCA	ATGCCCAAGG AGAATGGACT	CGGGAAGGAT	GCCTGCTTCG	GTGACTCAGG	TGGACCCTTG	720 780
	GGTCGGCCCA	ATCGGCCCGG	TGTCTACACC	AATATCAGCC	ACCACTTTGA	GTGGATCCAG	840
	AAGCTGATGG	CCCAGAGTGG	CATGTCCCAG	CCAGACCCCT	CCTGGCCACT	ACTCTTTTTC	900
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15		138 Protein					
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20		LLLARAGLRK					60
20		LLSHRWALTA NSPYDIALVK					120 180
	EALPSPHTLQ	EVQVAIINNS	MCNHLFLKYS	FRKDIFGDMV	CAGNAQGGKD	ACFGDSGGPL	240
	ACNKNGLWYQ PLLWALPLLG	IGVVSWGVGC	GRPNRPGVYT	NISHHPEWIQ	KLMAQSGMSQ	PDPSWPLLFF	300
25	FULMAUFULG			•			
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30		TOGGGGGGGGG		1			
		TGGGGCCGAA GACCCGGGTG					60 120
	CCGCGGGAGC	ATGGGCAGGA	GGATGCGGGG	CGCCGCCGCC	ACCGCGGGGC	TCTGGCTGCT	180
35		TCGCTGCTGG					240 300
	GCCCGCGCCT	CGCTTCCCTC	TGCCCCCGCC	CCTGGCGTGG	GACGCCCGCG	GCGGCTCCCT	360
		CGGGCGCTGC					420
		CCCAGGTGGC					480 540
40	GGAGGCCCAG	GCGGCGGCGT	GGCTGGAGGC	GGCTCGCGGC	GCCCGGATGG	TGGCCCTGGA	600
		TGCGGGCGCA TACGGCATCA					660 720
		CTGGGCCTCC					780
45		CAGTGGGCGC					840
40		AGCCTGACAC GAGGACGGCC					900 960
	CCTCAGCCAG	GCGGAGCTGG	TGGACCTAGT	ACAATGGACC	GACTTAATCC	TTTTCGACTA	1020
		AACTTCGACC CGTGCCACCA					1080
50		GCGGGCTTGG					1140 1200
1		TTGCAGTCAG					1260
		GGACAGGACG GAGCTGGCCG					1320 1380
55	CGACTTCCTC	GCCAAGCACA	TTTTGCACTG	TAAGGCCAAG	TACGGCCGCC	GGTCTGGGAC	1440
5 5		CGGGAGGAAA					1500 1560
		AGCTTTTCAC					1620
		GAGGACGAAC					1680
60		TCTTTACTGT					1740 1800
	TCCCTTTCCG	AAAAAGGAAA	ACTTGCGTTT	GAGCCGTTGA	GCTAATTCTG	CAATTTTCTA	1860
		CCTTTGTTCC					1920 1980
						GCAGACCTTG	2040
65	ACAATTTGCC	TGACTCATTC	CTGACCTCTT	GTCATTTTGG	CCTGAAGGCT	ACAAATTCAG	
		ACGATGATGT				AACCGACCAA GCACTTTATT	2160 2220
	TTGTTTTGAT	TTTCATTTTT	TATTAAGAAA	AAATTTTATT	TTACAGAATT	TACCTTCTCT	2280
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80	YGINPEQIQG	EALSYYLARL	LGLQRHVPPL	ALARVEARGA	QWAQVQEELR	AAHWTEGSVV	240
50						DLILFDYLTA GMWDKYNEPL	300 360
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		GCTGGCAGGT					180
		AAATGCCTGT					240
10		CTCGGAGCCA TCCACCACTA					300 360
		AGAAGGTGGG					420
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۰.		GCAAGAGCAC					300
35		GCGGAAGACC					360
		GCTGTGCTTG					420 480
		CTGTTTGGTT AAAGAACCAA					540
40	TTGCAGGGAG	CCTTCCCTTG	CACTGTGCTG	CTCTCACAGA	TCGGTGTCTG	GGCTCAGCCA	600
40		ACCTGCCTAA TCAACTCTCA					660
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50 55	Protein Acci None	ession #: 2 11	IP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGACTGCGTC GAACCCGGGC GCCTACCTG GCGCTACCTG GAACATCACA GACTGTGGCC	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT GCTCTCGCTG GCTGTGTACC GTGAAAAATG AGCCAGGGCC	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA CTGCAGGCAG	60 120 180 240 300 360 420 480
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50 55	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequi AGGTGAACAG TCCGCTGGCT TACCCGATTC GGCCTCCAT GGAGCTCGCT CACTGCCCAC TCACTGCCCAC TCACTGCCCAC TCACTACTTATT AGTTCTGGTC GCGCATGGTG GCGCATGGTG CTGGCAGACC	ession #: 2 11	CP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE 1#: NM_0022 222 21 CCAGCTCCGC CCCGGC CCCGG AGCAGCCCAG AGCAGGCCGA GCTACACCAA GCTACACCAA GCTACACCAA GCTACACCAA ACTAGACGGAT GCTTACACCAA ACTAGACGAA ACTAGACGAA ACATGCAAA ACATGCAAA	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCTGCGTC GAACCCGGC GCGCTACCTG GAACCCGGC GCGACTGGT GAACATCACA GACTGTGGCC GGTCCTGTGGC GATGCTGTGCCTGTGCCAATGACCTA TAGCAACACA	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCCGCCT AGCCTCTTCG CTCTGGCTG AGCCTGTTACC GTGAAAAATG AGCCAGGGCC TCAGGGTCAG GAGCTGGACT GAGCTGGACT GAGCTGGACT GAGCTGGACT GAGCTGGACT GACTACCTGG	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA CTGCAGGCAG AAGACCAGCA CAGGGAGAAAAACCAGCA CCAGTGATGAA	60 120 180 240 300 360 420 480 540
50 55 60	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA CTGCCGCTCAT GGAGCTCGCT CACTGCCCAC TCACATTATT AGTTCTGGTC GCCATGGTG CTGGCAGCCG GTGCCAGCTG GTGCCACC GTGCCACCGCCCCC	ression #: 2 11	CP_050184.1 21 FSPGPILPST MGLSPKRETT MGLSPKRETT MGLSPKRETT PURICE 1 #: NM_002: 3229 21 CCAGCTCCGC CCAGCCCCAG AGGAGGCCGG AGGAGCAGCA AGGAGGCGGA AGGAGGAGA GGCTACACCAA AGGTGGAGT GCTTGGAGT GCTTGGAGT GCTTGCAGG AGATGTGCAA GTGGGAGGAGA AGGTGCGAGG AGGTGCGAGG AGGTGCAGG AGGTGCAA GTGGGAGT GCTTCACCCA AGTGGGAGG AGTGGGAGG AGTGGCAGGAGG AGTGGGAGG AGTGGGAGG AGTGGCAAGG AGTGGCAAG	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC GAACCCGGGC GCACTACTG CCGGACTGGT GAACATCACA GACTGTGGCC GATGATGACACACACACAC CCAGAACACT CCAGAACACT	LLVSPPCAPP EKKVSQWA 41	S1 GGACCCGGT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCACT ACCCTGGCA AGACCAGCG CAGTGATGA AAGACCACCG CAGTGATGA AAGACCACCG CCAGTGATGA GCGCCCCGG	60 120 180 240 300 420 480 540 600 720
50 55 60	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA CTGTGCGCTC TACCGGATTC CGCACTCAT AGTTCTGGTC GCGCATGGTG CTGCAGAGCT GTGCCAGCTG TCGCAGAGCT GTGCCAGCTG TCGCAGAGCT GTGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAACATATT	ession #: 2 11 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession tence: 742 11 GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA CGGCAGACAG AAGGACATGA AAGGACATGCT TACCACACG GCCACAGCG GTGCACAGCG GTGCACAGCG GTGCACAGCG GTGCACAGCG GTGCACAGCG GTGCACAGCG GTGCACAGCG GTGCACAGGA	CP_050184.1 21 FSPGPILPST MGLSPKRETT MGLSPKRETT Quence 1 #: NM_0022 229 21 CCAGCTCCGC CCGGCCCCAG AGGAGGCCGA AGGAGGCCGA AGGAGGCCGA GCTACACCAA GTGAGCGAT GCTACACCAA ACGTGCGAGT ACGTGCGAGT ACGTGCAGAG ACGTGCGAGA ACGTGCACA ACAGCTACAT	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGGGCCC CGGCTGCGTC GAACCCGGGC GCGCTACCTG GAACATCACA GACTGTGGCC GGTGCTGGCC GGTGCTGGCC CGTGCTGGCC CAATGACACA CCAGAACACT CAATGACACCT CATTCAGCGC	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCGGCT GCTCTGGCT GCTGTTACC GTGAAAAATG AGCCAGGCC TCAGGGTCAG GACTACTGG GACTACTGG GACTACTGG AAGAGATGGA AAGAGTGGG AAGAGTTGG AAGAGTTGG	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACTCTGAGCAG AAGACCAGCA CAGCAGCAG AAGACCAGCA CAGCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCAG AAGACCAGCATATATAGA AGACCGCGGA ACTTATCTGA	60 120 180 240 300 360 420 480 540 600 660 720 780
50 55 60 65	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequility AGGTGAACAG TCCGCTGGCA TACCCGATTC CGCCTCCAT GGACTCGCT CACTGCCCAC TCACTATATT AGTTCTGGTC CGCGAGGTG CTGCAGACC GTGCAGACC GTGCAGACC GTGCAGACC GTGCTACAT AGGCAGCTG TGCCTACAT AGGCAGCTG AGGCAGACC AGGCAGACC AGGCAGACC AGGCAGACC AGGCAGACC AGGCAGACC AGGCAGCTTC AGGCAGCTTC AGGCAGCTTC	ession #: 2 11	IP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCCCC CGGCTGCCC GAACCCGGGC GAACCCGGGC GAACATCACA GACTGTGGC CAATGACAT CAGAACACATCACA CCAGAACACA CAGAACACT CAACACTCAT CACATTGTG CACATTGTG CACATTGTG CACATTGTG CACATTGTG CACATTGTG	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCGGCTG GCTCTCGGCTG GCTGTACA GCTCTTCTGCTG CTCAGGTCAG AGCCAGGCC CAGAGGCCC CAGGGTCAG GAGTACCTGG GACTACCTGG GACTACCTGG GACTACCTGA AAGAGTGGA ATTGGGTACA ACAGGTGCCC	S1 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACCCTGGCCA ACCCTGGCCA ACCCTGGCCA ACCCTGGCCA ACCCTGCCA ACCCTGCCA ACCCTGCCA ACCCTGCCA ACCCTGCCA ACCCTGCCA ACCCTGCCA ACCCTGCAC ACCCTGCCA ACCCTGCAC ACCCCCCGG ACTTATCTGA ACCAGCACCG CACGGCACCG CACGGCACCG	60 120 180 240 300 420 480 540 600 720
50 55 60	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA CTGCCCAC TACCCGATTC CGCCTCCAT GGAGCTCGCT CACTGCCCAC TCACATTATT AGTTCTGGTC GCCATGGTC GTGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAGCTG TGCCAGCTTC AGGCAGCTTC ACATATTAC ACATATTGGGC	ression #: 2 11	IP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCTACCTG GAACACCGGG GCGCTACCTG CAACATCACA ACATCACA TAGCAACAC GATTCAGAC GATTCAGGC AAACCTCTT GAACCTCTTTCG GAACACTCTTCG GATTCAGGC AAACCTCTTTTCG GAGGCAGGC	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCGCCT AGCCTCTTCG GCTGTTACC GTGAAAAATG AGCCTGGACT GACTACCTGG GACTACCTGG GACTACCTGG ATTGGTACA AATGGGTCGA ATTGGTACA ATTGGTACA GACTACCTGG CGGAGACCTGC GGAGACCTGC	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA ACGACGAGCAG AAGACCAGCG CCAGTGATGA GCACCCCGGG ACTTATCTGA CGATGCAGGCAT GCGCCCCGGG ACTTATCTGA CGATGCAGCC GGAGGACCC GGAGGACGCA GGAGGACCC	60 120 180 300 360 420 540 600 720 780 840 900 960
50 55 60 65	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA CTGTGCGCTC TACCCGATTC GGAGCTCGCAC TCACATTATT AGTTCTGGTC GCGCAGCC GTGCCAGCT GTGCCAGCT GTGCAGCT GTGCCAGCT AGTATAGTTAC AGGCAGCTTC AGTATAGTTAC AGGCAGCTTC ACATTAGTTAC AGGCAGCTTC ACATTAGTTAC AGGCAGCTTC ACATTAGGGC GGTGCTGGAG	ession #: 2 11	COMPANY OF THE PROPERTY OF THE	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGGGCCC CGGCTGCGTC GGAACCCGGGC GGCGTACCTG GAACATCACA GACTGTGGCC GGTGCTGGGC CAATGACACA CCAGAACACT CAAGAACACT CACCATTGTG CACCATTGTG CACCATTGTG CGGGGCAGGC TTTTGGCAGC TTTTTGGCAGC	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCGGCT GCTCTGGCT GCTGTTACC GTGAAAAATG AGCCAGGCC TCAGGGTCAG GAGCTCACT GACTACTGG AAGCATGGACT AAGAGTCGG AATGGTACA ACAGTGCCC GCGACACCTGG GCGACACCTGC GCAATTGCCC	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACTGCAGCAG AAGACCAGCA CAGCAGCAG AAGACCAGCA CAGCACCGG CCAGTGATGA GCGCCCCGG ACTTATCTGA CGATGCAGCAT CAGGGACCT CAGGGACCG CAGGGACCT TGGCAGACCT	60 120 180 240 300 360 420 6600 6600 720 780 840 900 1020
50 55 60 65	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA TCACCGATTC CGCCTCCAT GGAGCTCGT CACTGCCAC TCACTTATT AGTTCTGGTC GCGCATGGTG GGCATGGTG TGCCACAC TGCACAC TGCCACAC TGCCACAC TGCCACAC TGCCACAC TGCCACAC TGCCACAC TGCACAC TCCACAC TCCA	ression #: 2 11	IP_050184.1 21 FSPGPILPST MGLSPKRETT MGLSPKR	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCCCC GGACCGGCCC GAACCCGGG GAACATCACA ACATGACAC CAGAACAC CCAGAACAC GATTCAGGC AAACCTCTAT CACCATTGTG GGAGGCAGGC TTTTGGCAGC GGGCCCCCC GAACCAGGG GGACCCCCC GAACCAGGGG	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCGGCT AGCCTCTTCG GCTGTACC GTGAAAAATG GACTACCTGG GACTACCTG GACTACCTG GACTACCTG AACAGTGGA ATTGGTACA AACAGTGGCC GGAGACCTGC GCAATTGCCC TACTACTCG GGAACCTCC GGACCTCCT TACTACT	S1 GGACCCGGT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCACT ACCCTGGCCA AGACCAGCA AAGACCAGCG CAGTGATGA AGACGGCAT AGACGGCAT GCGCCCCGG ACTTATCTGA CGATGATGA GGAGCACT TGCAGGCACT TGCAGGCACT TGCAGGCACT TGCAGGCACT TGCAGGCACT TGCAGGCACT TGCAGGCACT TGCAGGCACCT TGCAGGAACT TCCCTGCTCA	60 120 180 300 360 420 540 600 720 780 840 900 960
50 55 60 65 70	Protein Acci NVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA CGCCTCCAT GGAGCTCGATTC CACTGCTC CACTGCTAT AGTTCTGGTC GCGCATGGTG CTGCCAGCAGACC GTGCCAGCAGCC GTGCCAGCAGCC GTGCCAGCC GTGCAGCC GTGCCAGCC GTGCCAGCC GTGCCAGCC GTGCCAGCC GTGCCAGCC GTGCCAGCC GTGCCAGCC GCCCCCCCCCC	ession #: 2 11 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession lence: 742 11 GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGG GTGCCGATG AAGGACATG TACCACACG GCAAGTGCT TACCACACG GGCACAGCG TGGAAAGGA AAGGACATGT TACCACACG GGCACCAGCG GGCACCAGCG GGCACCAGCG GGCACCAGCG GGCACCAGCG GGCACCAGCG GGCACCAGCG GGCACCAGCG GGCACCAGCG TGGAAAGGAA AAGGACCCAG ATCCTGCACC GCGGTGTTCT GCCTCGCACG GGGTGCCACC GCGTGCCATCT CTTCTTCATG	CP_050184.1 21 21 FSPGPILPST MGLSPKRETT MGLSPKRETT MGLSPKRETT MENCE 1 #: NM_0022 229 21 CCAGCTCCGC CCGGCCCCAG AGGAGGCCGA AGGAGGCCGA AGGAGGCCGA AGGAGGCCGA AGGAGGCAGA AGGAGCACA ACGTGCAGAG AGAGCACA AGGACCACA AGGACCACA AGGACCACA AGGCCCAAAAACA TGGGGGCCTA ACCTCCTGGT AGCCCCAGTGG	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGGCGCCCC CGGCTGCGTC GAACCCGGGC GCGCTACCTG GAACATCACA GACTGTGGCC GGTGCTGG CAATGACCTA GATTCAGCG AAACCTCTAT CACCATTGTG CGAGGCAGGC TTTTGGCAGC GGACCACTCTTTG CGAGGCAGGC CTCTGCTTT	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCGGCTG GCTGTTACC GTGAAAAATG AGCCTGGCTG AGCCTGGCTG AGCAGGCCC TCAGGGTCAG GAGTACCTGG AGCAGGCCC AATACCTGG ATGAGGTCAG ATTAGGTACA ATTAGGTACA GGAGACCTGC GGAGACCTGC GGAGACCTCC GGACACTCCC GGACACCTCC GGACACCTCC GGACACCCCC GGACACCTCC GGACACCCCC GGTTTATCTCG	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA CTGCAGCAG AGACCAGCG CAGTGATGA GGACCAGCG CAGTGATGA GGACCGCCCGG ACTTATCTGA CGATGCAGCA CGAGGACACT ACAGGCACCT AGAGGACACT AGAGGACACT AGAGGACCT AGAGGACCT AGAGGACCT AGAGGACCT AGAGGACCT AGAGGACCT TCGCCAGCAT TCGCCAGCAT	60 120 180 300 360 420 540 660 720 780 840 960 1020 1080 1140
50 55 60 65	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA TCACCTCCAT TACCCGATTC CGCCTCCAT AGTTCTGGTC GCGCATGGTC CTGCCAGCTG CTGCCAGCTG CTGCCAGCTG CTGCCAGCTG CTGCCAGCTG CGCCATGGTA CGTGCAGACC GTGTCAGACC GTGTCAGAC GTATAGTTAC AGGCAGCTTC ACATATGGTC ACATATGGTC ACATATGGTC CGCTTCACAC GTGTTGGACATC CTGGTACATC CTGTCACATC CTCACTC CTCACTC CTCACTC CTGTCACATC CTCACTC	ession #: 2 11	CP_050184.1 21 FSPGPILPST MGLSPKRETT MGLSPKRETT MGLSPKRETT MGLSPKRETT PLENCE #: NM_0022 1229 CCAGCTCCGC CCGGCCCCAG AGGAGGCCGAG AGGAGGCCGA AGGAGGCGGAGGA GGTACACCAA GTGAGCGGAGGA GGTACACCAA ACGTGAGGA ACGTGAGGA ACGTGAGCA ACGTGAGCA ACGTGAGCA ACGTGCAA ACGTCACA ACGGCTCAC ACGCTCAC ACGCTCAC ACGCTCAC ACGCTCAC ACGCTCAC ACGCTCAC ACGCTCACCA ACGCTCACCA ACGCTCACCA ACGCCCACTGG ATTTCTTCAT GCCCCAGTGG GATTTCAGGA	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCCCC CGGCTGCGTC GAACCCGGGC GGCTACCTG GAACATCACA GACTGTGGCC CAGTGCTGTGG CAATGACAA CCAGAACACT CACCATTGTG GAACCTTAT CACCATTGTG GGAGGCAGGC TTTTGGCAGC GGAGCAGGC CTCTGCCTTT TATTGCTGTG	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGCGCCCAC GTCTCGGCTG GCTCTTCGCTG GCTGTTACC GTGAAAAATG AGCAGGGCC TCAGGGTCAG GAGCTGGCTG GAGTACTTCG GTGTACTCG GTGTACTCG GTGTACTCG GGAGCTGGC GGAGCTGCC GGAGACCTGC GCATTGCCC TACTACTTCG GGAACTTCC GGAACTCCT GGAACTCCT GGAACTCCT GGAACTCCT GGAACTCCT GGAACTCCT	VMNGPRELDG 51 GGACCCCGCT GCGGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCAC TGCAGGCAG AGACCAGCA CCAGTGATGA AGACGGCAC CAGTGATGA AGACGGCAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGGAACA TCGCAGGAACA TCGCCGCCT TGGCAGACCT AGAGGAAAGA TCCCTGCTCA TGGCCACCAT TTGAAGGCTT TTGAAGGCTT	60 120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1080 1140 1260
50 55 60 65 70	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA TACCCGATTC GGCCTCCAT GGAGCTCGCT CACTGCCAC TCACATTATT AGTTCTGGTC GGCGATGGT GGCGAGACC GTGCAGACC GTGCAGACC GTGCAGACC GTGCAGACC GTATTAGTTAC AGGCAGCTTC ACATTATT AGTTCTGGTC GCGCATGGTG CCCTCACTC CGTCTACCAC GGACAAAGTG GGACAAAGTG GGCAAAAGTG	ession #: 2 11	CP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE 1 #: NM_0022 229 21 CCAGCTCOGC CCAGGCCCAGA AGCAGGCAGCA GCTACACCAA GCTACACCAA GCTACACCAA GCTACACCAA GCTACACCAA GCTACACCAA ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC TGCGGGCCCAA ACAGCTACAC TGCGGGCCCAA ACCTCCTGGT ATGTCTTCAT GCCCCAGTGG ACAGTACGCC ACAGTACAC ACAGTACAC ACAGCTACAC ACGCCCCAGTGG ATGTCTTCAGA ACAGTACGCC	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCTGCTC GAACCCGGGC GCGCTGCTG GAACATCACA GATTGTGGCC GGTGCTGTG CAATGACTA CCAGAACACT CATTCAGCGC AAACCTCTAT CACCATTGTG GGAGGCAGGC TTTTGGCAGC CTCTGCCTTT TATTGCTGT TATGGCGC TTATGCTGT TATGGCGCT TTATGCTGT TATGGCGCT TTATGCTGT TATGGCGCT	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGCCCCAC GTCTCGGCTG GCTCTTCGGCTG GCTGAAAAATG GACTACCTGGGTAAC GACTACCTGGGTAAC GACTACCTGGGTAAAAATG GACTACCTGGGTAC AAGAGTGGAAC ACAGGTGCCC GGAGACCTGC GCAATTGCCC GGAGACCTCC GGAACCTCC GGTTATATCTC GGAACCTCCT GGTACCTCC GGTTATCCCT GTAGACAGC CTTAGACAGC CTTAGACAGC	VMNGPRELDG 51 GGACCCCGCT GCGGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCAC TGCAGGCAG AGACCAGCA CCAGTGATGA AGACGGCAC CAGTGATGA AGACGGCAC CGAGGACAC CGAGGACAC CGAGGACAC CGAGGAACA TCGCAGGAACA TCGCCGCCT TGGCAGACCT AGAGGAAAGA TCCCTGCTCA TGGCCACCAT TTGAAGGCTT TTGAAGGCTT	60 120 180 300 360 420 540 660 720 780 840 960 1020 1080 1140
50 55 60 65 70	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA CTGTGCGCTC TACCGATTC GGAGCTCGTGCAC GGACTAGTT AGTTCTGGTC GCGCAGCT CACATTATT AGTTCTGGTC GGCAGCT CACATGGTA GGAGCTTC CTGCCAGCT CTGCCAGCT TGCCAGCT TGCCAGCT TGCCAGCT TGCCAGCT TGCTACAAC GTATAGTTAC ACATATGGT ACATATGGT ACATATGGA GGAGCAGCT TCACTCTGGAG GAACAATGGA GGAGATAGGG CCCCTCACTC TGGTGACATC GGGCAAAGTG AATCCATGGA GAATCGGA GCAGATGGA	ession #: 2 11	CABARACAT AGGACTACAC ACTICACA ACATICACA ACATICACA ACATICACA ACATICACA ACATICACA ACATICACA ACATICACACA ACATICACACA ACATICACACA ACATICACACACACACACACACACACACACACACACACAC	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCTGCGTC GAACCCGGGC GGCTACCTG GAACATCACA GATTGTGGCC CGGTCTGTG CAATGACATA CACATTGTG GAACCATTCTA CACCATTGTG GAACCATCTAT TAGCAGCG GAACCAGGC CTCTGCCTTT TATTGCTGTC TAATGGCCAC AGACCATCTA CACCATGTGC GAACCAGGC GAACCAGGC CTCTGCCTTT TATTGCTGTC TAATGGCCAC AGACCTTCTA	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCGGCT GCTCTTCGGCT GCTGTTACC GTGAAAAATG AGCCTGTACCT GAGTACCTGG GAGTACCTGG AAGCAGGCC TAAGCAGTCGG ATTGGGTAA ACAGTGGG ATTGGGTACA GGAGACCTGC GGAGACCTGC GGAATTGCCC TACTTACTT	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA ACGCCCGG AAGACCAGCA AGACGGCAT ACACGGCAC ACGCACCGG ACTTATCTGA GGAGGCAT CACGGCACCT ACAGGACCT TTGAAGGCTT CCCAGCAGGT TCCAGCAGGT TCCAGCAGGT TCCAGCAGCC TGTCAGTGG TGTCAGCCCA	60 120 180 240 300 420 480 540 600 660 720 840 900 1020 1080 1140 1260 1320 1380 1440
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50 55 60 65 70	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA TCACCCCACT TACCCGATTC GGCCTCCAT GGACTCGCT CACTCCCAC TCACTCCCAC TCACTACTATAT AGTTTTGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG TGCTCACAC TGGCAGACC GTGCAGACC GTGCAGACC GTGCAGACC GTGCAGACC GTGCAGACC GTATAGTTAC AGGCAGCTTC ACATATGGGC GGTCACAAC GGAACAATGAT GGAACAATGAT GGAACATGGAC CCTCACTC CGTCACTC CGGCAAAGTG AATCCATGGA GCAGATGGAT CATTTGCTTGC CCACCTGGAC CACTCTGGAC CACTCTTCC CA	dession #: 2 11	CP_050184.1 21 FSPGPILPST MGLSPKRETT GUENCE #: NM_0022 229 21 CCAGCTCOGC CCGGGCCCCAG AGCAGGCAGCA GCTACACCAA GCTACACCAA GCTACACCAA GCTACACCAA GCAGCTCACA CAGCTCCAG AGCAGCACCA AGCACCAA ACCTCCTGGT ATGTCTCAT CCCCAGGTACT CACTTCACC GACTTCACC GACTTCACC CGCCAGTCAT CGCCAGTCAC CCCCGGGACCC ACCCCGGCC TCTCCATGCC TCTCCATGCC	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCGCCCC GAACCCGGG GCGCTACCTG GAACATCAC GATTCAGGC CCAGACACT GATTCAGGC AAACCTCTAT CACCATTGTG GGAGGCAGGC TITTGGCAGC CTCTGCCTT TATTGCTGC TATTGCTGT TATGGCTC GGACCACCC GAACCTCTC CAACCTCTC CCACCCCCCCCC CCCCCCCC	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG GGGCCCCAC GTCTCCGGCT GCTCTCGGCT GCTGTACC GTGAAAAATG GACTACCTG GACTGCACT GAGCATGGACT AAGGATGGACT CGGACACTGG GCTTATCCG GCACTACCTG GCACTACCTG GCACTACCTG GCACTACTCCT GGAACCTCCT GGAACCTCCT TGTGCAAGC CCACAAGACCT TCTGGCAAGC TCTGGCAAGC TCTGGCAAGC TCTGTGCAAG CCTTTGCAG CCCTTGCCAGAACC TCCTGCAGAACC TCCTGCAGAACC TCCTGCAGAACC TCCTGCAGAACC TCCTGCAGAACC TCCTGCAGAACC	VMNGPRELDG 51 GGACCCCCCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCAC TGCCCCAC ACCCTGGCCA AGACCAGCAC AGACGACCA CAGTGATGA GCAGCACCG CAGTGATGA GCAGCACCG GCAGGACCCT GCAGCACCT ACAGCACCG GCAGGACCCT AGAGGAACCA TCCCTGCTCA TTGAAGGCT TCCAGCAGCA TCCCTGCTCA TTGAAGGCT TCCAGCAGCA TCCCTGCTCA TCCCAGCACCT TCCAGCACCA TCCCAGCACCT TCCAGCACCA TCCCAGCACCT TCCCAGCACCA TCCCAGCACCA TCCCAGCACCA TCCCAGCACCA TCCCAGCACCA TCCCAGCACCA TCCCAGCACCA TCCCAGCACCA TCCCCCCCCCC	60 120 240 300 360 420 480 540 660 720 780 900 960 1020 1320 1340 140 1500 1500 1560 1680 1740

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CGTGACGAAC ACCCGGACCT CGGAGCGCTC CGGGGAGGAC GCCCACGAGG CGCTGCTCAC
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                                                                                         2940
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                                                                                          3060
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                                                                                         3120
                                                                                         3180
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                                                                                          3240
                                                                                          3300
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                                                                                         3480
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                                                                                          4020
                                                                                          4080
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                                                                                          4320
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55
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                                                                                           180
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                                                                                           360
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                                                                                           420
60
                                                                                           480
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                                                                                           720
65
                                                                                           780
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                                                                                           960
         SIPTINMENK TTWFSVDIDS ELVEELPAEI ELWLVLVAVG AGLLLLGLII LLLWKCGFFK 1020
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                                                                                             60
                                                                                           120
80
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TCACATTATT GAGGACATGT GGCTTGGAGT GACTGTGGCC AGCCAGGGCC CTGCAGGCAG
                                                                                            420
85
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	CCCCATCCTC	CCCN N COCCOR	ACGTGCGAGG	CNATCACCES	CACCICCACI	CCACTCATCA	600
			AGATGTGCAA				600
							660
			GTGGCTTCAC				720
5			ACAGCTACAT				780
J			AGGACCAAGG				840
			CCAAAAACAT				900
			TGCTGAGCCA				960
			TGGGCGCCTA				1020
10			ACCTCCTGGT				1080
10	GGAAGTAGGG	GGTGCCATCT	ATGTCTTCAT	GAACCAGGCG	GGAACCTCCT	TCCCTGCTCA	1140
	CCCCTCACTC	CTTCTTCATG	GCCCCAGTGG	CTCTGCCTTT	GGTTTATCTG	TGGCCAGCAT	1200
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			CCGGGAACCC				1620
			ACCGCCGGCC				1680
20			TCTCCATGCC				1740
~0			ACAAACTCCG				
							1800
			GCCCCCGGCT				1860
			TGGAGAACCA				1920
25			GCAACTTGCA				1980
23			AGTACAGCAG				2040
			CGGAGCGCTC				2100
			TGCTGCTGTC				2160
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			CAATGGGGGA				2520
			AAGTCAGCAA				2580
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55							-
			CTGGGGACAG				2700
			AGGGCCCCCC				2760
			CCTGTGCCAC				2820
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			CCACCATCAA				3000
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55							3780
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			CGGCAACGTA				4020
60			GGACCAATTC				4080
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65	ACTCCCCAGC	CCCAGCCCCT	TCCATGGTAC	TGTAGCAGGG	GAATTCCCTC	CCCCTCCTTG	4440
	TGCCTTCTTT	GTATATAGGC	TTCTCACCGC	GACCAATAAA	CAGCTCCCAG	TTTGT	
		-			-		
	Seg ID NO:	148 Protein	n semience				
		cession #: 1					
70	1	11	21	31	41	51	
	î	i*	1	1	1.	1	
	MCDCDCDXDD	ADDIATORY	I LMVAAGGCVV	I CADAT PERM	INTERMINA	I T.DVIVQUAT UP	60
			PDGYTNRTGA				120
75			AHRYTQVLWS				180
15						EWDLSEYSYK	240
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•						RQPQQVIHGE	420
00			DENFYPOLLV				480
80	DPALCTATSC	VQVELCFAYN	QSAGNPNYRR	NITLAYTLEA	DRDRRPPRLR	Fagsesavfh	540
	GFFSMPEMRC	QKLELLLMDN	LRDKLRPIII	SMNYSLPLRM	PDRPRLGLRS	LDAYPILNQA	600
			CESNLOMRAA				660
			PALLLSSVRP				720
						LQSFFGGTVM	780
85						LYPTEITVEG	840
		. oor marery	- GE HOUSEVO		- 101000000		

5	VLTCATGRAH SIPTIMMENK	CVWLECPIPD TTWFSVDIDS	apvvtnytyk Elveelpabi	QRRRRQLDPG ARVWNSTFIE ELWLVLVAVG TKKHWVTSWQ	DYRDFDRVRV AGLLLLGLII		900 960 1020	
J		149 DNA sec ld Accession sence:	#: NM_0064	124.1				
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				GCCCAGCCCA			120	
				GATAAAAGCA			180	
16				CTTCTGCCGT			240	
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				TTTTTCGTGT GCAGGACAGT			420 480	
				GGGGTGCTGG			540	
20				ATGGTGTCCT			600	
				ATTGGAACGT			660	
				TTCAGAAGAG			720	
				GTGCTCTTGC GAGAGCTTCC			780 840	
25				CCCTTCACAA			900	
				GATGAAAAAG			960	
				ACCCAGATTA			1020	
				ACGGATGGCA			1080	
30						TTTCCACCTC	1140	
50				ATACTCTCCC		CACTGTCATC	1200 1260	
						CTACCTGGCC	1320	
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25						ACTCACGCTG	1440	
35						CCCTGGCAAT	1500	
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						GGGGCTGGGC	1620 1680	
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						GCGCTGCTGC	1920	
				TGCTTGCTGT			1980	
45						TGTCCCTGTC	2040 2100	
						TGTCAGGGAT	2160	
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	ACCTCGAGGA	GATTTGCTCC	CCATTAGCGA	ATGAAATTGA	TGCAGTCCTA	AAAAAAAA		
50	Cam ID NO.	150 Duebed						
50		150 Protein cession #: 1			•			
	1	11	21	31	41	51		
	1	1	1	1	1	1		
55				KSKETNKTON			60	
55				ILCFFQGIGR VLVTVLVQSS			120	
				RRAFAGATVH			180 240	
				FTKLIVQLDK			300	
~				DGIQNWTMKN			360	
60	DLAVGTILLI	LSLLVLCGCL	IMIVKILGSV	LKGQVATVIK	KTINTDFPFP	PAWLTGYLAI	420	
						LAALASPGNA	480	
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						AQEGQDVPVK	660	
65		SREAQGEVPA						
		151 DNA se						
		id Accession uence: 11						
70	1	11	21	31 .	41	51		
	Ī	ī	Ī	Ī	1	Ĭ		
				AGCGGCTGCC			60	
				TOGCTGGAAA			120	
75				CATAAGATCC CCTATAAATA			180	
				ATATTTATAC			240 300	
				AAGAAGAAGA			360	
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QΛ				CTCCCAGAAA			480	
80						CAGTGTCAGG	540	
				GGGATCTTTA		TGTCCCAGGA	600	
						AAATAGCCGT	660 720	
0.0						GAACAGTOGG		
85						ACAGCAGATT	840	
					32	6	•	
					J2			

5	AATGGAGTGC ACACAGATAG AGCTTAGCAG	CACAGCAGAT AGCTAAGCTT	TCCAAAAGCT TGAGTCTGGA CAGCTCAAAC	AGCGAAGAAG GTTCCTAATA CAGAATGGCT ACGGAATTTG ACATTATGA	CTGAGAGCCT TTATTCCCTC	GGAGTCATTA TAATGAAGTG	900 960 1020 1080
10		152 Protein ession #: 2		31	41	51	
10	GYADIHGDLL RPDNHRKKPH	PINNDDNYHK IVISMPQDFR	AVSTANPLLR PVSSIIDVDI	 SLERSKPGKF IFIQKKEEAD LPETHRRVRL VNDEVLEVNG	YSAFGTDTLI YKYGTEKPLG	KKKNVLTNVL FYIRDGSSVR	60 120 180 240
15	NLIITVRPAN	QRNNVVRNSR VPNTESLESL	TSGSSGQSTD	NSLLGYPQQI QNGPIPSNEV	EPSFEPEDED	SEEDDIIIED	300 360
20	Nucleic Act	153 DNA sec ld Accession Lence: 23	#: NM_003	064.2			
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30	TGGCCAATGT TGACTTGAAG ATTCCTGCCA .CCTGAGACTT	TTGATGCTTA TGTTGCATGG TATGGAGGAG GGCTCCACCA	ACCCCCCAA GCATGTGTGG GCTCTGGAGT CTGATATCCT	TTTCTGTGAG GAAATCCTGC CCTGCTCTGT CCTTTGGGGA AAATAAACGA	ATGGATGGCC GTTTCCCCTG GTGGTCCAGG AAGGCTTGGC	AGTGCAAGCG TGAAAGCTTG TCCTTTCCAC ACACAGCAGG	300 360 420 480 540
35	Seq ID NO:	154 Protein	n sequence				
40		KCLDPVDTPN		31 KAGVCPPKKS VTYGQCLMLN			60 120
45	Nucleic Ac:	155 DNA sec id Accession Lence: 199.	n #: NM_001	306.1			
	1 AATTCGGCAC	11 GAGGGCAGGT	21 GCAGGCGCAC	31 GCGGCGAGAG	41 CGTATGGAGC	51 CGAGCCGTTA	60
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55	GACCTTCAGG CTAGTGGCGC AAGATCACCA GTGTCCTGGT	CGGCCCGCGC TGGTGGCAGG TCGTGGCAGG CGGCCAACAC	CCTCATCGTG CCAGTGCACC CGTGCTGTTC CATTATCCGG	GTGTACGACT GTGGCCATCC AACTGCGTGC CTTCTCGCCG GACTTCTACA	TGCTGGCCGC AGGACGACAC CCCTGCTCAC ACCCCGTGGT	CTTCGGGCTG GGCCAAGGCC CCTCGTGCCG GCCCGAGGCG	420 480 540 600 660
60	CTGGGGGGCG AAGGTCGTCT GACCGCAAGG CAACACCACC	CGCTGCTCTG ACTCCGCGCC ACTACGTCTA ACCACCACCG	CTGCTCGTGT GCGCTCCACC AGGGACAGAC CGAGCTGGAG	GTGGGCTGGG CCCCCACGCG GGCCCGGGAG GCAGGGAGAC CGCGCACCAG	AGAAGAAGTA CCAGCCTGGG CCCACCACCA GCCATCCAGC	CACGGCCACC CACAGGCTAC CCACCACCAC GTGCAGCCTT	720 780 840 900 960
65	TCCCCAGCAG GCATGGACTG ACCACCCCGT	CCACGGCTTT TGAAACCTCA CGAGCCCCAT	GCGGGCCGGG CCCTTCTGGA CGGGCCGCTG	GCACGGGGCC	CGGGGCCCAG TGGGTGACCG GCGCTGGGCA	GGACCAACCT CCAATACTTG GGGACCGGCA	
70		156 Protei cession #: 1		31	41	51	
75	MQCKVYDSLL GVLFLLAALL	ALPQDLQAAR TLVPVSWSAN	ALIVVAILLA TIIRDFYNPV	AFGLLVALVG	AQCTNCVQDD AGLYVGWAAA	MNCVVQSTGQ TAKAKITIVA ALQLLGGALL	60 120 180
80	Nucleic Ac	157 DNA se id Accessio uence: 15	n.#: NM_005	564			
	1	11	21	31	41	51 I	
85				GCCCTGTTGG CCACCTCTGA		TGCCCAGGCC TCTGCAGCAG	60 120

5	ATTOTCAGAG GACAAGAGCT AGGACTITTG CCTGGATTAA GTGTTCTTCA ACCAAGGAGC	AAGACAAAGA ACAATGTCAC TTCCAGGTTG CGAGTTACCT AGAAAGTTTC	CCCGCAAAAG CTCCGTCCTG CCAGCCCGGC CGTCCGAGTG TCAAAACAGG ACTAAAGGAG	ATGTATGCCA TTTAGGAAAA GAGTTCACGC GTGAGCACCA GAGTACTTCA AACTTCATCC	CCATCTATGA AGAAGTGTGA TGGGCAACAT ACTACAACCA AGATCACCCT GCTTCTCCAA	AGGGAATGCA GCTGAAAGAA CTACTGGATC TAAGAGTTAC GCATGCTATG CTACGGGAGA ATATCTGGGC CGGCTGA	180 240 300 360 420 480 540
10		158 Protein cession #: 1 11		31	41	51	
15	ILREDKDPQK	MYATIYELKE VSTNYNQHAM	DKSYNVTSVL	PRKKKCDYWI	RTFVPGCQPG	WYVVGLAGNA EFTLGNIKSY NFIRPSKYLG	60 120 180
20	Nucleic Ac:	159 DNA sec ld Accession mence: 268	#: NM_006	353.1			
	1	11	21 	31 	41	51 Ì	
25	ATCGGGCAGA	GCTCGGGTTC GGTCTCACAG CTGCAGTTAA	CAGCCAAGGA	ACCTGGGGCC	CGCTCCTCCC	CCCTCCAGGC	60 120 180
	CAGGATCATC CGAGAAGACG	AAGGGGTTCG CGGCTACTCT	AGTGCAAGCC GTGGGGCGAC	TCACTCCCAG GCTCATCGCC	CCCTGGCAGG CCCAGATGGC	CAGCCCTGTT TCCTGACAGC	240 300
30	GGAGGGCTGT CAGCCTCCCC	CTCAAGCCCC GAGCAGACCC AACAAAGACC	GGACAGCCAC ACCGCAATGA	TGAGTCCTTC CATCATGCTG	CCCCACCCCG GTGAAGATGG	GCTTCAACAA CATCGCCAGT	360 420 480
35	CAGCTGCCTC CTTGCGATGC	TGGGCTGTGC ATTTCCGGCT GCCAACATCA	GGGGCAGCAC CCATCATTGA	GTCCAGCCCC GCACCAGAAG	CAGTTACGCC TGTGAGAACG	TGCCTCACAC CCTACCCCGG	540 600 660
<i>J J</i>	GGGTGACTCC CCAGGATCCG	GACACCATGG GGGGGCCCTC TGTGCGATCA	TGGTCTGTAA CCCGAAAGCC	CCAGTCTCTT	CAAGGCATTA ACGAAAGTCT	TCTCCTGGGG GCAAATATGT	720 780 840
40	ACCCTCCATT CAAGACCCTC AATCAACCTG GACTCTGGGA	CAGGAGACGA TCCACTTGGT TACGAACATT GGGTTCGAAA ATGACAACAC ATATCAAGGT	GTTTGGTTCC CTTTGGGCCT TCAGTGAGAC CTGGTTTGTT	TGTTCACTCT CCTGGACTAC CTGGATTCAA CTCTGTTGTA	GTTAATAAGA AGGAGATGCT ATTCTGCCTT TCCCCAGCCC	AACCCTAAGC GTCACTTAAT GAAATATTGT	900 960 1020 1080 1140
45	Seq ID NO: Protein Acc	160 Proteir	P_006844.1				
	1	11	21	31 	41	51	
50	AHCLKPRYIV SITWAVRPLT	LATGLVGGET HLGQHNLQKE LSSRCVTAGT VQEGGKDSCQ	EGCEQTRTAT SCLISGWGST	ESPPHPGFNN SSPQLRLPHT	SLPNKDHRND LRCANITIIE	IMLVKMASPV HQKCENAYPG	60 120 180 240

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1	1.	A method of detecting an ovarian cancer-associated transcript in a cell
2	from a patient, the me	ethod comprising contacting a biological sample from the patient with a
3	polynucleotide that se	electively hybridizes to a sequence at least 80% identical to a sequence

- 4 as shown in Tables 1-26.
- 1 2. The method of claim 1, wherein the biological sample comprises 2 isolated nucleic acids.
- 1 3. The method of claim 2, wherein the nucleic acids are mRNA.
- 1 4. The method of claim 2, further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 5. The method of claim 1, wherein the polynucleotide comprises a sequence as shown in Tables 1-26.
- 1 6. The method of claim 1, wherein the polynucleotide is immobilized on 2 a solid surface.
- The method of claim 1, wherein the patient is undergoing a therapeutic regimen to treat ovarian cancer.
- 1 8. The method of claim 1, wherein the patient is suspected of having 2 ovarian cancer.
- 1 9. An isolated nucleic acid molecule consisting of a polynucleotide 2 sequence as shown in Tables 1-26.
- 1 10. The nucleic acid molecule of claim 9, which is labeled.
- 1 11. An expression vector comprising the nucleic acid of claim 9.
- 1 12. A host cell comprising the expression vector of claim 11.
- 1 13. An isolated polypeptide which is encoded by a nucleic acid molecule 2 having polynucleotide sequence as shown in Tables 1-26.

i	14.	An antibody that specifically binds a polypeptide of claim 13.				
1	' 15.	The antibody of claim 14, further conjugated to an effector component.				
1 2	16. fluorescent label.	The antibody of claim 15, wherein the effector component is a				
1	17.	The antibody of claim 15, wherein the effector component is a				
2	radioisotope or a c	ytotoxic chemical.				
1	18.	The antibody of claim 15, which is an antibody fragment.				
1	. 19.	The antibody of claim 15, which is a humanized antibody				
1	20.	A method of detecting an ovarian cancer cell in a biological sample				
2	from a patient, the method comprising contacting the biological sample with an antibody of					
3	claim 14.					
1	21.	The method of claim 20, wherein the antibody is further conjugated to				
2	an effector component.					
	-					
1	22.	The method of claim 21, wherein the effector component is a				
2	fluorescent label.					
1	23.	A method for identifying a compound that modulates an ovarian				
2	cancer-associated	polypeptide, the method comprising the steps of:				
3	(i) o	contacting the compound with an ovarian cancer-associated polypeptide,				
4	the polypeptide en	coded by a polynucleotide that selectively hybridizes to a sequence at least				
5	80% identical to a	sequence as shown in Tables 1-26; and				
6	(ii)	determining the functional effect of the compound upon the polypeptide.				
1	24.	A drug screening assay comprising the steps of				
2	(i) :	administering a test compound to a mammal having ovarian cancer or a cel				
3	isolated therefrom;					
4	(ii)	comparing the level of gene expression of a polynucleotide that selectively				
5		uence at least 80% identical to a sequence as shown in Tables 1-26 in a				

6 treated cell or mammal with the level of gene expression of the polynucleotide in a control

- 7 cell or mammal, wherein a test compound that modulates the level of expression of the
- 8 polynucleotide is a candidate for the treatment of ovarian cancer.